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METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION

This is a Continuation-In-Part of Serial No. 08/360,107 filed December 20, 1994, which is a  
5 Continuation-In-Part of Serial No. 08/255,208 filed June 7, 1994, which is a Continuation-In-Part of Serial No. 08/073,028 filed June 7, 1993, each of which is incorporated herein by reference in its entirety. This invention was made with Government  
10 support under Grant No. AI-30411-02 awarded by the National Institutes of Health. The Government has certain rights in the invention.

1. INTRODUCTION

15 The present invention relates, first, to DP178 (SEQ ID NO:1), a peptide corresponding to amino acids 638 to 673 of the HIV-1<sub>LAI</sub> transmembrane protein (TM) gp41, and portions or analogs of DP178 (SEQ ID NO:1), which exhibit anti-membrane fusion capability,  
20 antiviral activity, such as the ability to inhibit HIV transmission to uninfected CD-4<sup>+</sup> cells, or an ability to modulate intracellular processes involving coiled-coil peptide structures. Further, the invention relates to the use of DP178 (SEQ ID NO:1) and DP178  
25 portions and/or analogs as antifusogenic or antiviral compounds or as inhibitors of intracellular events involving coiled-coil peptide structures. The present invention also relates to peptides analogous to DP107 (SEQ ID NO:25), a peptide corresponding to amino acids  
30 558 to 595 of the HIV-1<sub>LAI</sub> transmembrane protein (TM) gp41, having amino acid sequences present in other viruses, such as enveloped viruses, and/or other organisms, and further relates to the uses of such peptides. These peptides exhibit anti-membrane fusion  
35 capability, antiviral activity, or the ability to

modulate intracellular processes involving coiled-coil peptide structures. The present invention additionally relates to methods for identifying compounds that disrupt the interaction between DP178 and DP107, and/or between DP107-like and DP178-like peptides. Further, the invention relates to the use of the peptides of the invention as diagnostic agents. For example, a DP178 peptide may be used as an HIV subtype-specific diagnostic. The invention is demonstrated, first, by way of an Example wherein DP178 (SEQ ID:1), and a peptide whose sequence is homologous to DP178 are each shown to be potent, non-cytotoxic inhibitors of HIV-1 transfer to uninfected CD-4<sup>+</sup> cells. The invention is further demonstrated by Examples wherein peptides having structural and/or amino acid motif similarity to DP107 and DP178 are identified in a variety of viral and nonviral organisms, and in examples wherein a number of such identified peptides derived from several different viral systems are demonstrated to exhibit antiviral activity.

## 2. BACKGROUND OF THE INVENTION

### 2.1 MEMBRANE FUSION EVENTS

Membrane fusion is a ubiquitous cell biological process (for a review, see White, J.M., 1992, Science 258:917-924). Fusion events which mediate cellular housekeeping functions, such as endocytosis, constitutive secretion, and recycling of membrane components, occur continuously in all eukaryotic cells.

Additional fusion events occur in specialized cells. Intracellularly, for example, fusion events are involved in such processes as occur in regulated exocytosis of hormones, enzymes and neurotransmitters.

Intercellularly, such fusion events feature prominently in, for example, sperm-egg fusion and myoblast fusion.

Fusion events are also associated with disease states. For example, fusion events are involved in the formation of giant cells during inflammatory reactions, the entry of all enveloped viruses into cells, and, in the case of human immunodeficiency virus (HIV), for example, are responsible for the virally induced cell-cell fusion which leads to cell death.

## 2.2. THE HUMAN IMMUNODEFICIENCY VIRUS

The human immunodeficiency virus (HIV) has been implicated as the primary cause of the slowly degenerative immune system disease termed acquired immune deficiency syndrome (AIDS) (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo, R. et al., 1984, Science 224:500-503). There are at least two distinct types of HIV: HIV-1 (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo R. et al., 1984, Science 224:500-503) and HIV-2 (Clavel, F. et al., 1986, Science 233:343-346; Guyader, M. et al., 1987, Nature 326:662-669). Further, a large amount of genetic heterogeneity exists within populations of each of these types. Infection of human CD-4<sup>+</sup> T-lymphocytes with an HIV virus leads to depletion of the cell type and eventually to opportunistic infections, neurological dysfunctions, neoplastic growth, and ultimately death.

HIV is a member of the lentivirus family of retroviruses (Teich, N. et al., 1984, RNA Tumor Viruses, Weiss, R. et al., eds., CSH-Press, pp. 949-956). Retroviruses are small enveloped viruses that contain a diploid, single-stranded RNA genome, and

replicate via a DNA intermediate produced by a virally-encoded reverse transcriptase, an RNA-dependent DNA polymerase (Varmus, H., 1988, *Science* 240:1427-1439). Other retroviruses include, for example, oncogenic viruses such as human T-cell  
5 leukemia viruses (HTLV-I,-II,-III), and feline leukemia virus.

The HIV viral particle consists of a viral core, composed of capsid proteins, that contains the viral  
10 RNA genome and those enzymes required for early replicative events. Myristylated Gag protein forms an outer viral shell around the viral core, which is, in turn, surrounded by a lipid membrane enveloped derived from the infected cell membrane. The HIV enveloped  
15 surface glycoproteins are synthesized as a single 160 Kd precursor protein which is cleaved by a cellular protease during viral budding into two glycoproteins, gp41 and gp120. gp41 is a transmembrane protein and gp120 is an extracellular protein which remains non-covalently associated with gp41, possibly in a  
20 trimeric or multimeric form (Hammarskjold, M. and Rekosh, D., 1989, *Biochem. Biophys. Acta* 989:269-280).

HIV is targeted to CD-4<sup>+</sup> cells because the CD-4 cell surface protein acts as the cellular receptor for the HIV-1 virus (Dalglish, A. et al., 1984, *Nature* 312:763-767; Klatzmann et al., 1984, *Nature* 312:767-768; Maddon et al., 1986, *Cell* 47:333-348). Viral  
25 entry into cells is dependent upon gp120 binding the cellular CD-4<sup>+</sup> receptor molecules (McDougal, J.S. et al., 1986, *Science* 231:382-385; Maddon, P.J. et al.,  
30 1986, *Cell* 47:333-348) and thus explains HIV's tropism for CD-4<sup>+</sup> cells, while gp41 anchors the enveloped glycoprotein complex in the viral membrane.

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### 2.3. HIV TREATMENT

HIV infection is pandemic and HIV associated diseases represent a major world health problem. Although considerable effort is being put into the successful design of effective therapeutics, currently no curative anti-retroviral drugs against AIDS exist. In attempts to develop such drugs, several stages of the HIV life cycle have been considered as targets for therapeutic intervention (Mitsuya, H. et al., 1991, FASEB J. 5:2369-2381). For example, virally encoded reverse transcriptase has been one focus of drug development. A number of reverse-transcriptase-targeted drugs, including 2',3'-dideoxynucleoside analogs such as AZT, ddI, ddC, and d4T have been developed which have been shown to be active against HIV (Mitsuya, H. et al., 1991, Science 249:1533-1544). While beneficial, these nucleoside analogs are not curative, probably due to the rapid appearance of drug resistant HIV mutants (Lander, B. et al., 1989, Science 243:1731-1734). In addition, the drugs often exhibit toxic side effects such as bone marrow suppression, vomiting, and liver function abnormalities.

Attempts are also being made to develop drugs which can inhibit viral entry into the cell, the earliest stage of HIV infection. Here, the focus has thus far been on CD4, the cell surface receptor for HIV. Recombinant soluble CD4, for example, has been shown to inhibit infection of CD-4<sup>+</sup> T-cells by some HIV-1 strains (Smith, D.H. et al., 1987, Science 238:1704-1707). Certain primary HIV-1 isolates, however, are relatively less sensitive to inhibition by recombinant CD-4 (Daar, E. et al., 1990, Proc. Natl. Acad. Sci. USA 87:6574-6579). In addition,

recombinant soluble CD-4 clinical trials have produced inconclusive results (Schooley, R. et al., 1990, Ann. Int. Med. 112:247-253; Kahn, J.O. et al., 1990, Ann. Int. Med. 112:254-261; Yarchoan, R. et al., 1989, Proc. Vth Int. Conf. on AIDS, p. 564, MCP 137).

5       The late stages of HIV replication, which involve crucial virus-specific secondary processing of certain viral proteins, have also been suggested as possible anti-HIV drug targets. Late stage processing is dependent on the activity of a viral protease, and  
10       drugs are being developed which inhibit this protease (Erickson, J., 1990, Science 249:527-533). The clinical outcome of these candidate drugs is still in question.

15       Attention is also being given to the development of vaccines for the treatment of HIV infection. The HIV-1 enveloped proteins (gp160, gp120, gp41) have been shown to be the major antigens for anti-HIV antibodies present in AIDS patients (Barin, et al., 1985, Science 228:1094-1096). Thus far, therefore,  
20       these proteins seem to be the most promising candidates to act as antigens for anti-HIV vaccine development. To this end, several groups have begun to use various portions of gp160, gp120, and/or gp41 as immunogenic targets for the host immune system.  
25       See for example, Ivanoff, L. et al., U.S. Pat. No. 5,141,867; Saith, G. et al., WO 92/22,654; Shafferman, A., WO 91/09,872; Formoso, C. et al., WO 90/07,119. Clinical results concerning these candidate vaccines, however, still remain far in the future.

30       Thus, although a great deal of effort is being directed to the design and testing of anti-retroviral drugs, a truly effective, non-toxic treatment is still needed.

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### 3. SUMMARY OF THE INVENTION

The present invention relates, first, to DP178 (SEQ ID:1), a 36-amino acid synthetic peptide corresponding to amino acids 638 to 673 of the transmembrane protein (TM) gp41 from the HIV-1 isolate LAI (HIV-1<sub>LAI</sub>), which exhibits potent anti-HIV-1 activity. As evidenced by the Example presented below, in Section 6, the DP178 (SEQ ID:1) antiviral activity is so high that, on a weight basis, no other known anti-HIV agent is effective at concentrations as low as those at which DP178 (SEQ ID:1) exhibits its inhibitory effects.

The invention further relates to those portions and analogs of DP178 which also show such antiviral activity, and/or show anti-membrane fusion capability, or an ability to modulate intracellular processes involving coiled-coil peptide structures. The term "DP178 analog" refers to a peptide which contains an amino acid sequence corresponding to the DP178 peptide sequence present within the gp41 protein of HIV-1<sub>LAI</sub>, but found in viruses and/or organisms other than HIV-1<sub>LAI</sub>. Such DP178 analog peptides may, therefore, correspond to DP178-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1<sub>LAI</sub>, as well as non-enveloped viruses. Further, such analogous DP178 peptides may also correspond to DP178-like amino acid sequences present in nonviral organisms.

The invention further relates to peptides DP107 (SEQ ID NO:25) analogs. DP107 is a peptide corresponding to amino acids 558-595 of the HIV-1<sub>LAI</sub> transmembrane protein (TM) gp41. The term "DP107 analog" as used herein refers to a peptide which contains an amino acid sequence corresponding to the

DP107 peptide sequence present within the gp41 protein of HIV-1<sub>LAI</sub>, but found in viruses and organisms other than HIV-1<sub>LAI</sub>. Such DP107 analog peptides may, therefore, correspond to DP107-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1<sub>LAI</sub>, as well as non-enveloped viruses. Further, such DP107 analog peptides may also correspond to DP107-like amino acid sequences present in nonviral organisms.

Further, the peptides of the invention include DP107 analog and DP178 analog peptides having amino acid sequences recognized or identified by the 107x178x4, ALLMOTI5 and/or PLZIP search motifs described herein.

The peptides of the invention may, for example, exhibit antifusogenic activity, antiviral activity, and/or may have the ability to modulate intracellular processes which involve coiled-coil peptide structures. With respect to the antiviral activity of the peptides of the invention, such an antiviral activity includes, but is not limited to the inhibition of HIV transmission to uninfected CD-4<sup>+</sup> cells. Additionally, the antifusogenic capability, antiviral activity or intracellular modulatory activity of the peptides of the invention merely requires the presence of the peptides of the invention, and, specifically, does not require the stimulation of a host immune response directed against such peptides.

The peptides of the invention may be used, for example, as inhibitors of membrane fusion-associated events, such as, for example, the inhibition of human and non-human retroviral, especially HIV, transmission to uninfected cells. It is further contemplated that

the peptides of the invention may be used as modulators of intracellular events involving coiled-coil peptide structures.

The peptides of the invention may, alternatively, be used to identify compounds which may themselves exhibit antifusogenic, antiviral, or intracellular modulatory activity. Additional uses include, for example, the use of the peptides of the invention as organism or viral type and/or subtype-specific diagnostic tools.

The terms "antifusogenic" and "anti-membrane fusion", as used herein, refer to an agent's ability to inhibit or reduce the level of membrane fusion events between two or more moieties relative to the level of membrane fusion which occurs between said moieties in the absence of the peptide. The moieties may be, for example, cell membranes or viral structures, such as viral envelopes or pili. The term "antiviral", as used herein, refers to the compound's ability to inhibit viral infection of cells, via, for example, cell-cell fusion or free virus infection. Such infection may involve membrane fusion, as occurs in the case of enveloped viruses, or some other fusion event involving a viral structure and a cellular structure (e.g., such as the fusion of a viral pilus and bacterial membrane during bacterial conjugation).

It is also contemplated that the peptides of the invention may exhibit the ability to modulate intracellular events involving coiled-coil peptide structures. "Modulate", as used herein, refers to a stimulatory or inhibitory effect on the intracellular process of interest relative to the level or activity of such a process in the absence of a peptide of the invention.

Embodiments of the invention are demonstrated below wherein an extremely low concentration of DP178 (SEQ ID:1), and very low concentrations of a DP178 homolog (SEQ ID:3) are shown to be potent inhibitors of HIV-1 mediated CD-4<sup>+</sup> cell-cell fusion (i.e.,  
5 syncytial formation) and infection of CD-4<sup>+</sup> cells by cell-free virus. Further, it is shown that DP178 (SEQ ID:1) is not toxic to cells, even at concentrations 3 logs higher than the inhibitory DP-178 (SEQ ID:1) concentration.

10 The present invention is based, in part, on the surprising discovery that the DP107 and DP178 domains of the HIV gp41 protein non-covalently complex with each other, and that their interaction is required for the normal infectivity of the virus. This discovery  
15 is described in the Example presented, below, in Section 8. The invention, therefore, further relates to methods for identifying antifusogenic, including antiviral, compounds that disrupt the interaction between DP107 and DP178, and/or between DP107-like and  
20 DP178-like peptides.

Additional embodiments of the invention (specifically, the Examples presents in Sections 9-16 and 19-25, below) are demonstrated, below, wherein  
25 peptides, from a variety of viral and nonviral sources, having structural and/or amino acid motif similarity to DP107 and DP178 are identified, and search motifs for their identification are described. Further, Examples (in Sections 17, 18, 25-29) are presented wherein a number of the peptides of the  
30 invention are demonstrated exhibit substantial antiviral activity or activity predictive of antiviral activity.

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### 3.1. DEFINITIONS

Peptides are defined herein as organic compounds comprising two or more amino acids covalently joined by peptide bonds. Peptides may be referred to with  
5 respect to the number of constituent amino acids, i.e., a dipeptide contains two amino acid residues, a tripeptide contains three, etc. Peptides containing ten or fewer amino acids may be referred to as oligopeptides, while those with more than ten amino  
10 acid residues are polypeptides. Such peptides may also include any of the modifications and additional amino and carboxy groups as are described herein.

Peptide sequences defined herein are represented by one-letter symbols for amino acid residues as  
15 follows:

A (alanine)  
R (arginine)  
N (asparagine)  
D (aspartic acid)  
C (cysteine)  
20 Q (glutamine)  
E (glutamic acid)  
G (glycine)  
H (histidine)  
I (isoleucine)  
L (leucine)  
K (lysine)  
M (methionine)  
25 F (phenylalanine)  
P (proline)  
S (serine)  
T (threonine)  
W (tryptophan)  
Y (tyrosine)  
V (valine)

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#### 4. BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. Amino acid sequence of DP178 (SEQ ID:1) derived from HIV<sub>LAI</sub>; DP178 homologs derived from HIV-1<sub>SP2</sub> (DP-185; SEQ ID:3), HIV-1<sub>RF</sub> (SEQ ID:4), and HIV-1<sub>MN</sub> (SEQ ID:5); DP178 homologs derived from amino acid sequences of two prototypic HIV-2 isolates, namely, HIV-2<sub>rod</sub> (SEQ ID:6) and HIV-2<sub>NIH2</sub> (SEQ ID:7); control peptides: DP-180 (SEQ ID:2), a peptide incorporating the amino acid residues of DP178 in a scrambled sequence; DP-118 (SEQ ID:10) unrelated to DP178, which inhibits HIV-1 cell free virus infection; DP-125 (SEQ ID:8), unrelated to DP178, also inhibits HIV-1 cell free virus infection; DP-116 (SEQ ID:9), unrelated to DP178, is negative for inhibition of HIV-1 infection when tested using a cell-free virus infection assay. Throughout the figures, the one letter amino acid code is used.

FIG. 2. Inhibition of HIV-1 cell-free virus infection by synthetic peptides. IC<sub>50</sub> refers to the concentration of peptide that inhibits RT production from infected cells by 50% compared to the untreated control. Control: the level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 3. Inhibition of HIV-1 and HIV-2 cell-free virus infection by the synthetic peptide DP178 (SEQ ID:1). IC<sub>50</sub>: concentration of peptide that inhibits RT production by 50% compared to the untreated control. Control: Level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 4A-4B. Fusion Inhibition Assays. FIG 4A: DP178 (SEQ ID:1) inhibition of HIV-1 prototypic isolate-mediated syncytial formation; data represents the number of virus-induced syncytial per cell. FIG.



4B: DP-180 (SEQ ID:2) represents a scrambled control peptide; DP-185 (SEQ ID:3) represents a DP178 homolog derived from HIV-1<sub>SP2</sub> isolate; Control, refers to the number of syncytial produced in the absence of peptide.

5       FIG. 5. Fusion inhibition assay: HIV-1 vs. HIV-2. Data represents the number of virus-induced syncytial per well. ND: not done.

10       FIG. 6. Cytotoxicity study of DP178 (SEQ ID:1) and DP-116 (SEQ ID:9) on CEM cells. Cell proliferation data is shown.

15       FIG. 7. Schematic representation of HIV-gp41 and maltose binding protein (MBP)-gp41 fusion proteins. DP107 and DP178 are synthetic peptides based on the two putative helices of gp41. The letter P in the DP107 boxes denotes an Ile to Pro mutation at amino acid number 578. Amino acid residues are numbered according to Meyers et al., "Human Retroviruses and AIDS", 1991, Theoret. Biol. and Biophys. Group, Los Alamos Natl. Lab., Los Alamos, NM. The proteins are more fully described, below, in Section 8.1.1.

20       FIG. 8. A point mutation alters the conformation and anti-HIV activity of M41.

25       FIG. 9. Abrogation of DP178 anti-HIV activity. Cell fusion assays were carried out in the presence of 10 nM DP178 and various concentrations of M41Δ178 or M41PA178.

30       FIG. 10. Binding of DP178 to leucine zipper of gp41 analyzed by FAb-D ELISA.

35       FIG. 11A-B. Models for a structural transition in the HIV-1 TM protein. Two models are proposed which indicate a structural transition from a native oligomer to a fusogenic state following a trigger event (possibly gp120 binding to CD4). Common

features of both models include (1) the native state is held together by noncovalent protein-protein interactions to form the heterodimer of gp120/41 and other interactions, principally through gp41 interactive sites, to form homo-oligomers on the virus surface of the gp120/41 complexes; (2) shielding of the hydrophobic fusogenic peptide at the N-terminus (F) in the native state; and (3) the leucine zipper domain (DP107) exists as a homo-oligomer coiled coil only in the fusogenic state. The major differences in the two models include the structural state (native or fusogenic) in which the DP107 and DP178 domains are complexed to each other. In the first model (FIG. 11A) this interaction occurs in the native state and in the second (FIG. 11B), it occurs during the fusogenic state. When triggered, the fusion complex in the model depicted in (A) is generated through formation of coiled-coil interactions in homologous DP107 domains resulting in an extended  $\alpha$ -helix. This conformational change positions the fusion peptide for interaction with the cell membrane. In the second model (FIG. 11B), the fusogenic complex is stabilized by the association of the DP178 domain with the DP107 coiled-coil.

FIG. 12. Motif design using heptad repeat positioning of amino acids of known coiled-coils.

FIG. 13. Motif design using proposed heptad repeat positioning of amino acids of DP107 and DP178.

FIG. 14. Hybrid motif design crossing GCN4 and DP107.

FIG. 15. Hybrid motif design crossing GCN4 and DP178.

FIG. 16. Hybrid motif design 107x178x4, crossing DP107 and DP178. This motif was found to be

the most consistent at identifying relevant DP107-like and DP178-like peptide regions.

FIG. 17. Hybrid motif design crossing GCN4, DP107, and DP178.

5       FIG. 18. Hybrid motif design ALLMOTI5 crossing GCN4, DP107, DP178, c-Fos c-Jun, c-Myc, and Flu Loop 36.

FIG. 19. PLZIP motifs designed to identify N-terminal proline-leucine zipper motifs.

10       FIG. 20. Search results for HIV-1 (BRU isolate) enveloped protein gp41. Sequence search motif designations: Spades (♠): 107x178x4; Hearts (♥) ALLMOTI5; Clubs (♣): PLZIP; Diamonds (♦): transmembrane region (the putative transmembrane domains were identified using a PC/Gene program  
15       designed to search for such peptide regions). Asterisk (\*): Lupas method. The amino acid sequences identified by each motif are bracketed by the respective characters. Representative sequences  
20       chosen based on 107x178x4 searches are underlined and in bold. DP107 and DP178 sequences are marked, and additionally double-underlined and italicized.

FIG. 21. Search results for human respiratory syncytial virus (RSV) strain A2 fusion glycoprotein F1. Sequence search motif designations  
25       are as in FIG. 20.

FIG. 22. Search results for simian immunodeficiency virus (SIV) enveloped protein gp41 (AGM3 isolate). Sequence search motif designations  
30       are as in FIG. 20.

FIG. 23. Search results for canine distemper virus (strain Onderstepoort) fusion glycoprotein 1. Sequence search motif designations  
are as in FIG. 20.

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FIG. 24. Search results for newcastle disease virus (strain Australia-Victoria/32) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

5 FIG. 25. Search results for human parainfluenza 3 virus (strain NIH 47885) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

10 FIG. 26. Search results for influenza A virus (strain A/AICHI/2/68) hemagglutinin precursor HA2. Sequence search designations are as in FIG. 20.

FIG. 27A-D. Respiratory Syncytial Virus (RSV) peptide antiviral and circular dichroism data. FIG. 27A-B: Peptides derived from the F2 DP178/DP107-like region. Antiviral and CD data. FIG. 27C-D: 15 Peptides derived from the F1 DP107-like region. Peptide and CD data.

Antiviral activity (AV) is represented by the following qualitative symbols:

20 "-", negative antiviral activity;  
"+/-", antiviral activity at greater than 100µg/ml;  
"+", antiviral activity at between 50-100µg/ml;  
"++", antiviral activity at between 20-50µg/ml;  
25 "+++", antiviral activity at between 1-20µg/ml;  
"++++", antiviral activity at <1µg/ml.

CD data, referring to the level of helicity is represented by the following qualitative symbol:

30 "-", no helicity;  
"+", 25-50% helicity;  
"++", 50-75% helicity;  
"+++" 75-100% helicity.

35 IC<sub>50</sub> refers to the concentration of peptide necessary to produce only 50% of the number of syncytial relative to infected control cultures

containing no peptide.  $IC_{50}$  values were obtained using purified peptides only.

5       FIG. 28A-B. Respiratory Syncytial Virus (RSV) DP178-like region (F1) peptide antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as in FIG. 27A-D.  $IC_{50}$  values were obtained using purified peptides only.

10       FIG. 29A-B. Peptides derived from the HPIV3 F1 DP107-like region. Peptide antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as in FIG. 27A-D. Purified peptides were used to obtain  $IC_{50}$  values, except where the values are marked by an asterisk (\*), in which cases, the  $IC_{50}$  values were obtained using a crude peptide preparation.

15       FIG. 29C. HPIV3 peptide T-184 CD spectrum at 1°C in 0.1M NaCl 10mM  $KPO_4$ , pH 7.0. The data demonstrates the peptide's helical secondary structure ( $\theta_{222/208}=1.2$ ) over a wide range of concentrations (100-1500 $\mu$ M). This evidence is consistent with the peptide forming a helical coiled-coil structure.

20       FIG. 30A-B. Peptides derived from the HPIV3 F1 DP178-like region. Peptide antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as in FIG. 27A-D. Purified peptides were used to obtain  $IC_{50}$  values, except where the values are marked by an asterisk (\*), in which cases, the  $IC_{50}$  values were obtained using a crude peptide preparation.

25       FIG. 31. Motif search results for simian immunodeficiency virus (SIV) isolate MM251, enveloped polyprotein gp41. Sequence search designations are as in FIG. 20.

30       FIG. 32. Motif search results for Epstein-Barr Virus (Strain B95-8), glycoprotein gp110 precursor (designated gp115). BALF4. Sequence search designations are as in FIG. 20.

FIG. 33. Motif search results for Epstein-Barr Virus (Strain B95-8), BZLF1 trans-activator protein (designated EB1 or Zebra). Sequence search designations are as in FIG. 20. Additionally, "e" refers to a well known DNA binding domain and "+" refers to a well known dimerization domain, as defined by Flemington and Speck (Flemington, E. and Speck, S.H., 1990, Proc. Natl. Acad. Sci. USA 87:9459-9463).

FIG. 34. Motif search results for measles virus (strain Edmonston), fusion glycoprotein F1. Sequence search designations are as in FIG. 20.

FIG. 35. Motif search results for Hepatitis B Virus (Subtype AYW), major surface antigen precursor S. Sequence search designations are as in FIG. 20.

FIG. 36. Motif search results for simian Mason-Pfizer monkey virus, enveloped (TM) protein gp20. Sequence search designations are as in FIG. 20.

FIG. 37. Motif search results for Pseudomonas aeruginosa, fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 38. Motif search results for Neisseria gonorrhoeae fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 39. Motif search results for Hemophilus influenzae fimbrial protein. Sequence search designations are as in FIG. 20.

FIG. 40. Motif search results for Staphylococcus aureus, toxic shock syndrome toxin-1. Sequence search designations are as in FIG. 20.

FIG. 41. Motif search results for Staphylococcus aureus enterotoxin Type E. Sequence search designations are as in FIG. 20.

FIG. 42. Motif search results for Staphylococcus aureus enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 43. Motif search results for Escherichia coli, heat labile enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 44. Motif search results for human c-fos proto-oncoprotein. Sequence search designations  
5 are as in FIG. 20.

FIG. 45. Motif search results for human lupus KU autoantigen protein P70. Sequence search designations are as in FIG. 20.

FIG. 46. Motif search results for human  
10 zinc finger protein 10. Sequence search designations are as in FIG. 20.

FIG. 47. Measles virus (MeV) fusion protein DP178-like region antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as in FIG. 27A-D.  
15  $IC_{50}$  values were obtained using purified peptides.

FIG. 48. Simian immunodeficiency virus (SIV) TM (fusion) protein DP178-like region antiviral data. Antiviral symbols are as in FIG. 27A-D "NT", not tested.  
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FIG. 49A-C. DP178-derived peptide antiviral data. The peptides listed herein were derived from the region surrounding the HIV-1 BRU isolate DP178 region (e.g., gp41 amino acid residues 615-717).

In instances where peptides contained DP178 point  
25 mutations, the mutated amino acid residues are shown with a shaded background. In instances in which the test peptide has had an amino and/or carboxy-terminal group added or removed (apart from the standard amido- and acetyl- blocking groups found on such peptides),  
30 such modifications are indicated. FIG. 49A: The column to the immediate right of the name of the test peptide indicates the size of the test peptide and points out whether the peptide is derived from a one  
35 amino acid peptide "walk" across the DP178 region.

The next column to the right indicates whether the test peptide contains a point mutation, while the column to its right indicates whether certain amino acid residues have been added to or removed from the DP178-derived amino acid sequence. FIG 49B: The  
5 column to the immediate right of the test peptide name indicates whether the peptide represents a DP178 truncation, the next column to the right points out whether the peptide contains a point mutation, and the  
10 column to its right indicates whether the peptide contains amino acids which have been added to or removed from the DP178 sequence itself. FIG. 49C: The column to the immediate right of the test peptide name indicates whether the test peptide contains a  
15 point mutation, while the column to its right indicates whether amino acid residues have been added to or removed from the DP178 sequence itself.  $IC_{50}$  is as defined in FIG. 27A-D, and  $IC_{50}$  values were obtained using purified peptides except where marked with an  
20 asterisk (\*), in which case the  $IC_{50}$  was obtained using a crude peptide preparation.

FIG. 50. DP107 and DP107 gp41 region truncated peptide antiviral data.  $IC_{50}$  as defined in FIG. 27A-D, and  $IC_{50}$  values were obtained using  
25 purified peptides except where marked with an asterisk (\*), in which case the  $IC_{50}$  was obtained using a crude peptide preparation.

FIG. 51A-B. Epstein-Barr virus Strain B95-8 BZLF1 DP178/DP107 analog region peptide walks and electrophoretic mobility shift assay results. The  
30 peptides (T-423 to T-446, FIG. 51A; T-447 to T-461, FIG. 51B) represent one amino acid residue "walks" through the EBV Zebra protein region from amino acid residue 173 to 246.

35



The amino acid residue within this region which corresponds to the first amino acid residue of each peptide is listed to the left of each peptide, while the amino acid residue within this region which corresponds to the last amino acid residue of each peptide is listed to the right of each peptide. The length of each test peptide is listed at the far right of each line, under the heading "Res".

"ACT" refers to a test peptide's ability to inhibit Zebra binding to its response element. "+" refers to a visible, but incomplete, abrogation of the response element/Zebra homodimer complex; "+++" refers to a complete abrogation of the complex; and "-" represents a lack of complex disruption.

FIG. 52A-B. Hepatitis B virus subtype AYW major surface antigen precursor S protein DP178/DP107 analog region and peptide walks. 52A depicts Domain I (S protein amino acid residues 174-220), which contains a potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain I. 52B depicts Domain II (S protein amino acid residues 233-291), which contains a second potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain II.

#### 5. DETAILED DESCRIPTION OF THE INVENTION

Described herein are peptides which may exhibit antifusogenic activity, antiviral capability, and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. The peptides described include, first, DP178 (SEQ ID NO:1), a gp41-derived 36 amino acid peptide and fragments and analogs of DP178.

In addition, the peptides of the invention described herein include peptides which are DP107 analogs. DP107 (SEQ ID NO:25) is a 38 amino acid peptide corresponding to residues 558 to 595 of the HIV-1<sub>LAI</sub> transmembrane (TM) gp41 protein. Such DP107  
5 analogs may exhibit antifusogenic capability, antiviral activity or an ability to modulate intracellular processes involving coiled-coil structures.

Further, peptides of the invention include DP107  
10 and DP178 are described herein having amino acid sequences recognized by the 107x178x4, ALLMOTI5, and PLZIP search motifs. Such motifs are also discussed.

Also described here are antifusogenic, antiviral, intracellular modulatory, and diagnostic uses of the  
15 peptides of the invention. Further, procedures are described for the use of the peptides of the invention for the identification of compounds exhibiting antifusogenic, antiviral or intracellular modulatory activity.

While not limited to any theory of operation, the  
20 following model is proposed to explain the potent anti-HIV activity of DP178, based, in part, on the experiments described in the Examples, infra. In the HIV protein, gp41, DP178 corresponds to a putative  $\alpha$ -  
25 helix region located in the C-terminal end of the gp41 ectodomain, and appears to associate with a distal site on gp41 whose interactive structure is influenced by the leucine zipper motif, a coiled-coil structure, referred to as DP107. The association of these two  
30 domains may reflect a molecular linkage or "molecular clasp" intimately involved in the fusion process. It is of interest that mutations in the C-terminal  $\alpha$ -helix motif of gp41 (i.e., the D178 domain) tend to  
35 enhance the fusion ability of gp41, whereas mutations

in the leucine zipper region (i.e., the DP107 domain) decrease or abolish the fusion ability of the viral protein. It may be that the leucine zipper motif is involved in membrane fusion while the C-terminal  $\alpha$ -helix motif serves as a molecular safety to regulate the availability of the leucine zipper during virus-induced membrane fusion.

On the basis of the foregoing, two models are proposed of gp41-mediated membrane fusion which are schematically shown in FIG. 11A-B. The reason for proposing two models is that the temporal nature of the interaction between the regions defined by DP107 and DP178 cannot, as yet, be pinpointed. Each model envisions two conformations for gp41 - one in a "native" state as it might be found on a resting virion. The other in a "fusogenic" state to reflect conformational changes triggered following binding of gp120 to CD4 and just prior to fusion with the target cell membrane. The strong binding affinity between gp120 and CD4 may actually represent the trigger for the fusion process obviating the need for a pH change such as occurs for viruses that fuse within intracellular vesicles. The two major features of both models are: (1) the leucine zipper sequences (DP107) in each chain of oligomeric enveloped are held apart in the native state and are only allowed access to one another in the fusogenic state so as to form the extremely stable coiled-coils, and (2) association of the DP178 and DP107 sites as they exist in gp41 occur either in the native or fusogenic state. FIG. 11A depicts DP178/DP107 interaction in the native state as a molecular clasp. On the other hand, if one assumes that the most stable form of the enveloped occurs in the fusogenic state, the model in FIG. 11B can be considered.

When synthesized as peptides, both DP107 and DP178 are potent inhibitors of HIV infection and fusion, probably by virtue of their ability to form complexes with viral gp41 and interfere with its fusogenic process; e.g., during the structural transition of the viral protein from the native structure to the fusogenic state, the DP178 and DP107 peptides may gain access to their respective binding sites on the viral gp41, and exert a disruptive influence. DP107 peptides which demonstrate anti-HIV activity are described in Applicants' co-pending application Serial No. 08/264,531, filed June 23, 1994, which is incorporated by reference herein in its entirety.

As shown in the Examples, infra, a truncated recombinant gp41 protein corresponding to the ectodomain of gp41 containing both DP107 and DP178 domains (excluding the fusion peptide, transmembrane region and cytoplasmic domain of gp41) did not inhibit HIV-1 induced fusion. However, when a single mutation was introduced to disrupt the coiled-coil structure of the DP107 domain -- a mutation which results in a total loss of biological activity of DP107 peptides -- the inactive recombinant protein was transformed to an active inhibitor of HIV-1 induced fusion. This transformation may result from liberation of the potent DP178 domain from a molecular clasp with the leucine zipper, DP107 domain.

For clarity of discussion, the invention will be described primarily for DP178 peptide inhibitors of HIV. However, the principles may be analogously applied to other viruses, both enveloped and nonenveloped, and to other non-viral organisms.

#### 5.1. DP178 AND DP178-LIKE PEPTIDES

The DP178 peptide (SEQ ID:1) of the invention corresponds to amino acid residues 638 to 673 of the transmembrane protein gp41 from the HIV-1<sub>LAI</sub> isolate, and has the 36 amino acid sequence (reading from amino to carboxy terminus):

NH<sub>2</sub>-YTSLIHSLEESQNQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:1)

In addition to the full-length DP178 (SEQ ID:1) 36-mer, the peptides of the invention may include truncations of the DP178 (SEQ ID:1) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. Truncations of DP178 (SEQ ID:1) peptides may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide), as shown in Tables I and IA, below. Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH<sub>2</sub>) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

TABLE I  
DP178 (SEQ ID:1) CARBOXY TRUNCATIONS

X-YTS-Z  
 X-YTSL-Z  
 X-YTSLI-Z  
 X-YTSLIH-Z  
 5 X-YTSLIHS-Z  
 X-YTSLIHSL-Z  
 X-YTSLIHSLI-Z  
 X-YTSLIHSLIE-Z  
 X-YTSLIHSLIEE-Z  
 X-YTSLIHSLIEES-Z  
 X-YTSLIHSLIEESQ-Z  
 10 X-YTSLIHSLIEESQN-Z  
 X-YTSLIHSLIEESQNNQ-Z  
 X-YTSLIHSLIEESQNNQQ-Z  
 X-YTSLIHSLIEESQNNQQE-Z  
 X-YTSLIHSLIEESQNNQQEK-Z  
 X-YTSLIHSLIEESQNNQQEKN-Z  
 X-YTSLIHSLIEESQNNQQEKNE-Z  
 X-YTSLIHSLIEESQNNQQEKNEQ-Z  
 15 X-YTSLIHSLIEESQNNQQEKNEQE-Z  
 X-YTSLIHSLIEESQNNQQEKNEQEL-Z  
 X-YTSLIHSLIEESQNNQQEKNEQELL-Z  
 X-YTSLIHSLIEESQNNQQEKNEQELLE-Z  
 X-YTSLIHSLIEESQNNQQEKNEQELLEL-Z  
 X-YTSLIHSLIEESQNNQQEKNEQELLELD-Z  
 X-YTSLIHSLIEESQNNQQEKNEQELLELDK-Z  
 20 X-YTSLIHSLIEESQNNQQEKNEQELLELDKW-Z  
 X-YTSLIHSLIEESQNNQQEKNEQELLELDKWA-Z  
 X-YTSLIHSLIEESQNNQQEKNEQELLELDKWAS-Z  
 X-YTSLIHSLIEESQNNQQEKNEQELLELDKWASL-Z  
 X-YTSLIHSLIEESQNNQQEKNEQELLELDKWASLW-Z  
 X-YTSLIHSLIEESQNNQQEKNEQELLELDKWASLWN-Z  
 X-YTSLIHSLIEESQNNQQEKNEQELLELDKWASLWNW-Z  
 X-YTSLIHSLIEESQNNQQEKNEQELLELDKWASLWNWF-Z

25 The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxyl, dansyl, or  
 30 T-butyloxycarbonyl; an acetyl group; a 9-  
 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a  
 T-butyloxycarbonyl group; a macromolecular carrier  
 35 group including but not limited to lipid-fatty acid  
 conjugates, polyethylene glycol, or carbohydrates.

TABLE IA  
DP178 (SEQ ID:1) AMINO TRUNCATIONS

	X-NWF-Z
	X-WNWF-Z
	X-LWNWF-Z
5	X-SLWNWF-Z
	X-ASLWNWF-Z
	X-WASLWNWF-Z
	X-KWASLWNWF-Z
	X-DKWASLWNWF-Z
	X-LDKWASLWNWF-Z
	X-ELDKWASLWNWF-Z
10	X-LELDKWASLWNWF-Z
	X-LLELDKWASLWNWF-Z
	X-ELLELDKWASLWNWF-Z
	X-QELLELDKWASLWNWF-Z
	X-EQELLELDKWASLWNWF-Z
	X-NEQELLELDKWASLWNWF-Z
	X-KNEQELLELDKWASLWNWF-Z
	X-EKNEQELLELDKWASLWNWF-Z
15	X-QEKNEQELLELDKWASLWNWF-Z
	X-QQEKNEQELLELDKWASLWNWF-Z
	X-NQQEKNEQELLELDKWASLWNWF-Z
	X-QNQQEKNEQELLELDKWASLWNWF-Z
	X-SQNQQEKNEQELLELDKWASLWNWF-Z
	X-ESQNQQEKNEQELLELDKWASLWNWF-Z
	X-EESQNQQEKNEQELLELDKWASLWNWF-Z
20	X-IEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-LIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-SLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-HSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-IHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-LIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-SLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-TSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
25	X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the invention also include DP178-like peptides. "DP178-like", as used herein, refers, first, to DP178 and DP178 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-178-like" refers to peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP178. The DP178-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP178-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP178-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP178 peptides of the invention. Utilizing the DP178 and DP178 analog sequences described herein, the skilled artisan can readily compile DP178 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids of similar charge, size, and/or



hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids possessing  
5 dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The  
10 insertions may be made at the carboxy or amino terminal end of the DP178 or DP178 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that  
15 insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP178 (SEQ.ID:1) or DP178  
20 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to  
25 modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein  
30 regions either amino to or carboxy to the actual DP178 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP178  
35 region of the gp41 protein.

Deletions of DP178 (SEQ ID:1) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP178 or DP178-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are further described, below, in Section 5.3.

#### 5.2. DP107 AND DP107-LIKE PEPTIDES

Further, the peptides of the invention include peptides having amino acid sequences corresponding to DP107 analogs. DP107 is a 38 amino acid peptide which exhibits potent antiviral activity, and corresponds to residues 558 to 595 of HIV-1<sub>LAI</sub> transmembrane (TM) gp41 protein, as shown here:

NH<sub>2</sub>-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVEERYLKDQ-COOH  
(SEQ ID:25)

In addition to the full-length DP107 (SEQ ID:25) 38-mer, the peptides of the invention may include truncations of the DP107 (SEQ ID:25) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes

involving coiled-coil peptide structures. Truncations of DP107 (SEQ ID:25) peptides may comprise peptides of between 3 and 38 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 38-mer polypeptide), as shown in Tables II and IIA, below.

5 Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH<sub>2</sub>) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not

10 limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or

15 peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred

20 "X" or "Z" macromolecular group is a peptide group.

25

30

35

TABLE II  
DP107 (SEQ ID:25) CARBOXY TRUNCATIONS

```

X-NNL-Z
X-NNLL-Z
X-NNLLR-Z
5 X-NNLLRA-Z
X-NNLLRAI-Z
X-NNLLRAIE-Z
X-NNLLRAIEA-Z
X-NNLLRAIEAQ-Z
X-NNLLRAIEAQQ-Z
X-NNLLRAIEAQQH-Z
10 X-NNLLRAIEAQQHL-Z
X-NNLLRAIEAQQHLL-Z
X-NNLLRAIEAQQHLLQ-Z
X-NNLLRAIEAQQHLLQL-Z
X-NNLLRAIEAQQHLLQLT-Z
X-NNLLRAIEAQQHLLQLTV-Z
X-NNLLRAIEAQQHLLQLTVW-Z
X-NNLLRAIEAQQHLLQLTVWQ-Z
15 X-NNLLRAIEAQQHLLQLTVWQI-Z
X-NNLLRAIEAQQHLLQLTVWQIK-Z
X-NNLLRAIEAQQHLLQLTVWQIKQ-Z
X-NNLLRAIEAQQHLLQLTVWQIKQL-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQ-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQA-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQAR-Z
20 X-NNLLRAIEAQQHLLQLTVWQIKQLQARI-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARIL-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILA-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAV-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVE-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVER-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERY-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYL-Z
25 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLK-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKD-Z
X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-Z

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The one letter amino acid code is used.

Additionally,

30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IIA  
DP178 (SEQ ID:25) AMINO TRUNCATIONS

	X-KDQ-	Z
	X-LKDQ-	Z
5	X-YLKDQ-	Z
	X-RYLKDQ-	Z
	X-ERYLKDQ-	Z
	X-VERYLKDQ-	Z
	X-AVERYLKDQ-	Z
	X-LAVERYLKDQ-	Z
	X-ILAVERYLKDQ-	Z
	X-RILAVERYLKDQ-	Z
10	X-ARILAVERYLKDQ-	Z
	X-QARILAVERYLKDQ-	Z
	X-LQARILAVERYLKDQ-	Z
	X-QLQARILAVERYLKDQ-	Z
	X-KQLQARILAVERYLKDQ-	Z
	X-IKQLQARILAVERYLKDQ-	Z
	X-QIKQLQARILAVERYLKDQ-	Z
15	X-WQIKQLQARILAVERYLKDQ-	Z
	X-VWQIKQLQARILAVERYLKDQ-	Z
	X-TVWQIKQLQARILAVERYLKDQ-	Z
	X-LTVWQIKQLQARILAVERYLKDQ-	Z
	X-QLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LLQLTVWQIKQLQARILAVERYLKDQ-	Z
20	X-HLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-QHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-QQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-AQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-EAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-IEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-AIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-RAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
25	X-LLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-NLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z

The one letter amino acid code is used.

Additionally,

30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the invention also include DP107-like peptides. "DP107-like", as used herein, refers, first, to DP107 and DP107 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-107-like" refers to peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP107. The DP107-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP107-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP107-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP107 peptides of the invention. Utilizing the DP107 and DP107 analog sequences described herein, the skilled artisan can readily compile DP107 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids of similar charge, size, and/or

hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids possessing  
5 dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The  
10 insertions may be made at the carboxy or amino terminal end of the DP107 or DP107 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that  
15 insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP107 (SEQ.ID:25) or DP107  
20 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to  
25 modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein  
30 regions either amino to or carboxy to the actual DP107 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP107  
35 region of the gp41 protein.

Deletions of DP107 (SEQ ID:25) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP107 or DP107-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP107 and DP107 truncations are more fully described in Applicants' co-pending U.S. Patent Application Ser. No. 08/374,666, filed January 27, 1995, and which is incorporated herein by reference in its entirety. DP107 analogs are further described, below, in Section 5.3.

### 5.3. DP107 and DP178 ANALOGS

Peptides corresponding to analogs of the DP178, DP178 truncations, DP107 and DP107 truncation sequences of the invention, described, above, in Sections 5.1 and 5.2 may be found in other viruses, including, for example, non-HIV-1<sub>LAI</sub> enveloped viruses, non-enveloped viruses and other non-viral organisms.

The term "analog", as used herein, refers to a peptide which is recognized or identified via the 107x178x4, ALLMOTI5 and/or PLZIP search strategies discussed below. Further, such peptides may exhibit antifusogenic capability, antiviral activity, or the



ability to modulate intracellular processes involving coiled-coil structures.

Such DP178 and DP107 analogs may, for example, correspond to peptide sequences present in TM proteins of enveloped viruses and may, additionally correspond  
5 to peptide sequences present in non enveloped and non-viral organisms. Such peptides may exhibit antifusogenic activity, antiviral activity, most particularly antiviral activity which is specific to the virus in which their native sequences are found,  
10 or may exhibit an ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are peptides whose amino acid sequences are comprised of the amino acid sequences of peptide regions of, for example, other (*i.e.*, other  
15 than HIV-1<sub>LAI</sub>) viruses that correspond to the gp41 peptide region from which DP178 (SEQ ID:1) was derived. Such viruses may include, but are not limited to, other HIV-1 isolates and HIV-2 isolates. DP178 analogs derived from the corresponding gp41  
20 peptide region of other (*i.e.*, non HIV-1<sub>LAI</sub>) HIV-1 isolates may include, for example, peptide sequences as shown below.

25 NH<sub>2</sub>-YTNTIYTLLEESQNQQEKNEQEELLELDKWASLWNWF-COOH (DP-185; SEQ ID:3);

NH<sub>2</sub>-YTGIYNLLEESQNQQEKNEQEELLELDKWANLWNWF-COOH (SEQ ID:4);

30 NH<sub>2</sub>-YTSLIYSLLEKSQIQQEKNEQEELLELDKWASLWNWF-COOH (SEQ ID:5).

SEQ ID:3 (DP-185), SEQ ID:4, and SEQ ID:5 are derived from HIV-1<sub>SF2</sub>, HIV-1<sub>RF</sub>, and HIV-1<sub>MN</sub> isolates, respectively. Underlined amino acid residues refer to those residues that differ from the corresponding  
35 position in the DP178 (SEQ ID:1) peptide. One such

DP178 analog, DP-185 (SEQ ID:3), is described in the Example presented in Section 6, below, where it is demonstrated that DP-185 (SEQ ID:3) exhibits antiviral activity. The DP178 analogs of the invention may also include truncations, as described above. Further, the analogs of the invention modifications such those described for DP178 analogs in Section 5.1., above. It is preferred that the DP178 analogs of the invention represent peptides whose amino acid sequences correspond to the DP178 region of the gp41 protein, it is also contemplated that the peptides of the invention may, additionally, include amino sequences, ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178 amino acid sequence.

Striking similarities, as shown in FIG. 1, exist within the regions of HIV-1 and HIV-2 isolates which correspond to the DP178 sequence. A DP178 analog derived from the HIV-2<sub>NIH</sub> isolate has the 36 amino acid sequence (reading from amino to carboxy terminus):

NH<sub>2</sub>-LEANISQSLEQAQIQQEKMYELQKLNSWDVFTNWL-COOH (SEQ ID:7)

Table III and Table IV show some possible truncations of the HIV-2<sub>NIH</sub> DP178 analog, which may comprise peptides of between 3 and 36 amino acid residues (*i.e.*, peptides ranging in size from a tripeptide to a 36-mer polypeptide). Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH<sub>2</sub>) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; or a

covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached  
5 macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

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TABLE III

HIV-2<sub>NH2</sub> DP178 analog carboxy truncations.

	X-LEA-Z
	X-LEAN-Z
	X-LEANI-Z
	X-LEANIS-Z
5	X-LEANISQ-Z
	X-LEANISQS-Z
	X-LEANISQSL-Z
	X-LEANISQSLE-Z
	X-LEANISQSLEQ-Z
	X-LEANISQSLEQA-Z
	X-LEANISQSLEQAQ-Z
10	X-LEANISQSLEQAQI-Z
	X-LEANISQSLEQAQIQ-Z
	X-LEANISQSLEQAQIQQ-Z
	X-LEANISQSLEQAQIQQE-Z
	X-LEANISQSLEQAQIQQEK-Z
	X-LEANISQSLEQAQIQQEKN-Z
	X-LEANISQSLEQAQIQQEKNM-Z
	X-LEANISQSLEQAQIQQEKNMY-Z
15	X-LEANISQSLEQAQIQQEKNMYE-Z
	X-LEANISQSLEQAQIQQEKNMYEL-Z
	X-LEANISQSLEQAQIQQEKNMYELQ-Z
	X-LEANISQSLEQAQIQQEKNMYELQK-Z
	X-LEANISQSLEQAQIQQEKNMYELQKL-Z
	X-LEANISQSLEQAQIQQEKNMYELQKLN-Z
	X-LEANISQSLEQAQIQQEKNMYELQKLNS-Z
20	X-LEANISQSLEQAQIQQEKNMYELQKLNSW-Z
	X-LEANISQSLEQAQIQQEKNMYELQKLNSWD-Z
	X-LEANISQSLEQAQIQQEKNMYELQKLNSWDV-Z
	X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVF-Z
	X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFT-Z
	X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTN-Z
	X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNW-Z
25	X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IV

HIV-2<sub>NIH</sub> DP178 analog amino truncations.

	X-NWL-Z
	X-TNWL-Z
	X-FTNWL-Z
5	X-VFTNWL-Z
	X-DVFTNWL-Z
	X-WDVFTNWL-Z
	X-SWDVFTNWL-Z
	X-NSWDVFTNWL-Z
	X-LNSWDVFTNWL-Z
	X-KLNSWDVFTNWL-Z
	X-QKLNSWDVFTNWL-Z
10	X-LQKLNSWDVFTNWL-Z
	X-ELQKLNSWDVFTNWL-Z
	X-YELQKLNSWDVFTNWL-Z
	X-MYELQKLNSWDVFTNWL-Z
	X-NMYELQKLNSWDVFTNWL-Z
	X-KNMYELQKLNSWDVFTNWL-Z
	X-EKNMYELQKLNSWDVFTNWL-Z
15	X-QEKNMYELQKLNSWDVFTNWL-Z
	X-QQEKNMYELQKLNSWDVFTNWL-Z
	X-IQQEKNMYELQKLNSWDVFTNWL-Z
	X-QIQQEKNMYELQKLNSWDVFTNWL-Z
	X-AQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-QAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-EQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-LEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
20	X-SLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-QSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-SQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-ISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-NISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-ANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-EANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
25	X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

DP178 and DP107 analogs are recognized or identified, for example, by utilizing one or more of the 107x178x4, ALLMOTI5 or PLZIP computer-assisted search strategies described and demonstrated, below, in the Examples presented in Sections 9 through 16 and 19 through 25. The search strategy identifies additional peptide regions which are predicted to have structural and/or amino acid sequence features similar to those of DP107 and/or DP178.

The search strategies are described fully, below, in the Example presented in Section 9. While this search strategy is based, in part, on a primary amino acid motif deduced from DP107 and DP178, it is not based solely on searching for primary amino acid sequence homologies, as such protein sequence homologies exist within, but not between major groups of viruses. For example, primary amino acid sequence homology is high within the TM protein of different strains of HIV-1 or within the TM protein of different isolates of simian immunodeficiency virus (SIV). Primary amino acid sequence homology between HIV-1 and SIV, however, is low enough so as not to be useful. It is not possible, therefore, to find peptide regions similar to DP107 or DP178 within other viruses, or within non-viral organisms, whether structurally, or otherwise, based on primary sequence homology, alone.

Further, while it would be potentially useful to identify primary sequence arrangements of amino acids based on, for example, the physical chemical characteristics of different classes of amino acids rather than based on the specific amino acids themselves, such search strategies have, until now, proven inadequate. For example, a computer algorithm designed by Lupas et al. to identify coiled-coil propensities of regions within proteins (Lupas, A., et al., 1991 Science 252:1162-1164) is inadequate for

identifying protein regions analogous to DP107 or DP178.

Specifically, analysis of HIV-1 gp160 (containing both gp120 and gp41) using the Lupas algorithm does not identify the coiled-coil region within DP107. It does, however, identify a region within DP178 beginning eight amino acids N-terminal to the start of DP178 and ending eight amino acids from the C-terminus. The DP107 peptide has been shown experimentally to form a stable coiled coil. A search based on the Lupas search algorithm, therefore, would not have identified the DP107 coiled-coil region. Conversely, the Lupas algorithm identified the DP178 region as a potential coiled-coil motif. However, the peptide derived from the DP178 region failed to form a coiled coil in solution.

A possible explanation for the inability of the Lupas search algorithm to accurately identify coiled-coil sequences within the HIV-1 TM, is that the Lupas algorithm is based on the structure of coiled coils from proteins that are not structurally or functionally similar to the TM proteins of viruses, antiviral peptides (e.g. DP107 and DP178) of which are an object of this invention.

The computer search strategy of the invention, as demonstrated in the Examples presented below, in Sections 9 through 16 and 19 through 25, successfully identifies regions of proteins similar to DP107 or DP178. This search strategy was designed to be used with a commercially-available sequence database package, preferably PC/Gene.

A series of search motifs, the 107x178x4, ALLMOTI5 and PLZIP motifs, were designed and engineered to range in stringency from strict to broad, as discussed in this Section and in Section 9, with 107x178x4 being preferred. The sequences

identified via such search motifs, such as those listed in Tables V-XIV, below, potentially exhibit antifusogenic, such as antiviral, activity, may additionally be useful in the identification of antifusogenic, such as antiviral, compounds, and are  
5 intended to be within the scope of the invention.

Coiled-coiled sequences are thought to consist of heptad amino acid repeats. For ease of description, the amino acid positions within the heptad repeats are sometimes referred to as A through G, with the first  
10 position being A, the second B, etc. The motifs used to identify DP107-like and DP178-like sequences herein are designed to specifically search for and identify such heptad repeats. In the descriptions of each of the motifs described, below, amino acids enclosed by  
15 brackets , i.e., [], designate the only amino acid residues that are acceptable at the given position, while amino acids enclosed by braces, i.e., {}, designate the only amino acids which are unacceptable at the given heptad position. When a set of bracketed  
20 or braced amino acids is followed by a number in parentheses i.e., (), it refers to the number of subsequent amino acid positions for which the designated set of amino acids hold, e.g, a (2) means "for the next two heptad amino acid positions".

25 The ALLMOTI5 is written as follows:

{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-  
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-  
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-  
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-  
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-

30 Translating this motif, it would read: "at the first (A) position of the heptad, any amino acid residue except C, D, G, H, or P is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, or P is acceptable, at the fourth  
35 heptad position (D), any amino acid residue except C,



D, G, H, or P is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, or P is acceptable. This motif is designed to search for five consecutive heptad repeats (thus the repeat of the first line five times), meaning that it searches for 35-mer sized peptides. It may also be designed to search for 28-mers, by only repeating the initial motif four times. With respect to the ALLMOTI5 motif, a 35-mer search is preferred. Those viral (non-bacteriophage) sequences identified via such an ALLMOTI5 motif are listed in Table V, below, at the end of this Section. The viral sequences listed in Table V potentially exhibit antiviral activity, may be useful in the the identification of antiviral compounds, and are intended to be within the scope of the invention. In those instances wherein a single gene exhibits greater than one sequence recognized by the ALLMOTI5 search motif, the amino acid residue numbers of these sequences are listed under "Area 2", Area 3", etc. This convention is used for each of the Tables listed, below, at the end of this Section.

The 107x178x4 motif is written as follows:

[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-  
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-  
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-  
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-

Translating this motif, it would read: "at the first (A) position of the heptad, only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, M or P is acceptable, at the fourth position (D), only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, M or P is acceptable. This motif is designed to search for

four consecutive heptad repeats (thus the repeat of the first line four times), meaning that it searches for 28-mer sized peptides. It may also be designed to search for 35-mers, by repeating the initial motif five times. With respect to the 107x178x4 motif, a  
5 28-mer search is preferred.

Those viral (non-bacteriophage) sequences identified via such a 107x178x4 motif are listed in Table VI, below, at the end of this Section, with those viral (non-bacteriophage) sequences listed in  
10 Table VII, below at the end of this Section, being preferred.

The 107x178x4 search motif was also utilized to identify non-viral procaryotic protein sequences, as listed in Table VIII, below, at the end of this  
15 Section. Further, this search motif was used to reveal a number of human proteins. The results of this human protein 107x178x4 search is listed in Table IX, below, at the end of this Section. The sequences listed in Tables VIII and IX, therefore, reveal  
20 peptides which may be useful as antifusogenic compounds or in the identification of antifusogenic compounds, and are intended to be within the scope of the invention.

The PLZIP series of motifs are as listed in FIG.  
25 19. These motifs are designed to identify leucine zipper coiled-coil like heptads wherein at least one proline residue is present at some predefined distance N-terminal to the repeat. These PLZIP motifs find regions of proteins with similarities to HIV-1 DP178  
30 generally located just N-terminal to the transmembrane anchor. These motifs may be translated according to the same convention described above. Each line depicted in FIG. 19 represents a single, complete search motif. "X" in these motifs refers to any amino  
35 acid residue. In instances wherein a motif contains

two numbers within parentheses, this refers to a variable number of amino acid residues. For example, X (1,12) is translated to "the next one to twelve amino acid residues, inclusive; may be any amino acid".

5       Tables X through XIV, below, at the end of this Section, list sequences identified via searches conducted with such PLZIP motifs. Specifically, Table X lists viral sequences identified via PCTLZIP, P1CTLZIP and P2CTLZIP search motifs, Table XI lists  
10       viral sequences identified via P3CTLZIP, P4CTLZIP, P5CTLZIP and P6CTLZIP search motifs, Table XII lists viral sequences identified via P7CTLZIP, P8CTLZIP and P9CTLZIP search motifs, Table XIII lists viral  
15       sequences identified via P12LZIPC searches and Table XIV lists viral sequences identified via P23TLZIPC search motifs. The viral sequences listed in these tables represent peptides which potentially exhibit  
20       antiviral activity, may be useful in the identification of antiviral compounds, and are intended to be within the scope of the invention.

      The Examples presented in Sections 17, 18, 26 and 27 below, demonstrate that viral sequences identified via the motif searches described herein identify  
25       substantial antiviral characteristics. Specifically, the Example presented in Section 17 describes peptides with anti-respiratory syncytial virus activity, the Example presented in Section 18 describes peptides  
30       with anti-parainfluenza virus activity, the Example presented in Section 26 describes peptides with anti-measles virus activity and the Example presented in Section 27 describes peptides with anti-simian  
      immunodeficiency virus activity.

      The DP107 and DP178 analogs may, further, contain  
35       any of the additional groups described for DP178, above, in Section 5.1. For example, these peptides

may include any of the additional amino-terminal groups as described above for "X" groups, and may also include any of the carboxy-terminal groups as described, above, for "Z" groups.

5        Additionally, truncations of the identified DP107 and DP178 peptides are among the peptides of the invention. Further, such DP107 and DP178 analogs and DP107/DP178 analog truncations may exhibit one or more amino acid substitutions, insertion, and/or deletions. The DP178 analog amino acid substitutions, insertions  
10        and deletions, are as described, above, for DP178-like peptides in Section 5.1. The DP-107 analog amino acid substitutions, insertions and deletions are also as described, above, for DP107-like peptides in Section  
15        5.2.

      Tables XV through XXII, below, present representative examples of such DP107/DP178 truncations. Specifically, Table XV presents Respiratory Syncytial Virus F1 region DP107 analog carboxy truncations, Table XVI presents Respiratory  
20        Syncytial Virus F1 region DP107 analog amino truncations, Table XVII presents Respiratory Syncytial Virus F1 region DP178 analog carboxy truncations, Table XVIII presents Respiratory Syncytial Virus F1 region DP178 analog amino truncations, Table XIX  
25        presents Human Parainfluenza Virus 3 F1 region DP178 analog carboxy truncations, Table XX presents Human Parainfluenza Virus 3 F1 region DP178 analog amino truncations, Table XXI presents Human Parainfluenza Virus 3 F1 region DP107 analog carboxy truncations and  
30        Table XXII presents Human Parainfluenza Virus 3 F1 region DP107 analog amino truncations. Further, Table XXIII, below, presents DP107/DP178 analogs and analog truncations which exhibit substantial antiviral activity. These antiviral peptides are grouped  
35        according to the specific virus which they inhibit,

including respiratory syncytial virus, human  
parainfluenza virus 3, simian immunodeficiency virus  
and measles virus.

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TABLE V

ALLMOTIS SEARCH RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

PCGENE	ALLANTOIS	ALL Virens (de heterophaga)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
P19K TRV3	POTENTIAL 170 KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN P50)	113-151						
P19K TRV5	POTENTIAL 194 KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN 55N)	144-178	214-248	1045-1079	644-678	391-446	1135-1176	1135-1176
P33KD HSV6U	33 K KD PROTEIN	HERPES SIMPLEX VIRUS TYPE 6 (STRAIN UGANDA-1102)	228-262						
PAANT_HDVAM	DELTA ANTIGEN	HEPATITIS DELTA VIRUS (ISOLATE AMERICAN)	3-48	100-144					
PAANT_HDVB	DELTA ANTIGEN	HEPATITIS DELTA VIRUS (ISOLATE DJBO)	3-48	100-144					
PAANT_HDVT	DELTA ANTIGEN (ALPHA ANTIGEN)	HEPATITIS DELTA VIRUS (ISOLATE ITALIAN)	3-48	100-144					
PAANT_HDVLI	DELTA ANTIGEN	HEPATITIS DELTA VIRUS (ISOLATE JERANON-1)	3-48	100-144					
PAANT_HDVNI	DELTA ANTIGEN	HEPATITIS DELTA VIRUS (ISOLATE JAPANESE N-1)	3-48	100-144					
PAANT_HDVNI2	DELTA ANTIGEN	HEPATITIS DELTA VIRUS (ISOLATE JAPANESE N-2)	3-48	100-144					
PAANT_HDVNA	DELTA ANTIGEN	HEPATITIS DELTA VIRUS (ISOLATE NAJOUR)	3-48	100-144					
PAANT_HDVSI	DELTA ANTIGEN	HEPATITIS DELTA VIRUS (ISOLATE JAPANESE S-1)	1-49	100-144					
PAANT_HDVSI2	DELTA ANTIGEN	HEPATITIS DELTA VIRUS (ISOLATE JAPANESE S-2)	1-49	100-144					
PAANT_HDVSI3	DELTA ANTIGEN	HEPATITIS DELTA VIRUS (ISOLATE WOODCHUCK)	3-48	100-144					
PAANT_HDVW0	DELTA ANTIGEN	FOWLPOX VIRUS (ISOLATE IP-43)	71-110						
PATRI_F0WPM	ANTITHROMBIN-III HOMOLOG	VACCINIA VIRUS (STRAIN VR)	14-37	420-564	570-623				
PATIL_VACV	94 KD A-TYPE INCLUSION PROTEIN	VACCINIA VIRUS	423-525	571-565	571-623				
PATIL_VAVV	81 KD A-TYPE INCLUSION PROTEIN	VARIOLA VIRUS	304-345						
PATIL_HSV11	ALPHA TRANS-INDUCING FACTOR	HERPES SIMPLEX VIRUS (TYPE 1)	102-119	104-145					
PATIL_HSV1F	ALPHA TRANS-INDUCING FACTOR	HERPES SIMPLEX VIRUS (TYPE 1)	101-147	104-145					
PATIL_HSV1B	ALPHA TRANS-INDUCING FACTOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD-AP)	76-124	219-263					
PATIL_VACCC	POTENTIAL A-TYPE INCLUSION PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	79-124						
PATIL_VACCV	POTENTIAL A-TYPE INCLUSION PROTEIN	VACCINIA VIRUS	298-361	395-429					
PATIL_VZVD	ALPHA TRANS-INDUCING FACTOR	VARIOLA VIRUS	51-95						
PATIL_VACCV	POTENTIAL A-TYPE INCLUSION PROTEIN	VACCINIA VIRUS	178-219	324-381					
PATIL_HSV2	ALPHA TRANS-INDUCING PROTEIN (VMAW65)	HERPES SIMPLEX VIRUS (TYPE 2)	177-222	324-381					
PATIL_HSV2H	ALPHA TRANS-INDUCING PROTEIN (VMAW65)	HERPES SIMPLEX VIRUS (TYPE 2)	193-236						
PATIL_HSV2B	ALPHA TRANS-INDUCING PROTEIN	EQUINE HERPESVIRUS TYPE 1	241-289						
PATIL_VZVD	ALPHA TRANS-INDUCING PROTEIN	VARIOLA VIRUS	306-332						
PATIL_COWFX	A-TYPE INCLUSION PROTEIN	COWPOX VIRUS	14-37	425-526	572-629	1106-1150			
PBRL1_EBV	TRANSCRIPTION ACTIVATOR BR1F1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	90-131						
PCOAT_POVBA	COAT PROTEIN VP1	POLYOMAVIRUS BK	107-141						
PCOAT_POVBK	COAT PROTEIN VP1	POLYOMAVIRUS BK	107-141						
PCOAT_POVHA	COAT PROTEIN VP1	HAMSTER POLYOMAVIRUS	139-193						
PCOAT_SV40	COAT PROTEIN VP1	SIMIAN VIRUS 40	109-143						
PCOAT_BEDV	COAT PROTEIN VP2	RUDGERIGER FLEDDING DISEASE VIRUS	141-213						
PCOAL_POVBA	COAT PROTEIN VP2	POLYOMAVIRUS BK (STRAIN A5)	14-64	317-351					
PCOAL_POVBK	COAT PROTEIN VP2	POLYOMAVIRUS BK	14-64	317-351					
PCOAL_POVBO	COAT PROTEIN VP2	BOVINE POLYOMAVIRUS	35-76	153-216					
PCOAL_POVHA	COAT PROTEIN VP2	HAMSTER POLYOMAVIRUS	7-48	174-208					
PCOAL_POVIC	COAT PROTEIN VP2	POLYOMAVIRUS JC	14-64	231-267					
PCOAL_POVLY	COAT PROTEIN VP2	LYMPHOTROPIC POLYOMAVIRUS	14-78	156-206					
PCOAL_POVNO	COAT PROTEIN VP2	MOUSE POLYOMAVIRUS (STRAIN 1)	5-72	137-185					
PCOAL_POVNA	COAT PROTEIN VP2	MOUSE POLYOMAVIRUS	5-72	137-185					
PCOAL_POVNC	COAT PROTEIN VP2	MOUSE POLYOMAVIRUS	5-72	137-185					
PCOAL_POVAC	COAT PROTEIN VP2	MOUSE POLYOMAVIRUS	15-36	177-211					
PCOAL_SV40	COAT PROTEIN VP2	SIMIAN VIRUS 40	14-62	228-262	318-332				
PCOAT_ABMYW	COAT PROTEIN	ABUTLON MOSAIC VIRUS (ISOLATE WEST INDIA)	180-214						
PCOAT_ACLSV	COAT PROTEIN	APPLE CHLOROTIC LEAF SPOT VIRUS	154-188						
PCOAT_AEDBV	COAT PROTEIN VP1	AEDES DENSONUCLEOSIS VIRUS	243-284						
PCOAT_AMCV	COAT PROTEIN	ARTICHOKE MOTTLED CRINKLE VIRUS	36-70	100-134					
PCOAT_BLAY	COAT PROTEIN	BEAN LEAFROLL VIRUS	89-123						















PCGENE	ALLNOTIS	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
ELF1_RAB1	PROTEIN	YINUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PGAG_FU15V	GAG POLYPROTEIN	FUJINAMI SARCOMA VIRUS	57-94							
PGAG_GALV	GAG POLYPROTEIN	GIBBON APE LEUKEMIA VIRUS	391-444							
PGAG_HV1A2	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ARV25F2 ISOLATE)	87-133	294-328						
PGAG_HV1B1	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BIII10 ISOLATE)	90-131	292-326						
PGAG_HV1B5	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (III15 ISOLATE)	90-131	292-326						
PGAG_HV1B8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (III15 ISOLATE)	90-131	292-326						
PGAG_HV1C4	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-431 ISOLATE)	90-131	292-326						
PGAG_HV1E1	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ELI ISOLATE)	91-131	292-326						
PGAG_HV1H2	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (H102 ISOLATE)	90-131	292-326						
PGAG_HV1J3	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (H11 ISOLATE)	87-131	292-326						
PGAG_HV1R	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (IRC5F ISOLATE)	87-131	292-326						
PGAG_HV1MA	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (M14 ISOLATE)	90-131	292-326						
PGAG_HV1N5	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (N14 ISOLATE)	87-134	295-329						
PGAG_HV1N9	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NEW YORK-3 ISOLATE)	90-131	292-326						
PGAG_HV1OY	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE)	87-138	289-322						
PGAG_HV1P4	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (OVI1 ISOLATE)	90-131	292-326						
PGAG_HV1R8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (PV22 ISOLATE)	90-131	292-326						
PGAG_HV1U4	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RPHAT ISOLATE)	90-131	292-326						
PGAG_HV1W2	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (STRAIN UGANDAN)	87-137	292-326						
PGAG_HV1Z2	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (VNIJ2 ISOLATE)	292-326							
PGAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2CDC-214 ISOLATE)	87-132	293-327						
PGAG_PHA	RETROVIRUS-RELATED GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 3BLISY)	292-326							
PGAG_PMA	RETROVIRUS-RELATED GAG POLYPROTEIN	HAMSTER INTRACISTERNAL A-PARTICLE	91-137	320-357						
PGAG_SRY	GAG POLYPROTEIN	MURINE INTRACISTERNAL A-PARTICLE	67-103							
PGAG_PMA2	RETROVIRUS-RELATED GAG POLYPROTEIN	MURINE INTRACISTERNAL A-PARTICLE	80-133	138-172						
PGAG_SRY	GAG POLYPROTEIN	SHEEP PULMONARY ADENOMATOSIS VIRUS	470-504							
PGAG_MMTV8	GAG POLYPROTEIN	MURINE MAMMARY TUMOR VIRUS (STRAIN BR6)	81-151	156-190						
PGAG_MMTV9	GAG POLYPROTEIN	MURINE MAMMARY TUMOR VIRUS (STRAIN GR)	81-151	156-190						
PGAG_MPMV	GAG POLYPROTEIN	SIMIAN MASON-PFIZER VIRUS	222-260							
PGAG_SVLP	GAG POLYPROTEIN	ROUS SARCOMA VIRUS (STRAIN PRAGUE C)	57-94							
PGAG_SVLA	MAJOR COAT PROTEIN	SACCHARONYCES CERESIAE VIRUS L-A (SCV-L-A)	102-139							
PGAG_SFV1	GAG POLYPROTEIN	SIMIAN FOAMY VIRUS (TYPE 1)	128-177	178-416						
PGAG_SFV1L	GAG POLYPROTEIN	SIMIAN FOAMY VIRUS (TYPE 1 / STRAIN LK)	371-407	415-522						
PGAG_SIVAI	GAG POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGN153 ISOLATE)	302-336							
PGAG_SIVAI	GAG POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGN1 ISOLATE)	306-340							
PGAG_SIVAI	GAG POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGN1 / CLONE CR)	181-217	471-507						
PGAG_SIVAT	GAG POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (TYO-1 ISOLATE)	302-336							
PGAG_SIVCZ	GAG POLYPROTEIN	CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIVCPZ)	301-335							
PGAG_SIVGB	GAG POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE CR1)	161-204	221-367						
PGAG_SMSAV	GAG POLYPROTEIN	SIMIAN SARCOMA VIRUS	394-431							
PHL1_HSV11	PROBABLE HELICASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	172-206	769-820						
PHL1_HSV2H	PROBABLE HELICASE	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG5)	468-502	670-721						
PHL1_HSV3A	PROBABLE HELICASE	HERPES VIRUS SAMIRI (STRAIN 11)	158-203	413-449						
PHL1_VZV	PROBABLE HELICASE	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	445-517	782-821						
PHL1_CVBF	HEMAGGLUTININ-ESTERASE PRECURSOR	BOVINE CORONA VIRUS (STRAIN F15)	208-242							
PHL1_CVBL	HEMAGGLUTININ-ESTERASE PRECURSOR	BOVINE CORONA VIRUS (STRAIN LY-118)	208-242							
PHL1_CVBL	HEMAGGLUTININ-ESTERASE PRECURSOR	BOVINE CORONA VIRUS (STRAIN MEBIS)	208-242							
PHL1_CVBO	HEMAGGLUTININ-ESTERASE PRECURSOR	BOVINE CORONA VIRUS (STRAIN QUEBEC)	208-242							
PHL1_CVBOC	HEMAGGLUTININ-ESTERASE PRECURSOR	HUMAN CORONA VIRUS (STRAIN OC4)	208-242							
PHL1_LAUC	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/ALACHUA/268)	180-156							
PHL1_IABAN	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/BANGKOK/179)	364-440							
PHL1_IABUD	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN A/BUDDERGARHOKKAIDO/177)	378-454							









PCGENE	ALLNOTES	All Viruses (no better than 100%)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
FILENAME	PROTEIN	VIRUS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
PIEX9_ADE12	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 12	88-137							
PIEX9_ADE41	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 41	62-126							
PIEX9_ADE21	HEXON-ASSOCIATED PROTEIN	CANINE ADENOVIRUS TYPE 2	51-103							
PIEX9_ADE27	HEXON-ASSOCIATED PROTEIN	TUPAIA ADENOVIRUS	61-109							
PIEX_ADE01	HEXON PROTEIN	HUMAN ADENOVIRUS TYPE 2	341-386	583-624						
PIEX_ADE03	HEXON PROTEIN	HUMAN ADENOVIRUS TYPE 5	320-379	413-467						
PIEX_ADE04	HEXON PROTEIN	HUMAN ADENOVIRUS TYPE 40	303-352	408-449						
PIEX_ADE41	HEXON PROTEIN	HUMAN ADENOVIRUS TYPE 41	206-355	555-589						
PIEX_ADE43	HEXON PROTEIN	BOVINE ADENOVIRUS TYPE 41	201-346	385-419						
PIEX_COWPX	HOST RANGE PROTEIN	COWPOX VIRUS	220-395	455-489						
PIZB6_ASF17	LATE PROTEIN 12/28R	AFRICAN SWINE FEVER VIRUS (STRAIN BA11V)	110-151							
PIBMP_CAMV4	INCLUSION BODY MATRIX PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN D4)	3-44	378-419						
PIBMP_CAMV8	INCLUSION BODY MATRIX PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DARI 1)	379-420							
PIBMP_CAMV9	INCLUSION BODY MATRIX PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CH1-1841)	3-37	378-419						
PIBMP_CAMV10	INCLUSION BODY MATRIX PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DH1)	3-44	378-419						
PIBMP_CAMV11	INCLUSION BODY MATRIX PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN RDC)	3-37	378-419						
PIBMP_CAMV12	INCLUSION BODY MATRIX PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN S1JAPAN)	3-37	378-419						
PIBMP_CAMV13	INCLUSION BODY MATRIX PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN N78133)	3-37	378-419						
PIBMP_CAMV14	INCLUSION BODY MATRIX PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN PY147)	3-37	378-419						
PIBMP_CAMV15	INCLUSION BODY MATRIX PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	3-37	378-419						
PIBMP_CERV	INCLUSION BODY MATRIX PROTEIN	CARNATION ETCHED RING VIRUS	3-37							
PIBMP_DAVD	INCLUSION BODY MATRIX PROTEIN	FIGWORT MOSAIC VIRUS (STRAIN DXS)	3-37	372-406						
PIBMP_SODAV	INCLUSION BODY MATRIX PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	1-48	132-179						
PIBMP_HCMV1	PROBABLE PROCESSING AND TRANSPORT PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	51-98	290-324	498-532					
PIBMP_HSV11	PROCESSING AND TRANSPORT PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	331-365							
PIBMP_HSV12	PROCESSING AND TRANSPORT PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN ANGELOTTI)	331-365							
PIBMP_HSV13	PROCESSING AND TRANSPORT PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN F)	324-362							
PIBMP_HSV14	PROBABLE PROCESSING AND TRANSPORT PROTEIN	BOVINE HERPESVIRUS TYPE 2 (STRAIN BMV)	466-500							
PIBMP_HSV15	PROBABLE PROCESSING AND TRANSPORT PROTEIN	HERPESVIRUS TYPE 1 (ISOLATE HV535A)	241-375							
PIBMP_HSV16	PROBABLE PROCESSING AND TRANSPORT PROTEIN	HERPESVIRUS TYPE 1 (ISOLATE HV535A)	38-99	361-395						
PIBMP_HSV17	PROBABLE PROCESSING AND TRANSPORT PROTEIN	MURINE CYTOMEGALOVIRUS (STRAIN SMITH)	60-112	290-340						
PIBMP_HSV18	PROBABLE PROCESSING AND TRANSPORT PROTEIN	PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / DECKE)	299-333	303-337						
PIBMP_HSV19	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA)	190-224							
PIBMP_HSV20	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	BOVINE HERPESVIRUS TYPE 1 (STRAIN K22)	190-224							
PIBMP_HSV21	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	MAREK'S DISEASE HERPESVIRUS (STRAIN GA)	1022-1036							
PIBMP_HSV22	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	202-241							
PIBMP_HSV23	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	202-241							
PIBMP_HSV24	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	241-275							
PIBMP_HSV25	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	282-316							
PIBMP_HSV26	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	192-229							
PIBMP_HSV27	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	EQUINE HERPESVIRUS TYPE 4 (STRAIN 1942)	87-121							
PIBMP_HSV28	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	99-133							
PIBMP_HSV29	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	48-85							
PIBMP_HSV30	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	13-47							
PIBMP_HSV31	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	74-162							
PIBMP_HSV32	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	FELINE SARCOMA VIRUS (STRAIN HARDY-ZUCKERMAN 2)	280-314							
PIBMP_HSV33	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	ABELSON MURINE LEUKEMIA VIRUS	217-251							
PIBMP_HSV34	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	AKT8 MURINE LEUKEMIA VIRUS	172-227							
PIBMP_HSV35	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	FELINE SARCOMA VIRUS (STRAIN GARDNER-ARNSTEIN)	21-64							
PIBMP_HSV36	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	FELINE SARCOMA VIRUS (STRAIN GARDNER-ARNSTEIN)	210-232							
PIBMP_HSV37	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	FELINE SARCOMA VIRUS (STRAIN MCDONOUGH)	313-362							
PIBMP_HSV38	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PROTEIN	AVIAN SARCOMA VIRUS (STRAIN PC11)	65-99							

PGENE	ALLNOTIS	ALL Viruses (not bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7
FILENAME	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7
PKFAS_FUJIV	TYROSINE-PROTEIN KINASE TRANSFORMING PROT	FUJINAMI SARCONIA VIRUS	65-90		152-231				
PKITHI_ADEPV	THYMIDINE KINASE	ANISACTA MOORELINTONIOPOXVIRUS	47-81						
PKITHI_CAPVK	THYMIDINE KINASE	CAPRIOPOXVIRUS (STRAIN KS-1)	28-82						
PKITHI_EBV	THYMIDINE KINASE	EPSTEIN-BARR VIRUS (STRAIN B95-4)	228-262						
PKITHI_HSV11	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	431-472						
PKITHI_HSV12	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN CL101)	90-124						
PKITHI_HSV13	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN IFEM)	90-124						
PKITHI_HSV14	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN KOS)	90-124						
PKITHI_HSV15	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN SC16)	90-124						
PKITHI_HSV16	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN 11)	91-125						
PKITHI_HSV17	THYMIDINE KINASE	BOVINE HERPES VIRUS TYPE 3 (STRAIN WC11)	616-663						
PKITHI_HSV18	THYMIDINE KINASE	EQUINE HERPES VIRUS TYPE 4 (STRAIN 1942)	178-219						
PKITHI_HSV19	THYMIDINE KINASE	EQUINE HERPES VIRUS TYPE 1 (STRAIN AD47)	178-210						
PKITHI_HSV20	THYMIDINE KINASE	FELINE HERPES VIRUS (FELV) (STRAIN 1)	180-214						
PKITHI_HSV21	THYMIDINE KINASE	MARMOSET HERPES VIRUS	32-86						
PKITHI_HSV22	THYMIDINE KINASE	HERPES VIRUS SAIMIRI (STRAIN 11)	337-389						
PKITHI_HSV23	THYMIDINE KINASE	PSEUDORABIES VIRUS (STRAIN NIA-3)	161-202						
PKITHI_HSV24	THYMIDINE KINASE	AVIAN RETROVIRUS MH2	69-103						
PKITHI_HSV25	THYMIDINE KINASE	ICTALURID HERPES VIRUS 1	190-224						
PKITHI_HSV26	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	57-91		231-315				
PKITHI_HSV27	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	487-528		597-631				
PKITHI_HSV28	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	11-45						
PKITHI_HSV29	THYMIDINE KINASE	MORINE SARCONIA VIRUS M11	127-168						
PKITHI_HSV30	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	127-168						
PKITHI_HSV31	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN WR)	123-171						
PKITHI_HSV32	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	142-181						
PKITHI_HSV33	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN WR)	147-181						
PKITHI_HSV34	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	169-203						
PKITHI_HSV35	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN L-197)	116-170						
PKITHI_HSV36	THYMIDINE KINASE	VARIOLA VIRUS	169-203						
PKITHI_HSV37	THYMIDINE KINASE	AVIAN SARCONIA VIRUS (STRAIN UR)	111-145						
PKITHI_HSV38	THYMIDINE KINASE	AVIAN RETROVIRUS RFLJ0	15-66						
PKITHI_HSV39	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN WR)	135-169						
PKITHI_HSV40	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN Y7)	174-223						
PKITHI_HSV41	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 2	441-475						
PKITHI_HSV42	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 3	223-264						
PKITHI_HSV43	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 40	191-232		408-442				
PKITHI_HSV44	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 41	199-233						
PKITHI_HSV45	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 2	238-284						
PKITHI_HSV46	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 3	238-284						
PKITHI_HSV47	THYMIDINE KINASE	EPSTEIN-BARR VIRUS (STRAIN B95-4)	144-179						
PKITHI_HSV48	THYMIDINE KINASE	SHOPE FIBROMA VIRUS (STRAIN KASZA)	54-152						
PKITHI_HSV49	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	1-41		623-657				
PKITHI_HSV50	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN WR)	1-41		623-657				
PKITHI_HSV51	THYMIDINE KINASE	VARIOLA VIRUS	1-39		623-657				
PKITHI_HSV52	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	72-137		245-286				
PKITHI_HSV53	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN WR)	72-137		245-286				
PKITHI_HSV54	THYMIDINE KINASE	VARIOLA VIRUS	72-137		245-286				
PKITHI_HSV55	THYMIDINE KINASE	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	116-157						
PKITHI_HSV56	THYMIDINE KINASE	ODONTOLISSUM KINGSPOT VIRUS	51-90						
PKITHI_HSV57	THYMIDINE KINASE	PEPPER MILD MOTTLE VIRUS (STRAIN SPAIN)	26-66						
PKITHI_HSV58	THYMIDINE KINASE	TOBACCO MILD GREEN MOSAIC VIRUS (TANV STRAIN US)	29-66						

PCGENE	ALLNOTIS	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
PHOV_P1MYTO	MOVEMENT PROTEIN	TOBACCO MOSAIC VIRUS (STRAIN TONATOL)	37-66					
PHOV_P1MYVA	MOVEMENT PROTEIN	TOBACCO MOSAIC VIRUS (STRAIN LUIA)	37-80					
PHOV_P1MYVL	MOVEMENT PROTEIN	TOBACCO MOSAIC VIRUS (STRAIN LUI)	37-80					
PHOV_P1MYV	MOVEMENT PROTEIN	CHLORELLA VIRUS NC-1A	272-236					
PHOV_P1MYV	MODIFICATION METHYLASE CYBII	PARAMECILIUM BURSARIA CILLORELLA VIRUS I	116-164					
PHOV_P1MYV	MODIFICATION METHYLASE CYBII	AVIAN MYELOCYTOMATOSIS VIRUS CMII	229-266	173-419				
PHOV_P1MYV	MYC TRANSFORMING PROTEIN	AVIAN MYELOCYTOMATOSIS VIRUS NC29	230-267	176-420				
PHOV_P1MYV	MYC TRANSFORMING PROTEIN	AVIAN MYELOCYTOMATOSIS VIRUS HBI	230-267	176-420				
PHOV_P1MYV	MYC TRANSFORMING PROTEIN	AVIAN RETROVIRUS MIRE21	377-421					
PHOV_P1MYV	MYC TRANSFORMING PROTEIN	AVIAN RETROVIRUS OK10	224-261	170-414				
PHOV_P1MYV	MYC TRANSFORMING PROTEIN	FELINE LEUKEMIA VIRUS	393-437					
PHOV_P1MYV	MYC TRANSFORMING PROTEIN	FELINE LEUKEMIA VIRUS FTI	393-437					
PHOV_P1MYV	MYC TRANSFORMING PROTEIN	MURINE CORONA VIRUS MIV (STRAIN A59)	12-46					
PHOV_P1MYV	MYC TRANSFORMING PROTEIN	AINO VIRUS	177-211					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	BERNE VIRUS	46-83	122-156				
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A51008)	62-108	161-200	142-183			
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	BUNYAVIRUS GERMISTON	176-228					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	BUNYAVIRUS LA CROSSE	176-229					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	BUNYAVIRUS SNOWSHOE HARE	176-229					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	BUNYAVIRUS VIRUS	175-228					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	CRIMEAN-CONGO HEMORRHAGIC FEVER VIRUS (ISOLATE CAMO)	223-206	427-461				
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	CANINE DISTEMPER VIRUS (STRAIN ONDERS TEPPOKT)	137-174	176-217	154-402			
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	CHANDIPURA VIRUS (STRAIN 1633114)	40-84	321-369				
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	BOVINE CORONA VIRUS (STRAIN F15)	149-183					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	BOVINE CORONA VIRUS (STRAIN MEDUS)	149-183					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	CANINE ENTERIC CORONA VIRUS (STRAIN K378)	165-227					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	CANINE ENTERIC CORONA VIRUS (STRAIN OC4)	149-183					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	HUMAN CORONA VIRUS (STRAIN JIN)	12-46					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	MURINE CORONA VIRUS MIV (STRAIN JIN)	12-46					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONA VIRUS (S)	149-206					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONA VIRUS (S)	165-227					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	PORCINE RESPIRATORY CORONA VIRUS (STRAIN 86/137004 / BRU)	149-228					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	PORCINE RESPIRATORY CORONA VIRUS (STRAIN RM4)	149-228					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	RAT CORONA VIRUS (STRAIN 881)	12-46					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	TURKEY ENTERIC CORONA VIRUS	149-183					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	DUGBE VIRUS	230-206					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	FELINE INFECTIOUS PERITONITIS VIRUS (STRAIN 76-1146)	151-206					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	HANTAN VIRUS (STRAIN 76-118)	1-35	40-74	333-381			
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	HANTAN VIRUS (ISOLATE IC280)	237-297					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN)	62-145	161-200	248-303	342-380		
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	62-145	161-200	248-303	342-380		
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	HUMAN INFECTIOUS BRONCHITIS VIRUS (STRAIN GRAY)	186-227					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN KIB353)	186-220					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	JORDAN ARENA VIRUS	96-151					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	LASSA VIRUS (STRAIN GA391)	65-113	126-174				
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	LASSA VIRUS (STRAIN JOSIAH)	65-113	122-174	467-504			
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	LACTATE DEHYDROGENASE-ELEVATING VIRUS	3-40					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	LYMPHOCTIC CHLOROMENINGITIS VIRUS (STRAIN ABALSTRON)	45-117	460-497				
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	LYMPHOCTIC CHLOROMENINGITIS VIRUS (STRAIN WE)	45-117	460-497				
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	MAGUARI VIRUS	175-228					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	MEASLES VIRUS (STRAIN EDINBURGH)	188-226					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	MEASLES VIRUS (STRAIN HALL)	188-226					
PHOV_P1MYV	NUCLEOCAPSID PROTEIN	MEASLES VIRUS (STRAIN IP-3 CA)	188-226					

PGENE	ALLNOTES	All Virus (no description)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PNCAP_NEASY	NUCLEOCAPSID PROTEIN	MEASLES VIRUS (STRAIN YASAGATA-1)	188-226	363-411					
PNCAP_MOPFI	NUCLEOCAPSID PROTEIN	MOPEIA VIRUS	65-106	471-503					
PNCAP_MUMPI1	NUCLEOCAPSID PROTEIN	MUMPS VIRUS (STRAIN SBL-1)	214-235	500-514					
PNCAP_MUMPI4	NUCLEOCAPSID PROTEIN	MUMPS VIRUS (STRAIN NYAIARA VACCINE)	214-235		317-392				
PNCAP_PFIH	NUCLEOCAPSID PROTEIN	PROSPECT HILL VIRUS	1-35	40-74					
PNCAP_PFIHC	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C19)	212-272	441-510					
PNCAP_PFIHW	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN WASHINGTON1957)	212-272	441-510					
PNCAP_PFIHT	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIHARA)	214-266	344-378					
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TOSHIHARA)	200-403	446-490					
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 47885)	83-135	208-266		144-403			
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIHARA)	58-94	191-267					
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 4B VIRUS (STRAIN TOSHIHARA)	58-94	191-267					
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA 4C VIRUS (STRAIN 68-333)	65-112						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	PICHINDE ARENAY VIRUS	71-116	325-339					
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	PIRY VIRUS	1-35	40-75	317-392				
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	PUUMALA VIRUS (STRAIN HALLNAS 11)	1-35	40-75	317-392				
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	PUUMALA VIRUS (STRAIN SOTKANO)	1-35	40-75	317-392				
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	PUUMALA VIRUS (STRAIN SOTKANO)	91-141	248-303	144-403				
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	PUUMALA VIRUS (STRAIN SOTKANO)	131-167						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	RAHIES VIRUS (STRAIN AVOI)	212-272	345-404					
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	SENDAL VIRUS (STRAIN 2/HOST MUTANTS)	212-272	345-404					
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	SENDAL VIRUS (STRAIN ENDERS)	212-272	345-404					
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	SENDAL VIRUS (STRAIN 2)	212-272	345-404					
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	SEOL VIRUS (STRAIN SR-11)	1-35	40-74	317-381				
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	SIMIAN VIRUS 41	212-267	372-406	418-466				
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	SONCHUS YELLOW NET VIRUS	312-366						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	TACARIBE VIRUS	50-84	210-264					
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	TOSCARA VIRUS	212-249						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	TOMATO SPOTTED WILT VIRUS (BRAZILIAN ISOLATE CPNII/HR)	79-120						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	TOMATO SPOTTED WILT VIRUS (HAWAIIAN ISOLATE)	79-120						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	TOMATO SPOTTED WILT VIRUS (STRAIN LJ)	79-120						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	UUKUNIEMI VIRUS	31-102						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	VIRAL HEMORRHAGIC SEPTICEMIA VIRUS (STRAIN 07-71)	249-325						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	VIRAL HEMORRHAGIC SEPTICEMIA VIRUS (STRAIN MAKAI)	143-180	249-325					
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	VESICULAR STOMATITIS VIRUS (SEROTYPE INDIANA/STRAIN C42-108)	67-115						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	VESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY/STRAIN 67-115)	42-115						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	VESICULAR STOMATITIS VIRUS (STRAIN SAN JUAN)	2-48						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE BEN)	7-41						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194)	112-160						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	109-150						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE SOLIS)	108-149						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	96-140						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM/CLONE GR)	9-43	212-267					
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (F316/SNH4 ISOLATE)	9-43						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/BLACK DUCK/AUSTRALIA/702/71/81)	33-74						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/CANAL/INDONESIA/82)	50-91						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/CHICKEN/INDONESIA/1370/70)	349-383						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/CHICKEN/INDONESIA/1370/70)	349-383						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/CHICKEN/INDONESIA/1370/70)	14-48						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/CHICKEN/INDONESIA/1370/70)	14-48						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/CHICKEN/INDONESIA/1370/70)	10-47						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/CHICKEN/INDONESIA/1370/70)	5-44						
PNCAP_PFIH4	NUCLEOCAPSID PROTEIN	INFLUENZA A VIRUS (STRAIN A/CHICKEN/INDONESIA/1370/70)	50-91						





PCGENE	ALL MOTIFS	All Virus (no bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7
FILE NAME	PROTEIN	VIRUS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7
PPOLG_HCVH4	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IC-1)	364-398						
PPOLG_HCVH7	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE ICV-476)	364-398						
PPOLG_HCVH8	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IC177)	316-370						
PPOLG_HCVH9	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IC178)	248-282						
PPOLG_HCVI2	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE ICV-48)	352-398						
PPOLG_HCVI3	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IC-12)	352-398						
PPOLG_HCVI6	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IC-15)	364-398						
PPOLG_HCVI7	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IC-16)	364-401	1716-1750	2082-2116				
PPOLG_HCVI8	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IC-17)	364-398						
PPOLG_HCVI9	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IC-18)	364-398	1716-1750	2082-2116	2468-2502	2538-2572		
PPOLG_HCVI10	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE JAPANESE)	357-403	2311-2365					
PPOLG_HCVI11	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IC-17)	352-398	2311-2365					
PPOLG_HCVI12	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE TAIWAN)	352-398	2318-2365	2444-2503				
PPOLG_HCVI13	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IC-17)	2-43	101-135	203-237	870-904	1021-1055	1117-1151	
PPOLG_HCVI14	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN 43C)	2-43	101-135	203-237	870-904	1021-1055	1117-1151	
PPOLG_HCVI15	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN 18F)	2-43	101-135	203-237	870-904	1021-1055	1117-1151	
PPOLG_HCVI16	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN CRJ26)	2-43	101-135	203-237	870-904	1021-1055	1117-1151	
PPOLG_HCVI17	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN GA16)	2-43	101-135	203-237	870-904	1021-1055	1117-1151	
PPOLG_HCVI18	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN IC1-17)	80-114	182-216					
PPOLG_HCVI19	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN LA)	2-43	101-135	203-237	870-904	1021-1055	1117-1151	
PPOLG_HCVI20	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN M8B)	2-43	101-135	203-237	870-904	1021-1055	1117-1151	
PPOLG_HCVI21	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN AGN1-27)	2-43	101-135	203-237	870-904	1021-1055	1117-1151	
PPOLG_HCVI22	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN CY-145)	2-43	101-135	203-237	870-904	1021-1055	1117-1151	
PPOLG_HCVI23	GENOME POLYPROTEIN	HUMAN RHINOVIRUS 14 (HRV-14)	1020-1034	1393-1427	1479-1513	1877-1920			
PPOLG_HCVI24	GENOME POLYPROTEIN	HUMAN RHINOVIRUS 1A (HRV-1A)	362-396						
PPOLG_HCVI25	GENOME POLYPROTEIN	HUMAN RHINOVIRUS 1B (HRV-1B)	387-421	663-694	1131-1168				
PPOLG_HCVI26	GENOME POLYPROTEIN	HUMAN RHINOVIRUS 2 (HRV-2)	856-897	1176-1169	1552-1593				
PPOLG_HCVI27	GENOME POLYPROTEIN	HUMAN RHINOVIRUS 89 (HRV-89)	1566-1607						
PPOLG_HCVI28	GENOME POLYPROTEIN	HUMAN ENTEROVIRUS 70 (STRAIN 1670/71)	359-397	976-917	1032-1088	1403-1441	1896-1934		
PPOLG_HCVI29	STRUCTURAL POLYPROTEIN	AYAN INFECTION BURSAL DISEASE VIRUS (STRAIN OIF)	134-168	230-291	475-524				
PPOLG_HCVI30	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN SA-14)	74-122	211-256	539-576	980-1014	1409-1450	2463-2497	2719-2777
PPOLG_HCVI31	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN SA(V))	3322-3359	3387-3428					2782-2823
PPOLG_HCVI32	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN JAOAR5982)	74-122	211-256	539-576	980-1014	1409-1450	2463-2497	2719-2777
PPOLG_HCVI33	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN NAKAYAMA)	74-122	211-256	539-576	980-1014	1409-1450	2463-2497	2719-2777
PPOLG_HCVI34	GENOME POLYPROTEIN	KUNIN VIRUS (STRAIN MR046(C))	74-122	211-256	539-576	980-1014	1409-1450	2463-2497	2719-2777
PPOLG_HCVI35	GENOME POLYPROTEIN	LANGAT VIRUS (STRAIN TP21)	68-102	431-465	962-996	1431-1472	1972-1966	2356-2391	2967-3001
PPOLG_HCVI36	GENOME POLYPROTEIN	LANGAT VIRUS (STRAIN YELANTSEV)	3102-3145						
PPOLG_HCVI37	GENOME POLYPROTEIN	LOUPING ILL VIRUS (LI)	68-102	431-465					
PPOLG_HCVI38	GENOME POLYPROTEIN	LOUPING ILL VIRUS (STRAIN SB 18)	68-123	231-272	411-465				
PPOLG_HCVI39	GENOME POLYPROTEIN	MOSQUITO CELL FUSING AGENT (CFA FLAVIVIRUS)	131-183						
PPOLG_HCVI40	GENOME POLYPROTEIN	MURRAY VALLEY ENCEPHALITIS VIRUS	80-114	908-942	2049-2087	2610-2689	3016-3055	3290-3341	
PPOLG_HCVI41	GENOME POLYPROTEIN	ORINOTHALIM MOSAIC VIRUS	67-115	209-253	813-887	979-1013	1408-1449		
PPOLG_HCVI42	GENOME POLYPROTEIN	PEPPER MOTTLE VIRUS (CALIFORNIA ISOLATE)	481-515	946-984	1072-1106				
PPOLG_HCVI43	GENOME POLYPROTEIN	POLIOVIRUS TYPE 1 (STRAIN MANONEV)	55-100	207-248	377-411	704-738	872-907	1021-1035	1167-1201
PPOLG_HCVI44	GENOME POLYPROTEIN	POLIOVIRUS TYPE 1 (STRAIN SABIN)	1488-1539	1783-1821	1948-1982	2202-2236	2405-2439	2605-2639	3003-3037
PPOLG_HCVI45	GENOME POLYPROTEIN	POLIOVIRUS TYPE 2 (STRAIN LANSING)	9-43	1046-1101	1414-1448	1506-1548	1806-1840	1902-1947	
PPOLG_HCVI46	GENOME POLYPROTEIN		9-43	899-933	1047-1102	1415-1449	1501-1549	1610-1651	1808-1842
PPOLG_HCVI47	GENOME POLYPROTEIN		9-43	897-931	1045-1100	1413-1447	1502-1547	1608-1649	1808-1842
PPOLG_HCVI48	GENOME POLYPROTEIN								1902-1947



PCGENE	ALLNOTIS	All Viruses (no bacteriophage.gst)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PPOLG_P0L1J	GENOME POLYPROTEIN	POLIOVIRUS TYPE 1 (STRAIN W-2)	897-131	1003-1100	1413-1447	1502-1547	1601-1649	1806-1840	1901-1947	
PPOLG_P0L1L	GENOME POLYPROTEIN	POLIOVIRUS TYPE 1 (STRAIN 21127)	9-43	896-930	1044-1098	1412-1446	1498-1546	1607-1648	1805-1839	1901-1946
PPOLG_P0V1D	GENOME POLYPROTEIN	POLIOVIRUS TYPE 1 (STRAINS PILEON7 AND PILEON 12A) (JB)	9-43	896-930	1044-1098	1412-1446	1498-1546	1607-1648	1805-1839	1901-1946
PPOLG_P0V1E	GENOME POLYPROTEIN	PLUM POX POTVIRUS (STRAIN D)	164-208	441-503	728-769	815-867	921-955	1741-1782		
PPOLG_P0V1A	GENOME POLYPROTEIN	PLUM POX POTVIRUS (STRAIN EL ANAR)	116-157	784-818	1146-1197					
PPOLG_P0V1H	GENOME POLYPROTEIN	PLUM POX POTVIRUS (ISOLATE NAT)	164-208	403-437	722-768	814-873	920-954	1740-1781		
PPOLG_P0V1P	GENOME POLYPROTEIN	PLUM POX POTVIRUS (STRAIN RANKOVIC)	164-208	403-437	722-768	814-873	920-954	1740-1781		
PPOLG_P0V1W	GENOME POLYPROTEIN	PAPAYA RINGSPOT VIRUS (STRAIN P MUTANT HA)	68-102	431-468						
PPOLG_P0V1V	GENOME POLYPROTEIN	PAPAYA RINGSPOT VIRUS (STRAIN P MUTANT HA 5-1)	375-359							
PPOLG_P0V1C	GENOME POLYPROTEIN	PAPAYA RINGSPOT VIRUS (STRAIN W)	375-359							
PPOLG_P0V1U	GENOME POLYPROTEIN	PEA SEED-BORNE MOSAIC VIRUS (STRAIN DPDI)	253-315	355-389	579-589	935-976	984-1018	1080-1177	1588-1627	1808-1860
PPOLG_P0V1T	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN C)	1971-2015	2379-2413	2712-2746	2870-2907				
PPOLG_P0V1N	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN HUNGARIAN)	131-196	701-735	802-856					
PPOLG_P0V1O	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN N)	144-181	701-735	802-863	901-949	1401-1441	1492-1526	1728-1772	1777-1818
PPOLG_P0V1S	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN O)	2272-2306							
PPOLG_P0V1B	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN O)	140-196	211-245	701-735	802-863	1401-1441	1492-1526	1728-1772	1777-1818
PPOLG_P0V1T	GENOME POLYPROTEIN	PASSIONFRUIT WOOLINESS VIRUS (STRAIN SEVERE)	1929-1970							
PPOLG_P0V1V	GENOME POLYPROTEIN	PASSIONFRUIT WOOLINESS VIRUS (STRAIN TIP BRIGHT)	201-217	211-245	701-735	802-856				
PPOLG_P0V1W	GENOME POLYPROTEIN	PASSIONFRUIT WOOLINESS VIRUS (ISOLATE P-121)	203-237							
PPOLG_P0V1X	GENOME POLYPROTEIN	ST. LOUIS ENCEPHALITIS VIRUS (STRAIN MS1-7)	194-228	1111-1172	1379-1413	1838-1899	1930-1991	2703-2737		
PPOLG_P0V1Y	GENOME POLYPROTEIN	SWINE VESICULAR DISEASE VIRUS (STRAIN 107 76)	106-143	673-707	739-773	975-1009	1404-1438			
PPOLG_P0V1Z	GENOME POLYPROTEIN	SWINE VESICULAR DISEASE VIRUS (STRAIN LK62/72)	15-49	1034-1070	1379-1413	1890-1924				
PPOLG_P0V1A	GENOME POLYPROTEIN	TICK-BORNE ENCEPHALITIS VIRUS (STRAIN SOFIN)	15-49	1034-1070	1379-1413	1890-1924				
PPOLG_P0V1B	GENOME POLYPROTEIN	TICK-BORNE ENCEPHALITIS VIRUS (WESTERN SUBTYPE)	68-140	231-272	471-465	1158-1192	1431-1472	1929-1966	2182-2216	2335-2390
PPOLG_P0V1C	GENOME POLYPROTEIN	TICK-BORNE ENCEPHALITIS VIRUS (WESTERN SUBTYPE)	2965-2999	3051-3092	3100-3143					
PPOLG_P0V1D	GENOME POLYPROTEIN	TICK-BORNE ENCEPHALITIS VIRUS (WESTERN SUBTYPE)	68-140	231-272	471-465	1158-1192	1431-1472	1929-1966	2182-2216	2335-2390
PPOLG_P0V1E	GENOME POLYPROTEIN	TICK-BORNE ENCEPHALITIS VIRUS (WESTERN SUBTYPE)	3003-3017	3053-3094	3102-3145					
PPOLG_P0V1F	GENOME POLYPROTEIN	TICK-BORNE ENCEPHALITIS VIRUS (WESTERN SUBTYPE)	71-124	166-232	540-584	720-792	823-923	1148-1192	1416-1460	1494-1535
PPOLG_P0V1G	GENOME POLYPROTEIN	THEILER'S MURINE ENCEPHALOMYELITIS VIRUS (STRAIN BEAN)	1668-1702	1745-1781	1792-1826	2395-2434	2707-2821			
PPOLG_P0V1H	GENOME POLYPROTEIN	THEILER'S MURINE ENCEPHALOMYELITIS VIRUS (STRAIN DA)	1306-1340	1483-1518	1601-1635					
PPOLG_P0V1I	GENOME POLYPROTEIN	THEILER'S MURINE ENCEPHALOMYELITIS VIRUS (STRAIN DVII)	1304-1338	1481-1516	1599-1663					
PPOLG_P0V1J	GENOME POLYPROTEIN	THEILER'S MURINE ENCEPHALOMYELITIS VIRUS (STRAIN DVII)	1306-1340	1483-1518	1601-1635					
PPOLG_P0V1K	GENOME POLYPROTEIN	TOBACCO VEIN MOTTLING VIRUS	216-239	314-363	494-528	768-839	1443-1477			
PPOLG_P0V1L	GENOME POLYPROTEIN	TOBACCO VEIN MOTTLING VIRUS	34-68	409-449	667-704	761-813	851-885	969-1017	1031-1072	1643-1677
PPOLG_P0V1M	GENOME POLYPROTEIN	WATERMELON MOSAIC VIRUS II	1686-1725	2316-2374	2701-2749	2814-2848				
PPOLG_P0V1N	GENOME POLYPROTEIN	WEST NILE VIRUS	68-103	202-236						
PPOLG_P0V1O	GENOME POLYPROTEIN	WEST NILE VIRUS	74-108	207-231	847-881	973-1007	1413-1447	2461-2495	2533-2576	2771-2775
PPOLG_P0V1P	GENOME POLYPROTEIN	YELLOW FEVER VIRUS (STRAIN 17D)	3320-3357	3385-3426						
PPOLG_P0V1Q	GENOME POLYPROTEIN	YELLOW FEVER VIRUS (STRAIN 17D)	418-432	525-563	728-768	1388-1444	2231-2276	2477-2563	2938-2996	3097-3143
PPOLG_P0V1R	GENOME POLYPROTEIN	YELLOW FEVER VIRUS (STRAIN PASTEUR 17D-204)	418-432	525-563	728-768	1388-1444	2231-2276	2477-2563	2938-2996	3097-3143
PPOLG_P0V1S	GENOME POLYPROTEIN	YELLOW FEVER VIRUS (STRAIN PASTEUR 17D-204)	75-116	418-432	525-563	728-768				
PPOLG_P0V1T	GENOME POLYPROTEIN	POLIOVIRUS TYPE 1 (STRAIN MAHONEY)	9-43	1047-1102	1415-1449	1501-1549	1610-1651	1808-1842	1904-1949	
PPOLG_P0V1U	NON-STRUCTURAL POLYPROTEIN	VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TRINIDAD)	345-382	898-922	1945-1979					
PPOLG_P0V1V	NON-STRUCTURAL POLYPROTEIN	FELINE CALICIVIRUS (STRAIN CP/68 FIV)	310-344							
PPOLG_P0V1W	NON-STRUCTURAL POLYPROTEIN	FELINE CALICIVIRUS (STRAIN F9)	4-43	369-410	916-1020	1023-1061				
PPOLG_P0V1X	NON-STRUCTURAL POLYPROTEIN	HEPATITIS E VIRUS (STRAIN BURMA)	318-379	1139-1177						
PPOLG_P0V1Y	NON-STRUCTURAL POLYPROTEIN	HEPATITIS E VIRUS (STRAIN MEXICO)	318-379							
PPOLG_P0V1Z	NON-STRUCTURAL POLYPROTEIN	HEPATITIS E VIRUS (STRAIN MYANMAR)	318-379	1139-1184						
PPOLG_P0V1A	NON-STRUCTURAL POLYPROTEIN	HEPATITIS E VIRUS (STRAIN PAKISTAN)	317-378	1138-1176						
PPOLG_P0V1B	NON-STRUCTURAL POLYPROTEIN	MIDDELBURG VIRUS	922-977							

PGCENE	ALLNOTIS	All Viruses (no Bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
FILE NAME	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PPOLN_RBDV	NONSTRUCTURAL POLYPROTEIN	ONYONG-ONYONG VIRUS (STRAIN GULLU)	899-933	1942-1986	2444-2502					
PPOLN_RAVN	NONSTRUCTURAL POLYPROTEIN	RABBIT HEMORRHAGIC DISEASE VIRUS	188-214	306-347	409-437	1652-1716				
PPOLN_RAVT	NONSTRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN NB5092)	891-929	1978-1982	2414-2467					
PPOLN_RUBVT	NONSTRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN T44)	597-611	1083-1126						
PPOLN_SFV	NONSTRUCTURAL POLYPROTEIN	RUBELLA VIRUS (STRAIN THERIEN)	1506-1540	1531-1583	1720-1767	1862-1896				
PPOLN_SINDO	NONSTRUCTURAL POLYPROTEIN	SEXALIKI FOREST VIRUS	1094-1128	2338-2392						
PPOLN_SINDV	NONSTRUCTURAL POLYPROTEIN	SINDBIS VIRUS (SUBTYPE OCKELBO / STRAIN EDSBYN 82-3)	919-971	1491-1533	1961-1996	2444-2478				
PPOLA_EEAV	NONSTRUCTURAL POLYPROTEIN	SINDBIS VIRUS (STRAIN TRSP)	1491-1533	1939-1994	2442-2476					
PPOLS_EEAV	RNA REPLICASE POLYPROTEIN	EGGPLANT MOSAIC VIRUS	899-933	1121-1161						
PPOLS_EEAV1	STRUCTURAL POLYPROTEIN	EASTERN EQUINE ENCEPHALITIS VIRUS	372-406	914-931						
PPOLS_EEAVT	STRUCTURAL POLYPROTEIN	EASTERN EQUINE ENCEPHALITIS VIRUS (STRAIN VADJ) [TEN BRO]	372-407	915-933						
PPOLS_IBDV1	STRUCTURAL POLYPROTEIN	VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TC-83)	1216-1230							
PPOLS_IBDVA	STRUCTURAL POLYPROTEIN	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN TRINIDAD)	1216-1230							
PPOLS_IBDVC	STRUCTURAL POLYPROTEIN	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN 32709)	134-168	231-286	470-523					
PPOLS_IBDVE	STRUCTURAL POLYPROTEIN	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN AUSTRAL)	134-168	231-286	470-523					
PPOLS_IBDVP	STRUCTURAL POLYPROTEIN	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN CU-1)	134-168	231-286	470-523					
PPOLS_IBDVS	NONSTRUCTURAL POLYPROTEIN VP4	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN E)	134-168	231-286	304-340					
PPOLS_IPNV1	STRUCTURAL POLYPROTEIN	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN PBG-98)	115-149	212-267	451-504					
PPOLS_IPNVN	STRUCTURAL POLYPROTEIN	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN STC)	134-168	249-283	470-523					
PPOLS_ONVGO	STRUCTURAL POLYPROTEIN	INFECTIOUS PANCREATIC NECROSIS VIRUS (SEROTYPE JASPER)	69-103	723-785						
PPOLS_RAV2	STRUCTURAL POLYPROTEIN	INFECTIOUS PANCREATIC NECROSIS VIRUS (STRAIN NI)	716-766							
PPOLS_RAVN	STRUCTURAL POLYPROTEIN	ONYONG-ONYONG VIRUS (STRAIN GULLU)	1204-1238							
PPOLS_RAVT	STRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN 213970)	35-69							
PPOLS_RUBVH	STRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN NB5092)	169-403	919-973						
PPOLS_RUBVR	STRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN T44)	929-973							
PPOLS_RUBVT	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (VACCINE STRAIN HPV77)	999-1036							
PPOLS_SINDO	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (VACCINE STRAIN RA3702)	999-1036							
PPOLS_SINDV	STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (STRAIN THERIEN)	999-1036							
PPOLS_SINDW	STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (SUBTYPE OCKELBO / STRAIN EDSBYN 82-3)	362-396							
PPOLS_WEEV	STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (STRAINS HRSP AND HRLP)	362-396							
PPOLA_BAEVM	STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (WILD TYPE 58 DERIVED FROM STRAIN ARJ19)	14-46							
PPOLA_BLVAV	POL POLYPROTEIN	WESTERN EQUINE ENCEPHALITIS VIRUS	913-947							
PPOLA_BLV1	POL POLYPROTEIN	BABOON ENDOGENOUS VIRUS (STRAIN M7)	42-80	676-743	794-832	1001-1042				
PPOLA_CAEVC	POL POLYPROTEIN	BOVINE LEUKEMIA VIRUS (AUSTRALIAN ISOLATE)	623-673							
PPOLA_CAMVD	POL POLYPROTEIN	BOVINE LEUKEMIA VIRUS (JAPANESE ISOLATE BLV-1)	623-673							
PPOLA_COTMV	POL POLYPROTEIN	CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (STRAIN COBK)	879-934							
PPOLA_EIAPV	POL POLYPROTEIN	CALIFORNIA MOSAIC VIRUS (STRAIN DH)	177-211							
PPOLA_EIAPV	POL POLYPROTEIN	COMBILINA YELLOW MOTTLE VIRUS	87-121	333-367	447-498	838-876	1956-920	1310-1351		
PPOLA_EIAYV	POL POLYPROTEIN	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE 1369)	513-566	1022-1056						
PPOLA_FENNV1	POL POLYPROTEIN	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE CL23)	513-566	1022-1056						
PPOLA_FIVT2	POL POLYPROTEIN	EQUINE INFECTIOUS ANEMIA VIRUS (ISOLATE WYOMING)	513-563	1021-1035						
PPOLA_FIVSD	POL POLYPROTEIN	FELINE ENDGENOUS VIRUS ECEI	533-600	623-639	838-899					
PPOLA_FIVT3	POL POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALUMA)	429-473	606-663						
PPOLA_FIVD	POL POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO)	428-473	606-642						
PPOLA_FIVD	POL POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE Tm2)	428-472	595-662						
PPOLA_FIVD	POL POLYPROTEIN	FIGWORT MOSAIC VIRUS (STRAIN DXS)	403-437							
PPOLA_GALV	POL POLYPROTEIN	HUMAN SPINARETROVIRUS (FOAMY VIRUS)	140-174	217-236	285-326					
PPOLA_HTL1A	POL POLYPROTEIN	GIBBON APE LEUKEMIA VIRUS	528-562	673-740						
PPOLA_HTL1C	POL POLYPROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE I (STRAIN ATK)	676-711							
PPOLA_HV1A2	POL POLYPROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE I (CARIBBEAN ISOLATE)	676-711							
PPOLA_HV1B1	POL POLYPROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE I (ARV25F2 ISOLATE)	501-537	606-664						
PPOLA_HV1B3	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (BHI0 ISOLATE)	513-549	639-676						

FCGENE	ALLMOTIS	All Viruses (no Bacteriophages)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7
FILE NAME	PROTEIN	VIRUS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7
PPOL_HVIBR	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BIBS ISOLATE)	511-349	618-676					
PPOL_HVIEL	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BRU ISOLATE)	513-349	618-676					
PPOL_HVIRH	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ELI ISOLATE)	500-536	626-663					
PPOL_HVIRJ	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDR2 ISOLATE)	501-537	606-664					
PPOL_HVIMA	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (JRCF ISOLATE)	505-541	610-668					
PPOL_HVINI	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MAL ISOLATE)	476-536	601-663					
PPOL_HVINS	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NN ISOLATE)	504-540	609-667					
PPOL_HVIND	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NEW YORK-3 ISOL)	501-537	617-664					
PPOL_HVIDY	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE)	500-536	626-663					
PPOL_HVIPV	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (OYT ISOLATE)	501-537	606-664					
PPOL_HVIRH	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (PY22 ISOLATE)	513-349	693-678					
PPOL_HVIU4	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (REFRAIT ISOLATE)	500-536	602-663					
PPOL_HVIZ2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (STRAIN UGANDANI)	500-536	601-663					
PPOL_HVZBE	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (22CDC-234 ISOLA	500-536	626-663					
PPOL_HVZCA	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE BEN)	49-83	484-582	817-451				
PPOL_HVDI1	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE CAN2)	358-390	464-562	632-666				
PPOL_HVDI2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194)	502-600	671-705					
PPOL_HVDI3	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D205-7)	376-410	484-578	529-577	653-687			
PPOL_HVNZ0	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE GHANA-1)	464-562						
PPOL_HVNZ3	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE NIH-2)	44-78	336-390	631-667				
PPOL_HVZSB	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	352-391	465-583	634-668				
PPOL_HVZST	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE SOLIST)	46-80	471-562	633-667				
PPOL_PHA	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	484-518	522-577	653-687				
PPOL_SSV	PUTATIVE POL POLYPROTEIN	HAMSTER INTRACISTERIAL A-PARTICLE	462-503						
PPOL_MLVAK	POL POLYPROTEIN	SHEEP PULMONARY ADENOMATOSIS VIRUS	190-231						
PPOL_MLVAU	POL POLYPROTEIN	ACK MURINE LEUKEMIA VIRUS	325-392						
PPOL_MLVFS	POL POLYPROTEIN	ACK MURINE LEUKEMIA VIRUS	677-744						
PPOL_MLVFF	POL POLYPROTEIN	FRIEND MURINE LEUKEMIA VIRUS (ISOLATE 57)	682-749						
PPOL_MLVFP	POL POLYPROTEIN	FRIEND MURINE LEUKEMIA VIRUS (ISOLATE FD39)	682-749						
PPOL_MLVMO	POL POLYPROTEIN	FRIEND MURINE LEUKEMIA VIRUS (ISOLATE PVC-211)	682-749						
PPOL_MLVRO	POL POLYPROTEIN	MOLONEY MURINE LEUKEMIA VIRUS	677-744						
PPOL_MLVXK	POL POLYPROTEIN	RADIATION MURINE LEUKEMIA VIRUS	677-744						
PPOL_MPXY	POL POLYPROTEIN	RADIATION MURINE LEUKEMIA VIRUS (STRAIN KAPLAN)	63-129						
PPOL_OMYVS	POL POLYPROTEIN	SIAMAN MASON-PRIZER VIRUS	470-504	578-613					
PPOL_RVP	POL POLYPROTEIN	OYNRE LENTIVIRUS (STRAIN SA-OMYV)	470-503	855-910					
PPOL_RTV	POL POLYPROTEIN	OVINE SARCOMA VIRUS (STRAIN PRAGUE C)	646-684						
PPOL_RTBVP	POLYPROTEIN	RICE TUNGRO BACILLIFORM VIRUS	7-44	59-96	101-133	176-236	325-362	431-474	1405-1439
PPOL_SEVI	POLYPROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES)	7-44	59-96	101-133	176-236	325-362	431-474	1405-1439
PPOL_SEVIL	POL POLYPROTEIN	SIAMAN FOAMY VIRUS (TYPE I)	349-383	427-464	496-530				
PPOL_SIVA1	POL POLYPROTEIN	SIAMAN FOAMY VIRUS (TYPE 3 / STRAIN LK)	124-165	429-467	496-530				
PPOL_SIVA3	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (AGNI15 ISOLATE)	351-383	637-678	717-771	918-979			
PPOL_SIVA4	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (AGN286 ISOLATE)	45-86						
PPOL_SIVA1	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (AGN3 ISOLATE)	477-516	642-683	742-783				
PPOL_SIVA4	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM / CLONE GR	175-209	476-515	641-700	942-983	1020-1054		
PPOL_SIVCZ	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (TYO-1 ISOLATE)	657-698	737-798					
PPOL_SIVGB	POL POLYPROTEIN	CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIVCPZ2)	527-561	626-688					
PPOL_SIVM1	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (ISOLATE GB1)	6-37	446-483	629-673	793-827	915-946		
PPOL_SIVM4K	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (SM142-83 ISOLATE)	485-519	634-688					
PPOL_SIVS4	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (K5W ISOLATE)	485-519	634-688					
PPOL_SIVSP	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (F236SMH ISOLATE)	448-482	617-651					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					
PPOL_SIVYK	POL POLYPROTEIN	SIAMAN IMMUNODEFICIENCY VIRUS (PRIMC13 ISOLATE)	431-483	620-654					













PCGENE	ALLNOTES	ALL Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PRPP_BBSVA	RNA-DIRECTED RNA POLYMERASE	TOBACCO NECROSIS VIRUS (STRAIN D)	102-144							
PRPP_COVO	RNA POLYMERASE ALPHA SUBUNIT	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A31908)	99-158	160-216						
PRPP_HRSV	RNA POLYMERASE ALPHA SUBUNIT	CANINE DISTEMPER VIRUS (STRAIN ONDERSTPOORT)	312-373							
PRPP_HRSV1	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS	99-158	160-216						
PRPP_HRSV2	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN A2)	99-158	160-216						
PRPP_MEAS	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP A / STRAIN A2)	99-158	160-216						
PRPP_MEAS1	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP A / STRAIN A2)	99-158	160-216						
PRPP_MEAS2	RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN EDMONSTON)	315-374	460-495						
PRPP_MEAS3	RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN IP-3-CA)	315-374	460-495						
PRPP_MUMPE	RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN YAMAGATA-1)	315-374	460-495						
PRPP_MUMPE1	RNA POLYMERASE ALPHA SUBUNIT	MUMPS VIRUS (STRAIN SBL-1)	149-183	213-275						
PRPP_MUMPE2	RNA POLYMERASE ALPHA SUBUNIT	MUMPS VIRUS (STRAIN ENDERS)	214-276							
PRPP_MUMPE3	RNA POLYMERASE ALPHA SUBUNIT	MUMPS VIRUS (STRAIN MIYAIARA VACCINE)	214-276							
PRPP_NDVA	RNA POLYMERASE ALPHA SUBUNIT	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA/02)	100-134							
PRPP_NDVB	RNA POLYMERASE ALPHA SUBUNIT	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE C/45)	100-138							
PRPP_P11HB	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C13)	80-114	313-364	375-437					
PRPP_P11HC	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C19)	80-114	313-364	375-437					
PRPP_P11HD	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C14/71)	80-114	313-364	375-437					
PRPP_P11HE	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C14/71)	80-114	313-364	375-437					
PRPP_P11H	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C14/71)	80-114	313-364	375-437					
PRPP_P11T	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS	218-281							
PRPP_P11B	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIBA)	218-281							
PRPP_P11A	RNA POLYMERASE ALPHA SUBUNIT	BOVINE PARAINFLUENZA 3 VIRUS	31-130	414-470						
PRPP_P11A1	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 47885)	410-499							
PRPP_P11A2	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIBA)	4-38	222-285						
PRPP_P11A3	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 4B VIRUS (STRAIN 68-333)	222-285							
PRPP_P11A4	RNA POLYMERASE ALPHA SUBUNIT	PRY VIRUS	137-174							
PRPP_P11A5	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN AVOI)	93-127							
PRPP_P11A6	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN CYS-11)	93-127							
PRPP_P11A7	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN ERA, AND (STRAIN PM)	93-127							
PRPP_P11A8	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN P)	93-127							
PRPP_P11A9	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN SAD B19)	93-127							
PRPP_P11A10	RNA POLYMERASE ALPHA SUBUNIT	SENDAL VIRUS (STRAIN Z / HOST MUTANTS)	313-364	375-447						
PRPP_P11A11	RNA POLYMERASE ALPHA SUBUNIT	SENDAL VIRUS (STRAIN 694)	323-364	375-447						
PRPP_P11A12	RNA POLYMERASE ALPHA SUBUNIT	SENDAL VIRUS (STRAIN FUSHIMI)	313-364	375-447						
PRPP_P11A13	RNA POLYMERASE ALPHA SUBUNIT	SENDAL VIRUS (STRAIN HARRIS)	313-364	375-447						
PRPP_P11A14	RNA POLYMERASE ALPHA SUBUNIT	SENDAL VIRUS (STRAIN Z)	313-364	375-447						
PRPP_P11A15	RNA POLYMERASE ALPHA SUBUNIT	SENDAL VIRUS 5 (STRAIN W3)	205-278							
PRPP_P11A16	RNA POLYMERASE ALPHA SUBUNIT	SONCHUS YELLOW NET VIRUS	138-173	233-281						
PRPP_P11A17	RNA POLYMERASE ALPHA SUBUNIT	VELOCULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN C1-4)								
PRPP_P11A18	RNA POLYMERASE ALPHA SUBUNIT	VELOCULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN M-1)								
PRPP_P11A19	RNA POLYMERASE ALPHA SUBUNIT	VELOCULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN 1-37)								
PRPP_P11A20	RNA POLYMERASE ALPHA SUBUNIT	VELOCULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN 1-37)								
PRPP_P11A21	RNA POLYMERASE ALPHA SUBUNIT	VELOCULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN 1-37)								
PRPP_P11A22	RNA POLYMERASE ALPHA SUBUNIT	AMSACT A MOOREI ENTOMOPHAGUS	233-264	361-393						
PRPP_P11A23	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WR)	21-86							
PRPP_P11A24	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN COPENHAGEN)	118-167	225-266						
PRPP_P11A25	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WR)	118-167	225-266						

PGCENE	ALLMOTH	ALL Virens (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
QLEADAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PSPIA_VACC	SERINE PROTEINASE INHIBITOR 1	VARIOLA VIRUS	122-171	129-170						
PTC1_CVPI	SERINE PROTEINASE INHIBITOR 2	VACCINIA VIRUS (STRAIN COPIENHAGEN)	11-65							
PTA3_VACV	TYPE II RESTRICTION ENZYME CYAII	PARAMECIUM BURBARRIA CHLORELLA VIRUS 1	48-85							
PTAG1_FOPV	TRANS-ACTIVATOR PROTEIN A3	VACCINIA VIRUS (STRAIN WR, COPIENHAGEN, AND VARIOLA VI	95-133							
PTAG1_VACV	TRANS-ACTIVATOR PROTEIN FPO	FOWL POX VIRUS	3-51							
PTAG1_VAV	TRANS-ACTIVATOR PROTEIN CK1	VACCINIA VIRUS (STRAIN WR, COPIENHAGEN)	3-51							
PTA1A_BDV	TRANS-ACTIVATOR PROTEIN CK1	VARIOLA VIRUS	2-51							
PTA1A_POVBO	LARGE T ANTIGEN	BUDGERIGAR FLEDGLING DISEASE VIRUS	291-325	464-498						
PTA1A_POVHA	LARGE T ANTIGEN	BOVINE POLYOMIA VIRUS	303-337	495-537						
PTA1A_POVIC	LARGE T ANTIGEN	HANISTER POLYOMIA VIRUS	464-501	587-621						
PTA1A_POVLY	LARGE T ANTIGEN	POLYOMIA VIRUS JC	153-187	389-423						
PTA1A_POVAD	LARGE T ANTIGEN	LYMPHOTROPIC POLYOMIA VIRUS	3-41	206-258	437-478					
PTA1A_POVMA	LARGE T ANTIGEN	MOUSE POLYOMIA VIRUS (STRAIN 1)	509-544							
PTA1A_POVMC	LARGE T ANTIGEN	MOUSE POLYOMIA VIRUS (STRAIN A3)	507-542							
PTAM1_POVHA	LARGE T ANTIGEN	MOUSE POLYOMIA VIRUS (STRAIN CRAWFORD SMALL-PLAQUE)	504-539							
PTAM1_POVMA	MIDDLE T ANTIGEN	HANISTER POLYOMIA VIRUS	339-378							
PTAM1_POVMC	MIDDLE T ANTIGEN	MOUSE POLYOMIA VIRUS (STRAIN 3)	211-245	388-422						
PTASM_POVBO	MIDDLE T ANTIGEN	MOUSE POLYOMIA VIRUS (STRAIN A3)	192-226	369-403						
PTASM_POVLY	MIDDLE T ANTIGEN	MOUSE POLYOMIA VIRUS (STRAIN CRAWFORD SMALL-PLAQUE)	192-226	369-403						
PTATM_POVLY	SMALL T ANTIGEN	BOVINE POLYOMIA VIRUS	41-85							
PTATM_NPVAC	SMALL T ANTIGEN	LYMPHOTROPIC POLYOMIA VIRUS	2-41							
PTATM_NPVBM	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	AUTOGRAFIA CALIFORNICA NUCLEAR POLYOMIA VIRUS	408-442	48-480						
PTATM_NPVOP	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	BOMBYX MORI NUCLEAR POLYOMIA VIRUS	413-447	451-485						
PTATM_SIVAI	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	ORGANIA PSEUDOTUGATA MULTICAPSID POLYOMIA VIRUS	391-455	511-554						
PTATM_SIVAI	TAT PROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGM153 ISOLATE)	21-109							
PTATM_VLV	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM / CLONE GR	137-185							
PTATM_VLV1	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	VISNA LENTIVIRUS (STRAIN 1514)	28-74							
PTATM_VLV2	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	VISNA LENTIVIRUS (STRAIN 1514 / CLONE LVI-1K51)	40-74							
PTCB_FLV	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	VISNA LENTIVIRUS (STRAIN 1514 / CLONE LVI-1K52)	40-74							
PTGP_HSV11	T-CELL RECEPTOR BETA CHAIN PRECURSOR	FELINE LEUKEMIA VIRUS	279-321							
PTGP_HSV1A	TEGMENT PHOSPHOPROTEIN US9	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	27-61							
PTGP_HSV1B	NONSENSE									
PTGP_HSV1C	NONSENSE									
PTGP_HSV1D	NONSENSE									
PTGP_HSV1E	NONSENSE									
PTGP_HSV1F	NONSENSE									
PTGP_HSV1G	NONSENSE									
PTGP_HSV1H	NONSENSE									
PTGP_HSV1I	NONSENSE									
PTGP_HSV1J	NONSENSE									
PTGP_HSV1K	NONSENSE									
PTGP_HSV1L	NONSENSE									
PTGP_HSV1M	NONSENSE									
PTGP_HSV1N	NONSENSE									
PTGP_HSV1O	NONSENSE									
PTGP_HSV1P	NONSENSE									
PTGP_HSV1Q	NONSENSE									
PTGP_HSV1R	NONSENSE									
PTGP_HSV1S	NONSENSE									
PTGP_HSV1T	NONSENSE									
PTGP_HSV1U	NONSENSE									
PTGP_HSV1V	NONSENSE									
PTGP_HSV1W	NONSENSE									
PTGP_HSV1X	NONSENSE									
PTGP_HSV1Y	NONSENSE									
PTGP_HSV1Z	NONSENSE									
PTGP_HSV2A	NONSENSE									
PTGP_HSV2B	NONSENSE									
PTGP_HSV2C	NONSENSE									
PTGP_HSV2D	NONSENSE									
PTGP_HSV2E	NONSENSE									
PTGP_HSV2F	NONSENSE									
PTGP_HSV2G	NONSENSE									
PTGP_HSV2H	NONSENSE									
PTGP_HSV2I	NONSENSE									
PTGP_HSV2J	NONSENSE									
PTGP_HSV2K	NONSENSE									
PTGP_HSV2L	NONSENSE									
PTGP_HSV2M	NONSENSE									
PTGP_HSV2N	NONSENSE									
PTGP_HSV2O	NONSENSE									
PTGP_HSV2P	NONSENSE									
PTGP_HSV2Q	NONSENSE									
PTGP_HSV2R	NONSENSE									
PTGP_HSV2S	NONSENSE									
PTGP_HSV2T	NONSENSE									
PTGP_HSV2U	NONSENSE									
PTGP_HSV2V	NONSENSE									
PTGP_HSV2W	NONSENSE									
PTGP_HSV2X	NONSENSE									
PTGP_HSV2Y	NONSENSE									
PTGP_HSV2Z	NONSENSE									
PTGP_HSV3A	NONSENSE									
PTGP_HSV3B	NONSENSE									
PTGP_HSV3C	NONSENSE									
PTGP_HSV3D	NONSENSE									
PTGP_HSV3E	NONSENSE									
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PTGP_HSV3G	NONSENSE									
PTGP_HSV3H	NONSENSE									
PTGP_HSV3I	NONSENSE									
PTGP_HSV3J	NONSENSE									
PTGP_HSV3K	NONSENSE									
PTGP_HSV3L	NONSENSE									
PTGP_HSV3M	NONSENSE									
PTGP_HSV3N	NONSENSE									
PTGP_HSV3O	NONSENSE									
PTGP_HSV3P	NONSENSE									
PTGP_HSV3Q	NONSENSE									
PTGP_HSV3R	NONSENSE									
PTGP_HSV3S	NONSENSE									
PTGP_HSV3T	NONSENSE									
PTGP_HSV3U	NONSENSE									
PTGP_HSV3V	NONSENSE									
PTGP_HSV3W	NONSENSE									
PTGP_HSV3X	NONSENSE									
PTGP_HSV3Y	NONSENSE									
PTGP_HSV3Z	NONSENSE									
PTGP_HSV4A	NONSENSE									
PTGP_HSV4B	NONSENSE									
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PTGP_HSV4D	NONSENSE									
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PTGP_HSV4H	NONSENSE									
PTGP_HSV4I	NONSENSE									
PTGP_HSV4J	NONSENSE									
PTGP_HSV4K	NONSENSE									
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PTGP_HSV4M	NONSENSE									
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PTGP_HSV4P	NONSENSE									
PTGP_HSV4Q	NONSENSE									
PTGP_HSV4R	NONSENSE									
PTGP_HSV4S	NONSENSE									
PTGP_HSV4T	NONSENSE									
PTGP_HSV4U	NONSENSE									
PTGP_HSV4V	NONSENSE									
PTGP_HSV4W	NONSENSE									
PTGP_HSV4X	NONSENSE									
PTGP_HSV4Y	NONSENSE									
PTGP_HSV4Z	NONSENSE									
PTGP_HSV5A	NONSENSE									
PTGP_HSV5B	NONSENSE									
PTGP_HSV5C	NONSENSE									
PTGP_HSV5D	NONSENSE									
PTGP_HSV5E	NONSENSE									
PTGP_HSV5F	NONSENSE									
PTGP_HSV5G	NONSENSE									
PTGP_HSV5H	NONSENSE									
PTGP_HSV5I	NONSENSE									
PTGP_HSV5J	NONSENSE									
PTGP_HSV5K	NONSENSE									
PTGP_HSV5L	NONSENSE									
PTGP_HSV5M	NONSENSE									
PTGP_HSV5N	NONSENSE									
PTGP_HSV5O	NONSENSE									
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PTGP_HSV5Q	NONSENSE									
PTGP_HSV5R	NONSENSE									
PTGP_HSV5S	NONSENSE									
PTGP_HSV5T	NONSENSE									
PTGP_HSV5U	NONSENSE									
PTGP_HSV5V	NONSENSE									
PTGP_HSV5W	NONSENSE									
PTGP_HSV5X	NONSENSE									
PTGP_HSV5Y	NONSENSE									
PTGP_HSV5Z	NONSENSE									
PTGP_HSV6A	NONSENSE									
PTGP_HSV6B	NONSENSE									
PTGP_HSV6C	NONSENSE									
PTGP_HSV6D	NONSENSE									
PTGP_HSV6E	NONSENSE									
PTGP_HSV6F	NONSENSE									
PTGP_HSV6G	NONSENSE									
PTGP_HSV6H	NONSENSE									
PTGP_HSV6I	NONSENSE									
PTGP_HSV6J	NONSENSE									
PTGP_HSV6K	NONSENSE									
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PTGP_HSV6N	NONSENSE									
PTGP_HSV6O	NONSENSE									
PTGP_HSV6P	NONSENSE									
PTGP_HSV6Q	NONSENSE									
PTGP_HSV6R	NONSENSE									
PTGP_HSV6S	NONSENSE									
PTGP_HSV6T	NONSENSE									
PTGP_HSV6U	NONSENSE									
PTGP_HSV6V	NONSENSE									
PTGP_HSV6W	NONSENSE									
PTGP_HSV6X	NONSENSE									
PTGP_HSV6Y	NONSENSE									
PTGP_HSV6Z	NONSENSE									
PTGP_HSV7A	NONSENSE									

PCGENE	ALLNOTIS	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	VIRUS	441-491	497-538						AREA1
PUL01_AVS1	DNA TERMINAL PROTEIN	HUMAN ADENOVIRUS TYPE 12	441-491	497-538						AREA1
PTMAF_AVS4	TRANSFORMING PROTEIN JUN	AVIAN SARCOMA VIRUS (STRAIN 17)	210-284							
PTOP1_SFVKA	TRANSFORMING PROTEIN MAF	AVIAN MUSCULOPONEUROTIC FIBROSARCOMA VIRUS AS42	247-288	295-340						
PTOP2_SFVB7	DNA TOPOISOMERASE	SHOPE FIBROMA VIRUS (STRAIN KASZA)	127-183	269-310						
PTOP2_SFPMQ	DNA TOPOISOMERASE II	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	146-180	481-515	601-642	943-979	1034-1093	1123-1162		
PTSIS_SNSAV	DNA TOPOISOMERASE II	AFRICAN SWINE FEVER VIRUS (ISOLATE MALAWI LIL 2001)	146-180	480-514	600-641	902-936	944-978	1034-1091	1122-1161	
PTSYV_VZVDO	PDGF-RELATED TRANSFORMING PROTEIN P14-335	SRGAN SARCOMA VIRUS	16-71							
PUBIL_NPVOP	THYMIDYLATE SYNTHASE	VARIICELLA-ZOSTER VIRUS (STRAIN DUMAS)	215-260							
PUL01_HCAVA	UBIQUITIN-LIKE PROTEIN	ORGANIA PSEUDOTISUCATA MULTICAPSID POLYHEDROUS VIRUS	43-80							
PUL03_HSV11	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	169-203							
PUL03_HSV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	94-128							
PUL03_HSV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	94-128							
PUL04_HSV11	GENE 40 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADHP)	92-126							
PUL04_EBV	PROTEIN UL4	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	102-136							
PUL06_HCAVA	VIRION PROTEIN BBRF1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	104-145	313-347	376-410					
PUL06_HSV11	HYPOTHETICAL PROTEIN UL6	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	216-250							
PUL06_HSV2B	VIRION PROTEIN UL4	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	36-94	103-141	294-329	337-371	416-479			
PUL06_HSV3A	VIRION GENE 36 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADHP)	62-170	337-413	448-503					
PUL06_VZVDO	VIRION GENE 41 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	90-140	151-194	302-336	364-403				
PUL08_HCAVA	VIRION GENE 34 PROTEIN	VARIICELLA-ZOSTER VIRUS (STRAIN DUMAS)	87-131	330-409	704-738					
PUL09_HSV2B	HYPOTHETICAL PROTEIN UL8	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-50							
PUL09_VZVDO	ORIGIN OF REPLICATION BINDING PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADHP)	174-208							
PUL11_HCAVA	ORIGIN OF REPLICATION BINDING PROTEIN	VARIICELLA-ZOSTER VIRUS (STRAIN DUMAS)	122-163							
PUL11_HCAVA	NONSENSE									
PUL14_HCAVA	HYPOTHETICAL PROTEIN UL13	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	47-81	185-227						
PUL14_HSV2B	HYPOTHETICAL PROTEIN UL14	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	303-343							
PUL14_PAVNO	HYPOTHETICAL GENE 48 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADHP)	52-96	246-283						
PUL14_VZVDO	UL14 PROTEIN HOMOLOG	PSEUDORABIES VIRUS (STRAIN NIA-3)	43-93							
PUL16_HSV2B	HYPOTHETICAL GENE 46 PROTEIN	VARIICELLA-ZOSTER VIRUS (STRAIN DUMAS)	61-103							
PUL17_HSV6U	GENE 46 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADHP)	266-300							
PUL21_HSV2B	PROTEIN 10R	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	219-280							
PUL21_HCAVA	GENE 40 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADHP)	44-78	421-474						
PUL24_HCAVA	HYPOTHETICAL PROTEIN UL23	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	213-253							
PUL24_ILTVT	PROTEIN UL24 HOMOLOG	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	5-39							
PUL25_HCAVA	HYPOTHETICAL PROTEIN UL24	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE V8)	161-195							
PUL25_HSV11	HYPOTHETICAL PROTEIN UL25	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	235-241	331-399						
PUL25_HSV2B	VIRION PROTEIN UL25	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	370-411							
PUL31_HSV3A	VIRION PROTEIN UL31	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADHP)	364-413							
PUL31_ILTVT	VIRION GENE 19 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	29-92	183-231	365-408					
PUL31_VZVDO	64.1 KD VIRION PROTEIN	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE V8)	38-84	165-206						
PUL31_HCAVA	VIRION GENE 34 PROTEIN	VARIICELLA-ZOSTER VIRUS (STRAIN DUMAS)	340-388							
PUL31_HSV2B	HYPOTHETICAL PROTEIN UL31	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	244-285							
PUL31_VZVDO	GENE 29 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADHP)	131-187							
PUL31_HSV2B	GENE 27 PROTEIN	VARIICELLA-ZOSTER VIRUS (STRAIN DUMAS)	163-197							
PUL31_VZVDO	MAJOR ENVELOPE GLYCOPROTEIN 200	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADHP)	342-376							
PUL33_HCAVA	PROBABLE MAJOR ENVELOPE GLYCOPROTEIN 26	VARIICELLA-ZOSTER VIRUS (STRAIN DUMAS)	72-106	296-344						
PUL33_VZVDO	G-PROTEIN COUPLED RECEPTOR HOMOLOG UL33	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	94-135	309-352						
PUL34_EBV	GENE 23 PROTEIN	VARIICELLA-ZOSTER VIRUS (STRAIN DUMAS)	29-63							
PUL34_HCAVA	BBRF1 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)	159-200							
PUL34_HSV11	HYPOTHETICAL PROTEIN UL34	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	113-147							
PUL35_HCAVA	VIRION PROTEIN UL34	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	187-221							
PUL37_EBV	HYPOTHETICAL PROTEIN UL35	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	231-268							

FCGENE	ALLNOTIS	ALL Virus (no bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
FILE NAME	PROTEIN	VIRUS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
PUL37_HSV11	PROTEIN BOLF1	EPSTEIN-BARR VIRUS (STRAIN B95-3)	708-742							
PUL37_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	833-891							
PUL37_HSV11	PROTEIN BOLF1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD169)	82-137	311-345	614-648	713-750	781-822			
PUL37_HSV11	PROTEIN BOLF1	HERPESVIRUS SAIMIRI (STRAIN 11)	6-65	682-741						
PUL37_HSV11	PROTEIN BOLF1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	719-753	786-827						
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	10-51							
PUL37_HSV11	PROTEIN BOLF1	HOST SHUTOFF VIRION PROTEIN	330-366							
PUL37_HSV11	PROTEIN BOLF1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	134-168	221-263						
PUL37_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	138-172							
PUL37_HSV11	PROTEIN BOLF1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD169)	72-109							
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	312-363							
PUL37_HSV11	PROTEIN BOLF1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	96-137							
PUL37_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	96-137							
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	114-165	448-485	745-856					
PUL37_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	473-518							
PUL37_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	473-518							
PUL37_HSV11	PROTEIN BOLF1	BOVINE HERPESVIRUS TYPE 1 (STRAIN P8-2)	561-612							
PUL37_HSV11	PROTEIN BOLF1	EQUINE HERPESVIRUS TYPE 1 (STRAIN 1942)	183-246	582-620	825-866					
PUL37_HSV11	PROTEIN BOLF1	VARICELLA-ZOSTER VIRUS (STRAIN AD169)	219-253	371-412	817-866					
PUL37_HSV11	PROTEIN BOLF1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	84-135	156-209	664-701					
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	155-189							
PUL37_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	118-169							
PUL37_HSV11	PROTEIN BOLF1	EQUINE HERPESVIRUS TYPE 1 (STRAIN 1942)	121-162							
PUL37_HSV11	PROTEIN BOLF1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD169)	122-163							
PUL37_HSV11	PROTEIN BOLF1	EPSTEIN-BARR VIRUS (STRAIN B95-3)	183-255							
PUL37_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	189-223							
PUL37_HSV11	PROTEIN BOLF1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD169)	141-182	919-970						
PUL37_HSV11	PROTEIN BOLF1	VARICELLA-ZOSTER VIRUS (STRAIN 11)	445-483							
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN DUMAS)	301-342							
PUL37_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 1942)	12-48							
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	151-185							
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	32-21							
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	39-99							
PUL37_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 1942)	43-79							
PUL37_HSV11	PROTEIN BOLF1	HERPESVIRUS SAIMIRI (STRAIN 11)	729-770							
PUL37_HSV11	PROTEIN BOLF1	HERPESVIRUS SAIMIRI (STRAIN 11)	366-400	382-616						
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	357-391							
PUL37_HSV11	PROTEIN BOLF1	HERPESVIRUS SAIMIRI (STRAIN 11)	24-58							
PUL37_HSV11	PROTEIN BOLF1	EPSTEIN-BARR VIRUS (STRAIN B95-3)	107-144	188-222						
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	79-116							
PUL37_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 1942)	101-145	174-216						
PUL37_HSV11	PROTEIN BOLF1	HERPESVIRUS SAIMIRI (STRAIN 11)	88-122							
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	23-57	299-384						
PUL37_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 1942)	24-71	239-293						
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	21-51	231-270						
PUL37_HSV11	PROTEIN BOLF1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 1942)	31-101							
PUL37_HSV11	PROTEIN BOLF1	HERPESVIRUS SAIMIRI (STRAIN 11)	53-113							
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	45-100							
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-40	758-792						
PUL37_HSV11	PROTEIN BOLF1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	1-56	110-171	330-364	439-492	541-575			

PGENE	FILENAME	ALLNOTES	All Viruses (no bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PUNG_HSV11	PROTEIN	PROTEIN	VIRUS	84-125							
PUNG_HSV21	HYPOTHETICAL PROTEIN H10		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	227-265							
PUNG_HSV21	URACIL-DNA GLYCOSYLASE		HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	188-229							
PUNG_HSV21	URACIL-DNA GLYCOSYLASE		HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN 311)	148-189							
PUNG_HSV21	URACIL-DNA GLYCOSYLASE		HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HGS2)	135-176							
PUNG_HSV21	URACIL-DNA GLYCOSYLASE		HERPES VIRUS SAIMIRI (STRAIN 11)	81-115							
PUS02_HSV2B	URACIL-DNA GLYCOSYLASE		SHOPE FIBROMA VIRUS (STRAIN KASZA)	79-120							
PUS07_HSV2K	GENE 68 PROTEIN		EQUINE HERPES VIRUS TYPE 1 (STRAIN ABAP)	86-120							
PUS07_HSV2K	US1 PROTEIN		EQUINE HERPES VIRUS TYPE 1 (STRAIN KENTUCKY A)	2-36							
PUS11_HSV2A	HYPOTHETICAL PROTEIN H0LF3		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	3-51							
PUS14_HSV2A	HYPOTHETICAL PROTEIN H0LF1		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	187-225							
PUS18_HSV2A	HYPOTHETICAL PROTEIN H0LF4		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	294-335							
PUS31_HSV2A	MEMBRANE PROTEIN H0LF3		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	135-172							
PUS34_HSV2A	HYPOTHETICAL PROTEIN H0LF7		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	535-584							
PUS36_HSV2A	HYPOTHETICAL PROTEIN H0LF6		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-40							
PUS37_HSV2A	HYPOTHETICAL PROTEIN H0LF3		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	135-169							
PUS39_HSV2A	G-PROTEIN COUPLED RECEPTOR HOMOLOG U37		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	18-52							
PV131_ASVLE	HYPOTHETICAL PROTEIN H0RF3		ALFALFA MOSAIC VIRUS (STRAIN 437 / ISOLATE LEIDEN)	313-350							
PV143_NPVAC	123 KD PROTEIN		AUTOGRAPIA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	75-117							
PV18K_TRV3Y	HELICASE		TOBACCO RATTLE VIRUS (STRAIN PSG)	21-55							
PV18K_TRV3Y	16 KD PROTEIN		TOBACCO RATTLE VIRUS (STRAIN SYM)	4-66							
PV1A_BMV	16 KD PROTEIN		TOBACCO RATTLE VIRUS (STRAIN SYM)	11-59							
PV1A_BMV	1A PROTEIN		BROAD BEAN MOTTLE VIRUS	149-405							
PV1A_CMYV	1A PROTEIN		BROME MOSAIC VIRUS	348-411							
PV1A_CMYV	1A PROTEIN		COWPEA CHLOROTIC MOTTLE VIRUS	242-276							
PV1A_CMYV	1A PROTEIN		CUCUMBER MOSAIC VIRUS (STRAIN FNY)	393-434							
PV1A_CMYV	1A PROTEIN		CUCUMBER MOSAIC VIRUS (STRAIN O)	11-66							
PV1A_CMYV	1A PROTEIN		CUCUMBER MOSAIC VIRUS (STRAIN Q)	393-434							
PV1A_CMYV	1A PROTEIN		PEANUT STUNT VIRUS (STRAIN J)	11-66							
PV21K_HSV2H	1A PROTEIN		TOMATO ASPERM VIRUS	4-66							
PV21K_HSV2H	33.5 KD PROTEIN		TOMATO ASPERM VIRUS (STRAIN I12)	11-59							
PV21K_NPVAC	24 KD ANTIGEN		TURKEY HERPES VIRUS (STRAIN I12)	177-211							
PV21K_PLRV1	33 KD PROTEIN		BORNA DISEASE VIRUS	63-121							
PV21K_PLRV1	33 KD PROTEIN		AUTOGRAPIA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	4-30							
PV21K_PLRV1	33 KD PROTEIN		POTATO LEAFROLL VIRUS (STRAIN I)	116-150							
PV21K_PLRV1	33 KD PROTEIN		POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	116-150							
PV21K_PLRV1	33 KD PROTEIN		AFRICAN SWINE FEVER VIRUS (STRAIN L1517)	138-183							
PV21K_PLRV1	33 KD PROTEIN		EARLY BROWNING VIRUS	115-192							
PV21K_PLRV1	33 KD PROTEIN		TOBACCO RATTLE VIRUS (STRAIN SYM), AND (STRAIN PSG)	167-201							
PV21K_PLRV1	33 KD PROTEIN		TOBACCO RATTLE VIRUS (STRAIN TCM)	45-79							
PV21K_PLRV1	33 KD PROTEIN		COWPEA CHLOROTIC MOTTLE VIRUS	768-806							
PV21K_PLRV1	33 KD PROTEIN		CUCUMBER MOSAIC VIRUS (STRAIN FNY)	386-420							
PV21K_PLRV1	33 KD PROTEIN		PEANUT STUNT VIRUS (STRAIN J)	717-751							
PV21K_PLRV1	33 KD PROTEIN		TOMATO ASPERM VIRUS	722-756							
PV21K_PLRV1	33 KD PROTEIN		TOBACCO RATTLE VIRUS (STRAIN TCM)	105-218							
PV21K_PLRV1	33 KD PROTEIN		AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	51-87							
PV21K_PLRV1	33 KD PROTEIN		AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	54-102							
PV21K_PLRV1	33 KD PROTEIN		AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	151-192							
PV21K_PLRV1	33 KD PROTEIN		BROME MOSAIC VIRUS	151-199							
PV21K_PLRV1	33 KD PROTEIN		CUCUMBER MOSAIC VIRUS (STRAIN FNY)	11-45							
PV21K_PLRV1	33 KD PROTEIN		CUCUMBER MOSAIC VIRUS (STRAIN M)	215-255							
PV21K_PLRV1	33 KD PROTEIN		CUCUMBER MOSAIC VIRUS (STRAIN O)	215-255							
PV21K_PLRV1	33 KD PROTEIN		CUCUMBER MOSAIC VIRUS (STRAIN Y)	215-255							



ALLNOTES  
Nidif Search Results

PLGNAME	ALLNOTES	ALL Viruses (see bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PVA49_VACCC	PROTEIN A47	VARIOLA VIRUS	62-96	143-184						
PVA49_VACCC	PROTEIN A49	VACCINIA VIRUS (STRAIN COPENHAGEN)	3-40	126-160						
PVA49_VACCC	PROTEIN A49	VACCINIA VIRUS (STRAIN WR)	3-40	126-160						
PVA52_VACCC	PROTEIN A49	VARIOLA VIRUS	3-40	126-160						
PVA52_VACCC	PROTEIN A52	VACCINIA VIRUS (STRAIN COPENHAGEN)	91-132							
PVA52_VACCC	PROTEIN A52	VACCINIA VIRUS (STRAIN WR)	91-132							
PVA57_VACCC	GUANYLATE KINASE HOMOLOG	VACCINIA VIRUS (STRAIN COPENHAGEN)	134-168							
PVAL1_MSVK	GUANYLATE KINASE HOMOLOG	VACCINIA VIRUS (STRAIN WR)	134-168							
PVAL1_MSVN	ALI PROTEIN	MAIZE STREAK VIRUS (KENYAN ISOLATE)	220-269							
PVAL1_MSVN	ALI PROTEIN	MAIZE STREAK VIRUS (NIGERIAN ISOLATE)	228-262							
PVAL1_MSVN	ALI PROTEIN	MAIZE STREAK VIRUS (SOUTH AFRICAN ISOLATE)	228-262							
PVAL1_MSVN	ALI PROTEIN	SQUASH LEAF CURL VIRUS	117-151							
PVAL1_MSVN	ALI PROTEIN	TOBACCO YELLOW DWARF VIRUS (STRAIN AUSTRALIA)	191-225							
PVAL1_MSVN	ALI PROTEIN	ABUTILON MOSAIC VIRUS (ISOLATE WEST INDIA)	44-78	81-124						
PVAL1_MSVN	ALI PROTEIN	BEAN GOLDEN MOSAIC VIRUS	44-78	81-124						
PVAL1_MSVN	ALI PROTEIN	POTATY YELLOW MOSAIC VIRUS (ISOLATE VENEZUELA)	30-78	87-121						
PVAL1_MSVN	ALI PROTEIN	SQUASH LEAF CURL VIRUS	46-80	91-125						
PVAL1_MSVN	ALI PROTEIN	TOMATO GOLDEN MOSAIC VIRUS	44-78							
PVAL1_MSVN	ALI PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CN-1841)	22-70	84-127						
PVAL1_MSVN	ALI PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DRI)	22-70							
PVAL1_MSVN	ALI PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN BBC)	22-70	93-127						
PVAL1_MSVN	ALI PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN NY8153)	22-70	93-127						
PVAL1_MSVN	ALI PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN PV147)	22-70	93-127						
PVAL1_MSVN	ALI PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	22-70	93-130						
PVAL1_MSVN	ALI PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN W260)	36-70							
PVAL1_MSVN	ALI PROTEIN	CARNATION ETCHED RING VIRUS	99-138							
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN WR)	108-142							
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	89-123	331-372	496-530					
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN WR)	89-123	331-372						
PVAL1_MSVN	ALI PROTEIN	VARIOLA VIRUS	89-134	324-372	492-530					
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN LC16ND)	234-298							
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	234-298							
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN LISTER)	234-298							
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN WR)	234-298							
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN WR, AND (STRAIN COPENHAGEN))	28-62							
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-60							
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN WR)	337-375	491-532						
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	337-375	491-532						
PVAL1_MSVN	ALI PROTEIN	VARIOLA VIRUS	337-378	491-532						
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	82-121							
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN DAIEN I)	85-119							
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN WR)	85-119							
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	48-85							
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN WR)	61-95							
PVAL1_MSVN	ALI PROTEIN	BEAN GOLDEN MOSAIC VIRUS	139-193							
PVAL1_MSVN	ALI PROTEIN	SQUASH LEAF CURL VIRUS	139-193							
PVAL1_MSVN	ALI PROTEIN	TOMATO GOLDEN MOSAIC VIRUS	139-193							
PVAL1_MSVN	ALI PROTEIN	BEAN GOLDEN MOSAIC VIRUS	172-206							
PVAL1_MSVN	ALI PROTEIN	SQUASH LEAF CURL VIRUS	20-61							
PVAL1_MSVN	ALI PROTEIN	TOMATO GOLDEN MOSAIC VIRUS	25-59							
PVAL1_MSVN	ALI PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	37-42	262-302	391-442					

PCGENE	ALLIOTIS	ALL Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PVC04_SFVKA	PROTEIN C1	VACCINIA VIRUS (STRAIN WR)	32-82	362-202	391-442					
PVC04_VACCC	PROTEIN C4	SHOPE FIBRONA VIRUS (STRAIN KASZA)	175-223	374-408						
PVC04_VACCV	PROTEIN C4	VACCINIA VIRUS (STRAIN COPENHAGEN)	12-46							
PVC04_VAVR	PROTEIN C4	VACCINIA VIRUS (STRAIN WR)	12-46							
PVC03_SFVKA	PROTEIN C4	VARIOLA VIRUS	12-46							
PVC03_VACCC	HYPOHETICAL PROTEIN C3	SHOPE FIBRONA VIRUS (STRAIN KASZA)	82-115							
PVC03_VACCV	PROTEIN C3	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-68							
PVC03_VAVR	PROTEIN C3	VACCINIA VIRUS (STRAIN WR)	31-68							
PVC08_SFVKA	PROTEIN C5	VARIOLA VIRUS	32-70	72-121						
PVC09_SFVKA	HYPOHETICAL PROTEIN C4	SHOPE FIBRONA VIRUS (STRAIN KASZA)	45-86							
PVC09_VACCC	HYPOHETICAL PROTEIN C9	SHOPE FIBRONA VIRUS (STRAIN KASZA)	63-106							
PVC09_VACCV	PROTEIN C9	VACCINIA VIRUS (STRAIN COPENHAGEN)	82-116	168-226	289-323	575-612				
PVC10_VACCC	PROTEIN C9	VACCINIA VIRUS (STRAIN WR)	82-116	168-226	289-323	575-612				
PVC10_VACCV	PROTEIN C10	VACCINIA VIRUS (STRAIN COPENHAGEN)	136-180							
PVC10_VAVR	PROTEIN C10	VACCINIA VIRUS (STRAIN WR)	136-176							
PVC12_SFVKA	PROTEIN C10	VARIOLA VIRUS	136-170							
PVC17_SFVKA	HYPOHETICAL PROTEIN C12	SHOPE FIBRONA VIRUS (STRAIN KASZA)	2-36							
PVC16_VACCC	PROTEIN C13	SHOPE FIBRONA VIRUS (STRAIN KASZA)	3-66	117-182	189-240					
PVC17_VACCC	PROTEIN C13	VACCINIA VIRUS (STRAIN COPENHAGEN)	142-176							
PVC18_VACCC	PROTEIN C13	VACCINIA VIRUS (STRAIN COPENHAGEN)	100-155	323-339						
PVC19_SFVKA	PROTEIN C13	VACCINIA VIRUS (STRAIN COPENHAGEN)	40-98							
PVC19_VACCC	PROTEIN C19	SHOPE FIBRONA VIRUS (STRAIN KASZA)	56-97							
PVCAP_EBV	PROTEIN C13	VACCINIA VIRUS (STRAIN COPENHAGEN)	218-232							
PVCAP_HCNVA	MAJOR CAPSID PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	150-184	670-709						
PVCAP_HSV1	MAJOR CAPSID PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	136-174	191-225	260-294					
PVCAP_HSV6	MAJOR CAPSID PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	116-173	308-316						
PVCAP_HSV6B	MAJOR CAPSID PROTEIN	HERPES SIMPLEX VIRUS	136-174	320-366	311-382					
PVCAP_HSV8A	MAJOR CAPSID PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	150-184	304-352						
PVCAP_PV15	MAJOR CAPSID PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	479-520	673-714	715-799					
PVCAP_VZV0	MAJOR CAPSID PROTEIN	PSEUDORABIES VIRUS (STRAIN INDIANA S)	101-160	292-326						
PVC01_NPVAC	MAJOR CAPSID PROTEIN	VARIOLA-ZOSTER VIRUS (STRAIN DUMAS)	128-198	316-330						
PVD03_FOWP1	DNA-BINDING PROTEIN	AUTOGRAFA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	110-248							
PVD03_VACCC	92.6 KD PROTEIN	FOWLPOX VIRUS (STRAIN FP-1)	145-181							
PVD03_VACCV	PROTEIN D5	VACCINIA VIRUS (STRAIN COPENHAGEN)	123-157							
PVD03_VAVR	PROTEIN D5	VACCINIA VIRUS (STRAIN WR)	123-157							
PVD09_VACCC	PROTEIN D5	VARIOLA VIRUS	123-157							
PVD09_VACCV	PROTEIN D9	VACCINIA VIRUS (STRAIN COPENHAGEN)	126-160							
PVD09_VAVR	PROTEIN D9	VACCINIA VIRUS (STRAIN WR)	126-160							
PVD10_FOWP1	PROTEIN D9	VARIOLA VIRUS	126-160							
PVD10_SFVKA	PROTEIN D10	FOWLPOX VIRUS (STRAIN FP-1)	65-99	188-222						
PVD10_VAVR	PROTEIN D10	SHOPE FIBRONA VIRUS (STRAIN KASZA)	4-33							
PVDBP_CANYC	PROTEIN D10	VARIOLA VIRUS	67-103							
PVDBP_CAMVD	DNA-BINDING PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CM-1841)	1-35							
PVDBP_CAMVE	DNA-BINDING PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN D11)	1-35							
PVDBP_CAMVH	DNA-BINDING PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN BDC)	1-35							
PVDBP_CAMVS	DNA-BINDING PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN NY115)	1-35							
PVE02_VACCC	DNA-BINDING PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	1-35							
PVE02_VACCV	PROTEIN E3	VACCINIA VIRUS (STRAIN COPENHAGEN)	282-316							
PVE02_VAVR	PROTEIN E2	VACCINIA VIRUS (STRAIN WR)	282-316							
PVE03_VACCC	PROTEIN E3	VARIOLA VIRUS	282-316							
PVE03_VACCV	PROTEIN E3	VACCINIA VIRUS (STRAIN COPENHAGEN)	17-61							
PVE03_VAVR	PROTEIN E3	VACCINIA VIRUS (STRAIN WR)	17-61							













PEptide	ALLNOTES	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
ELISA NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PVGLG_BRSVC	SPIKE GLYCOPROTEIN PRECURSOR	BOVINE EPHEMERAL FEVER VIRUS	506-612	104-118						
PVGLG_HRSV1	MAJOR SURFACE GLYCOPROTEIN G	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COPEHAGE)	30-70							
PVGLG_HRSV2	MAJOR SURFACE GLYCOPROTEIN G	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN)	30-81							
PVGLG_HRSV3	MAJOR SURFACE GLYCOPROTEIN G	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RSD042)	30-85							
PVGLG_HRSV4	MAJOR SURFACE GLYCOPROTEIN G	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RSD1734)	30-85							
PVGLG_HRSV5	MAJOR SURFACE GLYCOPROTEIN G	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RSD1857)	30-107							
PVGLG_HRSV6	MAJOR SURFACE GLYCOPROTEIN G	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RSD1900)	30-85							
PVGLG_HRSV7	MAJOR SURFACE GLYCOPROTEIN G	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RSD256)	30-85							
PVGLG_HRSV8	MAJOR SURFACE GLYCOPROTEIN G	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RSD614)	30-85							
PVGLG_HRSV9	MAJOR SURFACE GLYCOPROTEIN G	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN)	30-81							
PVGLG_HRSV10	MAJOR SURFACE GLYCOPROTEIN G	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	30-67							
PVGLG_HRSV11	MAJOR SURFACE GLYCOPROTEIN G	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	35-85							
PVGLG_HRSV12	MAJOR SURFACE GLYCOPROTEIN G	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP A / STRAIN)	271-305							
PVGLG_SIGMA	GLYCOPROTEIN G PRECURSOR	EQUINE HERPESVIRUS TYPE 4 (STRAIN 1942)	344-381	464-498						
PVGLG_SYNV	SPIKE GLYCOPROTEIN PRECURSOR	SIGMA VIRUS	448-523							
PVGLG_VHSV0	SPIKE GLYCOPROTEIN PRECURSOR	SONCHUS YELLOW NET VIRUS	448-523							
PVGLG_VSVIG	SPIKE GLYCOPROTEIN PRECURSOR	VIRAL HEMORRHAGIC SEPTICEMIA VIRUS (STRAIN 07-71)	363-397							
PVGLG_EBV	SPIKE GLYCOPROTEIN PRECURSOR	VESICULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN G476-510)	33-87	160-201	316-330	653-694				
PVGLG_HCNVA	GLYCOPROTEIN GP3 PRECURSOR	EPSTEIN-BARR VIRUS (STRAIN D95-4)	103-137	270-311	693-741					
PVGLG_HCNVT	GLYCOPROTEIN H PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	102-136	692-740						
PVGLG_HSV1	GLYCOPROTEIN H PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN TOWNIE)	447-481							
PVGLG_HSV2	GLYCOPROTEIN H PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	447-481							
PVGLG_HSV3	GLYCOPROTEIN H PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN IFEN)	447-481							
PVGLG_HSV4	GLYCOPROTEIN H PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 4 / STRAIN COOPER)	357-406							
PVGLG_HSV5	GLYCOPROTEIN H PRECURSOR	BOVINE HERPESVIRUS TYPE 1 (STRAIN COOPER)	364-416							
PVGLG_HSV6	GLYCOPROTEIN H PRECURSOR	EQUINE HERPESVIRUS TYPE 4 (STRAIN 1942)	314-379	414-455						
PVGLG_HSV7	GLYCOPROTEIN H PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD47) AND (ISOLATE HV)	327-372	407-448						
PVGLG_HCNVS	GLYCOPROTEIN H PRECURSOR	HERPESVIRUS SAIMIRI (STRAIN 11)	32-66	374-433	664-712					
PVGLG_PVKA	GLYCOPROTEIN H PRECURSOR	MURINE CYTOMEGALOVIRUS (STRAIN SMITH)	440-474							
PVGLG_PVNI	GLYCOPROTEIN H PRECURSOR	PSEUDORABIES VIRUS (STRAIN KAPLAN)	326-260							
PVGLG_PVNI	GLYCOPROTEIN H PRECURSOR	PSEUDORABIES VIRUS (STRAIN NIA-3)	226-260							
PVGLG_VZV0	GLYCOPROTEIN H PRECURSOR	PSEUDORABIES VIRUS (STRAIN RICE)	226-260							
PVGLG_HCNVA	PROBABLE GLYCOPROTEIN H PRECURSOR	VARICELLA-ZOSTER VIRUS (STRAIN DUNIAS)	455-506							
PVGLG_BUNGE	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	43-111	323-359						
PVGLG_BUNL7	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	BUNYAVIRUS GERMISTON	512-567	683-737	1228-1262					
PVGLG_BUNSH	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	BUNYAVIRUS LA CROSSE (ISOLATE L74)	643-677	916-950						
PVGLG_BUNYW	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	BUNYAVIRUS SNOWSHOE HARE	643-677							
PVGLG_DUGBY	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	BUNYAVIRUS SNOWSHOE HARE	340-374	504-563	903-939					
PVGLG_HANTB	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	DUGBE VIRUS	937-989	1239-1300						
PVGLG_HANTH	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN B-1)	693-727							
PVGLG_HANTL	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN H010)	72-106							
PVGLG_HANTV	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN LEE)	72-106							
PVGLG_INSV	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN 76-118)	72-106							
PVGLG_PHV	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	IMPATIENS NECROTIC SPOT VIRUS	1067-1101							
PVGLG_PTPV	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	PROSPECT HILL VIRUS	73-111							
PVGLG_SEOU8	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	PUNTA TORO PHEBOVIRUS	149-251							
PVGLG_SEOUR	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	SEOU VIRUS (STRAIN 80-39)	693-727							
PVGLG_SEOUS	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	SEOU VIRUS (STRAIN R2)	694-728							
PVGLG_BEV	IMMEDIATE EARLY GLYCOPROTEIN PRECURSOR	SEOU VIRUS (STRAIN SR-1)	693-730							
PVGLP_BEV	NONSTRUCTURAL GLYCOPROTEIN GNS PRECURSOR	BOVINE EPHEMERAL FEVER VIRUS	377-414	513-569						
PVGLX_PVRI	PEPLOMER GLYCOPROTEIN PRECURSOR	BERNE VIRUS	43-82	90-124	622-656	1128-1236				
PVGLY_JURN	SECRETED GLYCOPROTEIN G	PSEUDORABIES VIRUS (STRAIN RICE)	420-461							
PVGLY_LASSG	GLYCOPROTEIN POLYPROTEIN PRECURSOR	JUNIN ARENAVIRUS	303-349							

GENE	ALLIOTIS	All Viruses (no bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
FILENAME	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PVGLY_LASSJ	GLYCOPROTEIN POLYPROTEIN PRECURSOR	LASSA VIRUS (STRAIN GA391)	317-360	381-422						
PVGLY_LYCVB	GLYCOPROTEIN POLYPROTEIN PRECURSOR	LASSA VIRUS (STRAIN JOSIAH)	318-361	389-423						
PVGLY_LYCVW	GLYCOPROTEIN POLYPROTEIN PRECURSOR	LYMPHOCTIC CHOROMENINGITIS VIRUS (STRAIN ABRASTRON)	313-363	395-432						1
PVGLY_NOPEI	GLYCOPROTEIN POLYPROTEIN PRECURSOR	LYMPHOCTIC CHOROMENINGITIS VIRUS (STRAIN WE)	312-362	394-431						
PVGLY_TACV	GLYCOPROTEIN POLYPROTEIN PRECURSOR	MOPEIA VIRUS	316-359	393-432						
PVGLY_TACV3	GLYCOPROTEIN POLYPROTEIN PRECURSOR	PICHINDE ARENA VIRUS	314-375							
PVGLY_TACV7	GLYCOPROTEIN POLYPROTEIN PRECURSOR	TACARIBE VIRUS	315-363							
PVGLY_TACV7	GLYCOPROTEIN POLYPROTEIN PRECURSOR	TACARIBE VIRUS (STRAIN V5)	301-351	382-416						
PVGLY_TACV7	GLYCOPROTEIN POLYPROTEIN PRECURSOR	TACARIBE VIRUS (STRAIN V7)	302-350	381-415						
PVGNB_CNAV	GLYCOPROTEIN POLYPROTEIN PRECURSOR	TACARIBE VIRUS (STRAIN TRVL 11598)	301-351	382-416						
PVGNB_CNAV	GLYCOPROTEIN POLYPROTEIN PRECURSOR	COMPEA MOSAIC VIRUS	835-869							
PVGNB_CNAV	GENOME POLYPROTEIN II	COMPEA MOSAIC VIRUS	160-201							
PVGNB_CNAV	GENOME POLYPROTEIN M	COMPEA MOSAIC VIRUS	192-226	758-792	874-915					
PVGNB_CNAV	GENOME POLYPROTEIN N	COMPEA MOSAIC VIRUS	192-226	758-792	874-915					
PVGNB_CNAV	GENOME POLYPROTEIN M	RED CLOVER NOTTLE VIRUS	874-915	913-946						
PVGP_EBOV	PROBABLE MEMBRANE ANTIGEN GPB3	RED CLOVER NOTTLE VIRUS	94-149							
PVGP_EBOV	STRUCTURAL GLYCOPROTEIN PRECURSOR	EBOLA VIRUS	280-321	314-368	469-503					
PVGP_MABVP	STRUCTURAL GLYCOPROTEIN PRECURSOR	MARBURG VIRUS (STRAIN MUSOKE)	562-596							
PVGP_MABVP	STRUCTURAL GLYCOPROTEIN PRECURSOR	MARBURG VIRUS (STRAIN POPP)	562-596							
PVH02_VACCC	LATE PROTEIN H2	VACCINIA VIRUS (STRAIN COPENHAGEN)	58-92							
PVH02_VACCC	LATE PROTEIN H2	VACCINIA VIRUS (STRAIN WR)	58-94							
PVH02_VACCC	LATE PROTEIN H2	VARIOLA VIRUS	58-92							
PVH02_VACCC	PROTEIN H3	VACCINIA VIRUS (STRAIN COPENHAGEN)	118-185							
PVH02_VACCC	PROTEIN H3	VACCINIA VIRUS (STRAIN WR)	118-185							
PVH02_VACCC	PROTEIN H3	VARIOLA VIRUS	136-203							
PVH02_VACCC	PROBABLE HELICASE	LILY STAPTONLESS VIRUS	126-160							
PVH02_VACCC	HOST RANGE PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	216-279							
PVH02_VACCC	HOST RANGE PROTEIN	VACCINIA VIRUS (STRAIN WR)	216-279							
PVH02_VACCC	PROTEIN I3	VACCINIA VIRUS (STRAIN COPENHAGEN)	150-193	210-244						
PVH02_VACCC	PROTEIN I3	VACCINIA VIRUS (STRAIN WR)	150-193	210-244						
PVH02_VACCC	PROTEIN I3	VARIOLA VIRUS	150-193	210-244						
PVH02_VACCC	PROTEIN I6	VACCINIA VIRUS (STRAIN WR)	58-92							
PVH02_VACCC	PROTEIN I6	VARIOLA VIRUS	58-92							
PVH02_VACCC	PROTEIN I7	VARIOLA VIRUS	371-407							
PVH02_VACCC	PUTATIVE RNA HELICASE I8	VACCINIA VIRUS (STRAIN COPENHAGEN)	548-589							
PVH02_VACCC	PUTATIVE RNA HELICASE I8	VACCINIA VIRUS (STRAIN WR)	548-589							
PVH02_VACCC	PUTATIVE RNA HELICASE I8	VARIOLA VIRUS	548-589							
PVH02_VACCC	53 KD IMMEDIATE-EARLY PROTEIN I	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	78-112	171-205	368-402	416-450				
PVH02_VACCC	53 KD IMMEDIATE-EARLY PROTEIN I	HUMAN CYTOMEGALOVIRUS (STRAIN TOWNE)	78-112	171-205	368-402	416-450				
PVH02_VACCC	IMMEDIATE-EARLY PROTEIN I	MURINE CYTOMEGALOVIRUS (STRAIN SMITH)	244-297							
PVH02_VACCC	IMMEDIATE-EARLY PROTEIN I2	ORGVIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS	94-128	305-395						
PVH02_VACCC	IMMEDIATE-EARLY REGULATORY PROTEIN IE-N	AUTOGAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	277-407							
PVH02_VACCC	VIRION INFECTIVITY FACTOR	CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (STRAIN CORK)	23-92							
PVH02_VACCC	VIRION INFECTIVITY FACTOR	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALUMA)	53-94							
PVH02_VACCC	VIRION INFECTIVITY FACTOR	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO)	32-40							
PVH02_VACCC	VIRION INFECTIVITY FACTOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (ARV25F7 ISOLATE)	1-42	62-96						
PVH02_VACCC	VIRION INFECTIVITY FACTOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (BHI0.BRU.HXB2.PV)	1-42	62-96						
PVH02_VACCC	VIRION INFECTIVITY FACTOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (ELI ISOLATE)	1-42	62-96						
PVH02_VACCC	VIRION INFECTIVITY FACTOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (ELI ISOLATE)	1-42	62-96						
PVH02_VACCC	VIRION INFECTIVITY FACTOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (HCSF ISOLATE)	1-42	62-96						
PVH02_VACCC	VIRION INFECTIVITY FACTOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (MAL ISOLATE)	1-42	62-96						
PVH02_VACCC	VIRION INFECTIVITY FACTOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (MN ISOLATE)	1-42	62-96						
PVH02_VACCC	VIRION INFECTIVITY FACTOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (NEW YORK 3 ISOL)	1-42	62-96						







GENE	ALL NOTIS	ALL Viruses (no bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
HAEMAGGLUTININ	PROTEIN	VIRUS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
HAEMAGGLUTININ	MAJOR SURFACE ANTIGEN PRECURSOR	WOODCHUCK HEPATITIS VIRUS 1	210-247							
HAEMAGGLUTININ	PROBABLE MAJOR SURFACE ANTIGEN PRECURSOR	WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE)	210-247							
HAEMAGGLUTININ	MATRIX PROTEIN 1	DIORI VIRUS (STRAIN INDIAN/11/1961)	201-235							
HAEMAGGLUTININ	MATRIX (M1) PROTEIN	INFLUENZA A VIRUS (STRAIN MANN ARBOR/660)	92-126	174-222						
HAEMAGGLUTININ	MATRIX (M2) PROTEIN	INFLUENZA A VIRUS (STRAIN ADANGOK/179)	92-126	174-222						
HAEMAGGLUTININ	MATRIX (M3) PROTEIN	INFLUENZA A VIRUS (STRAIN ACAMIELA/NGOLIA/82)	31-79							
HAEMAGGLUTININ	MATRIX (M4) PROTEIN	INFLUENZA A VIRUS (STRAIN AFORT WARREN/150) AND (STR)	92-126	174-222						
HAEMAGGLUTININ	MATRIX (M5) PROTEIN	INFLUENZA A VIRUS (STRAIN AFOWL FLAQUE VIRUS/ROSTOCK)	92-126	174-222						
HAEMAGGLUTININ	MATRIX (M6) PROTEIN	INFLUENZA A VIRUS (STRAIN AFOWL FLAQUE VIRUS/VEYDRID)	92-126	174-222						
HAEMAGGLUTININ	MATRIX (M7) PROTEIN	INFLUENZA A VIRUS (STRAIN ALENINGRAD/134/57)	92-126	174-222						
HAEMAGGLUTININ	MATRIX (M8) PROTEIN	INFLUENZA A VIRUS (STRAIN ALENINGRAD/134/17/57)	92-126	174-222						
HAEMAGGLUTININ	MATRIX (M9) PROTEIN	INFLUENZA A VIRUS (STRAIN ANALL ARDNEW YORK/63/50/78)	92-126	174-222						
HAEMAGGLUTININ	MATRIX (M10) PROTEIN	INFLUENZA A VIRUS (STRAIN APURTO RICO/82/4)	92-126	174-222						
HAEMAGGLUTININ	MATRIX (M11) PROTEIN	INFLUENZA A VIRUS (STRAIN APURTO RICO/82/4)	92-126	174-222						
HAEMAGGLUTININ	MATRIX (M12) PROTEIN	INFLUENZA A VIRUS (STRAIN AODORN/10/77/3)	92-126	174-222						
HAEMAGGLUTININ	MATRIX (M13) PROTEIN	INFLUENZA A VIRUS (STRAIN AOWILSON-SMITH/10/3)	92-126	174-222						
HAEMAGGLUTININ	MATRIX (M14) PROTEIN	INFLUENZA A VIRUS (STRAIN ASWINE/5/0/15/0)	92-126	174-222						
HAEMAGGLUTININ	MATRIX (M15) PROTEIN	INFLUENZA B VIRUS (STRAIN BIANN ARBOR/1/66 [COLD-ADAPTE])	175-209							
HAEMAGGLUTININ	MATRIX (M16) PROTEIN	INFLUENZA B VIRUS (STRAIN BIANN ARBOR/1/66 [WILD-TYPE])	175-209							
HAEMAGGLUTININ	MATRIX (M17) PROTEIN	INFLUENZA B VIRUS (STRAIN BINGAPORE/22/79)	175-209							
HAEMAGGLUTININ	MATRIX (M18) PROTEIN	INFLUENZA B VIRUS (STRAIN BIANN ARBOR/1/66 [COLD-ADAPTE])	132-184							
HAEMAGGLUTININ	MATRIX (M19) PROTEIN	INFLUENZA B VIRUS (STRAIN BIANN ARBOR/1/66 [WILD-TYPE])	132-184							
HAEMAGGLUTININ	MATRIX (M20) PROTEIN	INFLUENZA B VIRUS (STRAIN BLEE/40)	132-184							
HAEMAGGLUTININ	MATRIX (M21) PROTEIN	INFLUENZA B VIRUS (STRAIN BINGAPORE/22/79)	132-184							
HAEMAGGLUTININ	MATRIX (M22) PROTEIN	INFLUENZA B VIRUS (STRAIN LAUSANNE)	46-80	143-197						
HAEMAGGLUTININ	MATRIX (M23) PROTEIN	MYXOMA VIRUS (STRAIN COPENHAGEN)	64-112							
HAEMAGGLUTININ	MATRIX (M24) PROTEIN	VACCINIA VIRUS (STRAIN WR)	64-112							
HAEMAGGLUTININ	MATRIX (M25) PROTEIN	BOVINE ROTAVIRUS (GROUP C / STRAIN SIINTOKU)	64-169							
HAEMAGGLUTININ	MATRIX (M26) PROTEIN	BOVINE ROTAVIRUS (GROUP C / STRAIN SIINTOKU)	64-117	121-169						
HAEMAGGLUTININ	MATRIX (M27) PROTEIN	ADENO-ASSOCIATED VIRUS 2	91-125	212-231						
HAEMAGGLUTININ	MATRIX (M28) PROTEIN	RICE STRIPE VIRUS	129-163							
HAEMAGGLUTININ	MATRIX (M29) PROTEIN	BOVINE PARVOVIRUS	221-235							
HAEMAGGLUTININ	MATRIX (M30) PROTEIN	ALUTIAN NINK DISEASE PARVOVIRUS (STRAIN G)	19-60	270-304						
HAEMAGGLUTININ	MATRIX (M31) PROTEIN	AEDS DENDROCYTOSIS VIRUS (STRAIN GY 002 003)	276-339	521-571	585-640	715-760	700-849			
HAEMAGGLUTININ	MATRIX (M32) PROTEIN	FELINE PANLEUKOPENIA VIRUS (STRAIN 193)	53-98							
HAEMAGGLUTININ	MATRIX (M33) PROTEIN	NINK ENTERITIS VIRUS (STRAIN ADASI/IRI)	53-98							
HAEMAGGLUTININ	MATRIX (M34) PROTEIN	MURINE MINUTE VIRUS (STRAIN MINVI)	35-91	261-297						
HAEMAGGLUTININ	MATRIX (M35) PROTEIN	MURINE MINUTE VIRUS	35-87	259-297						
HAEMAGGLUTININ	MATRIX (M36) PROTEIN	BOVINE PARVOVIRUS	181-222							
HAEMAGGLUTININ	MATRIX (M37) PROTEIN	CANINE PARVOVIRUS (STRAIN N)	53-98							
HAEMAGGLUTININ	MATRIX (M38) PROTEIN	HUMAN PARVOVIRUS III	216-270							
HAEMAGGLUTININ	MATRIX (M39) PROTEIN	HUMAN PARVOVIRUS III	35-76	259-297						
HAEMAGGLUTININ	MATRIX (M40) PROTEIN	PORCINE PARVOVIRUS (STRAIN NADL-2)	24-77	169-210	109-146					
HAEMAGGLUTININ	MATRIX (M41) PROTEIN	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	107-141							
HAEMAGGLUTININ	MATRIX (M42) PROTEIN	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	107-141							
HAEMAGGLUTININ	MATRIX (M43) PROTEIN	BLUETONGUE VIRUS (SEROTYPE 1 / ISOLATE AUSTRALIA)	107-141							
HAEMAGGLUTININ	MATRIX (M44) PROTEIN	BLUETONGUE VIRUS (SEROTYPE 1 / ISOLATE SOUTH AFRICA)	107-141							
HAEMAGGLUTININ	MATRIX (M45) PROTEIN	BLUETONGUE VIRUS (SEROTYPE 20 / ISOLATE AUSTRALIA)	107-141							
HAEMAGGLUTININ	MATRIX (M46) PROTEIN	EPIDEMIC HEMORRAGIC DISEASE VIRUS (SEROTYPE 2 / STRAIN)	401-454							
HAEMAGGLUTININ	MATRIX (M47) PROTEIN	INFLUENZA A VIRUS (STRAIN MANN ARBOR/660)	49-83							
HAEMAGGLUTININ	MATRIX (M48) PROTEIN	INFLUENZA A VIRUS (STRAIN ACAMIELA/NGOLIA/82)	37-71							









GENE	ALL NOTES	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
ELFEN	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PVORI_S1VEA	165 KD PROTEIN	POTATO VIRUS X (STRAIN CP) (PVX)	510-347							
PVORI_S1VEA	130 KD PROTEIN	STRAWBERRY MILD YELLOW EDGE-ASSOCIATED VIRUS (SMVE)	308-342	911-965						
PVORI_WCNVA	147 KD PROTEIN	WHITE CLOVER MOSAIC VIRUS (STRAIN M) (WCMV)	1240-1289							
PVORI_NPVAC	147 KD PROTEIN	WHITE CLOVER MOSAIC VIRUS (STRAIN O) (WCMV)	1240-1289							
PVORI_NPVOP	P10 PROTEIN	AUTOGRAPHIA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS (7-41)	7-41							
PVORI_RSDV	P10 PROTEIN	ORGANIA PSEUDOTUGATA MULTICAPSID POLYIHDROSIS VIRUS (7-50)	7-50							
PVORI_RSDV	PROTEIN S10	RICE BLACK STREAKED DWARF VIRUS (RSDV)	319-382	395-429	506-556					
PVORI_WTV	NONSTRUCTURAL PROTEIN PNS10	RICE GALL DWARF VIRUS (RGDV)	186-273							
PVORI_RDV	NONSTRUCTURAL PROTEIN PNS10	WOUND TUNOR VIRUS (WTV)	220-254							
PVORI_WTV	NONSTRUCTURAL PROTEIN PNS11	RICE DWARF VIRUS (RDV)	25-80	273-314						
PVORI_RDV	NONSTRUCTURAL PROTEIN PNS11	WOUND TUNOR VIRUS (WTV)	16-74							
PVORI_WTV	NONSTRUCTURAL PROTEIN P11	RICE DWARF VIRUS (RDV)	160-181							
PVORI_WTV	NONSTRUCTURAL PROTEIN P11	WOUND TUNOR VIRUS (WTV)	68-108							
PVORI_HSTED	NONSTRUCTURAL PROTEIN PNS12	WOUND TUNOR VIRUS (WTV)	68-108							
PVORI_HSTED	CAPSID ASSEMBLY AND DNA NATURATION PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P) (EHV-1)	189-231							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	41-82	146-180						
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	HERPES SIMPLEX VIRUS (TYPE 6) (STRAIN UGANDA-1102)	47-81							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	EBOLA VIRUS	166-200							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	HERPESVIRUS SANIRU (STRAIN 11)	36-77							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	HERPESVIRUS SANIRU (STRAIN 11)	41-78							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	ORGANIA PSEUDOTUGATA MULTICAPSID POLYIHDROSIS VIRUS (118-159)	118-159							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS) (VZV)	47-81							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4) (STRAIN VACC1)	136-188	270-304	410-465	614-662	684-720	976-1036		
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	BLUETONGUE VIRUS (SEROTYPE 10) (ISOLATE USA)	168-225							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	BLUETONGUE VIRUS (SEROTYPE 11) (ISOLATE USA)	77-111	559-593						
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	BLUETONGUE VIRUS (SEROTYPE 12) (ISOLATE USA)	77-111	168-209						
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	BLUETONGUE VIRUS (SEROTYPE 13) (ISOLATE SOUTH AFRICA)	119-153	576-610	608-702	461-495	891-929			
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	EPIDEMIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1) (EHDV1)	72-106	247-301	403-453	607-655	675-714			
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	BOVINE ROTAVIRUS (STRAIN 8F)	2-94	482-516	524-558	608-656	676-715			
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	BOVINE ROTAVIRUS (STRAIN 8F)	2-94	482-516	524-558	608-656	676-715			
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	PORCINE ROTAVIRUS (SEROTYPE 1) (STRAIN WA)	17-97	492-526	533-567	617-658	685-764			
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	PORCINE ROTAVIRUS (SEROTYPE 1) (STRAIN WA)	17-97	492-526	533-567	617-658	685-764			
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	SINIAN 11 ROTAVIRUS (STRAIN SA11)	1-50	52-99	194-228	515-551	599-643	705-746		
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	AFRICAN SWINE FEVER VIRUS (STRAIN E-73) (ASFV)	36-96	483-517	608-656	680-735				
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	AFRICAN SWINE FEVER VIRUS (STRAIN E-73) (ASFV)	29-89							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV)	227-261							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	EBOLA VIRUS	79-89							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	EBOLA VIRUS	80-119							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	AUTOGRAPHIA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS (USNPV)	14-102	224-258						
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	BONBYX MORI NUCLEAR POLYIHDROSIS VIRUS (USNPV)	54-102							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	VACCINIA VIRUS (STRAIN COPESTAGEN)	140-181							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	VACCINIA VIRUS (STRAIN L-1VP)	17-51							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	VACCINIA VIRUS (STRAIN WR)	140-181							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	VARICELLA VIRUS	141-182							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4) (STRAIN VACC1)	173-214	240-274	662-704					
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	BLUETONGUE VIRUS (SEROTYPE 10) (ISOLATE USA)	214-255	833-894						
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	BLUETONGUE VIRUS (SEROTYPE 11) (ISOLATE USA)	214-255	833-894						
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	BLUETONGUE VIRUS (SEROTYPE 12) (ISOLATE AUSTRALIA)	214-255	833-894						
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	EPIDEMIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1) (EHDV1)	208-246	798-832	831-892					
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	EPIDEMIC HEMORRHAGIC DISEASE VIRUS	208-246	715-770	798-832					
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	GRAPEVINE FANLEAF VIRUS (GFLV)	96-133							
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	RICE DWARF VIRUS (RDV)	799-337	817-872						
PVORI_HSTED	PROBABLE CAPSID PROTEIN VP23	PORCINE ROTAVIRUS (GROUP C) (STRAIN COWDEN)	24-58	229-263	379-395	406-446	640-688			

PCGENE	ALLNOTES	ALL VITAMIN (no Bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
ELUSANIE	PROTEIN	VIRUS								
PV100_EBV	INNER CORE PROTEIN VP3	SINIAN 11 ROTAVIRUS (STRAIN SA11)	26-76							
PV100_HSV1	CAPSID PROTEIN P40	EPSTEIN-BARR VIRUS (STRAIN D95-8) (HUMAN HERPESVIRUS 4)	431-467	331-365	451-492	662-696				
PV100_HSV2	CAPSID PROTEIN P40	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	206-257	599-633						
PV100_ILTVT	CAPSID PROTEIN P40	EQUINE HERPESVIRUS TYPE 1 (STRAIN AIMP) (EQU 1)	180-245							
PV100_SNCVC	CAPSID PROTEIN P40	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE VM)	1-35	509-557						
PV100_VZV	CAPSID PROTEIN P40	SINIAN CYTOMEGALOVIRUS (STRAIN COLUBUS)	457-488							
PV100_NPVAC	CAPSID PROTEIN P40	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS) (VZV)	167-246	486-522						
PV101_ROT51	STRUCTURAL GLYCOPROTEIN GP1	AUTOGRAPIA CALIFORNICA NUCLEAR POLYOMEDNOSIS VIRUS (1) 12-166								
PV102_ROT51	OUTER CAPSID PROTEIN VP4	SINIAN 11 ROTAVIRUS (STRAIN SA11)	1-35	484-518	528-630					
PV104_VACCC	OUTER CAPSID PROTEIN VP4	SINIAN 11 ROTAVIRUS (STRAIN SA11)	1-35	237-518	531-646					
PV104_VACCC	MAJOR CORE PROTEIN P4A PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	355-359	718-763	794-838	857-891				
PV104_VARV	MAJOR CORE PROTEIN P4A PRECURSOR	VACCINIA VIRUS (STRAIN WIR)	262-296	355-359	718-763	794-838	857-891			
PV104_FONPV	MAJOR CORE PROTEIN P4B PRECURSOR	VARICELLA-ZOSTER VIRUS	355-389	719-764	795-839	858-892				
PV104_VACCC	MAJOR CORE PROTEIN P4B PRECURSOR	FOWLPOX VIRUS	131-172	296-310						
PV104_VACCC	MAJOR CORE PROTEIN P4B PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	1-37	325-163	249-283					
PV104_VARV	MAJOR CORE PROTEIN P4B PRECURSOR	VACCINIA VIRUS (STRAIN WIR)	1-37	325-163	249-283					
PV104_BTIV10	MAJOR CORE PROTEIN P4B PRECURSOR	VARIOLA VIRUS	1-37	325-163	249-283					
PV104_BTIV11	VP4 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	579-617	619-653						
PV104_BTIV11	VP4 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	569-607	609-643						
PV104_BTIV11	VP4 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 12 / ISOLATE USA)	569-607	609-643						
PV104_NCDV	VP4 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	569-607	609-643						
PV104_RDV	OUTER CAPSID PROTEIN VP4	NEBRASKA CALF DIARRHEA VIRUS (STRAIN NCDV-LINCOLN)	484-518	528-630						
PV104_ROT84	NONSTRUCTURAL PROTEIN PNS4	RICE DWARF VIRUS (RDV)	388-437	444-478	627-679					
PV104_ROT84	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVIRUS (SEROTYPE 6 / STRAIN B641)	1-35	112-146	338-379	484-518	528-630			
PV104_ROT84	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVIRUS (STRAIN C486)	1-35	484-518	528-630					
PV104_ROT84	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVIRUS (STRAIN UK)	1-35	112-146	338-379	484-518	528-630			
PV104_ROT84	OUTER CAPSID PROTEIN VP4	EQUINE ROTAVIRUS (STRAIN H-2)	1-35	112-146	227-274	345-379	484-518	528-630		
PV104_ROT84	OUTER CAPSID PROTEIN VP4	ROTAVIRUS (GROUP B / STRAIN IDIR)	117-151	476-519	337-378	483-517	530-645			
PV104_ROT84	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 1076)	1-35	236-273	337-378	483-517	528-630			
PV104_ROT84	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN RV-5)	1-35	236-273	337-378	483-517	528-630			
PV104_ROT84	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 69M)	1-35	112-146	237-274	338-379	484-518	531-646		
PV104_ROT84	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN DS1)	1-35	236-273	337-378	483-517	528-630			
PV104_ROT84	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN K3)	1-35	237-274	345-379	484-518	528-588			
PV104_ROT84	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN KU)	1-35	237-274	483-517	527-652				
PV104_ROT84	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN L26)	1-35	236-273	337-378	483-517	527-632			
PV104_ROT84	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN M17)	1-35	337-378	483-517	530-645				
PV104_ROT84	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN M11)	1-35	237-274	338-379	484-518	531-645			
PV104_ROT84	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN P)	1-35	236-273	337-378	483-517	527-632			
PV104_ROT84	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN RBV)	1-38	91-146	227-274					
PV104_ROT84	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST THOMAS J)	1-35	236-273	337-378	483-517	530-644			
PV104_ROT84	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN VA70)	1-35	237-273	344-378	483-517	527-632			
PV104_ROT84	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	1-35	237-273	344-378	483-517	527-632			
PV104_ROT84	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN OSU)	112-146	484-518	528-639					
PV104_ROT84	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	6-40	127-161	241-278	293-334	380-614			
PV104_ROT84	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN GOTTFRIED)	1-35	236-273	337-378	483-517	530-564	569-638		
PV104_ROT84	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN YAI)	1-38	112-146	237-274	338-379	484-518	528-639		
PV104_ROT84	OUTER CAPSID PROTEIN VP4	RUESUS ROTAVIRUS	1-38	484-518	528-630	338-379	484-518	531-646		
PV104_ROT84	OUTER CAPSID PROTEIN VP4	SINIAN 11 ROTAVIRUS (STRAIN SA11-FEN)	1-35							
PV104_WTV	DE OUTER CAPSID PROTEIN VP4	SINIAN 11 ROTAVIRUS (STRAIN SA11-SEN)	1-35	237-274	345-379	484-518	531-646			
PV104_AHSV4	NONSTRUCTURAL PROTEIN PMS4	WOUND TUMOR VIRUS (WTV)	28-62	565-621						
PV105_BSD	OUTER CAPSID PROTEIN VP3	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4 / STRAIN VACC)	7-58	113-229						
PV105_BTIV10	OUTER CAPSID PROTEIN VP3	BROADHAVEN VIRUS (BRV)	45-46	98-226						



PCGENE	ALLIOTIS	All Viruses (no bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
FILENAME	PROTEIN	VIRUS	14-58	92-150	154-222	404-438				AREA.1
PVP5_BT1V11	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	14-58	92-150	154-222	404-438				
PVP5_BT1V11	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	14-58	92-150	154-222	404-438				
PVP5_BT1V1A	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	14-58	154-222	404-438					
PVP5_BT1V1S	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE AUSTRALIA)	14-58	92-143	148-222	404-438				
PVP5_BT1V2A	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE SOUTH AFRICA)	14-58	92-143	148-222	404-438				
PVP5_EIDV1	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	14-58	92-222	404-438					
PVP5_RDV	OUTER CAPSID PROTEIN VP5	EPIDEMIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1) (EIDV)	24-58	92-126	163-233	291-325				
PVP5_WTV	OUTER COAT PROTEIN P5	RICE DWARF VIRUS (RDV)	38-86	95-136	550-594					
PVP6_BT1V10	OUTER COAT PROTEIN P5	WOUND TUMOR VIRUS (WTV)	414-503	547-581	751-798					
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	163-215							
PVP6_BT1V10	OUTER COAT PROTEIN P5	MAIZE ROUGH DWARF VIRUS (MRDV)	128-202							
PVP6_BT1V10	OUTER COAT PROTEIN P5	AUTOGRAFIA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS (C)	29-96	351-386						
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	47-88	159-207	214-251					
PVP6_BT1V10	OUTER COAT PROTEIN P5	ORGANIA PSEUDOSUGATA MULTICAPSID POLYIHDROSIS VIRUS (C)	296-361	431-479						
PVP6_BT1V10	OUTER COAT PROTEIN P5	AUTOGRAFIA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS (C)	44-78	289-364	443-477					
PVP6_BT1V10	OUTER COAT PROTEIN P5	GALLERIA MELLONELLA NUCLEAR POLYIHDROSIS VIRUS (GN)	206-281							
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	159-211							
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	159-211							
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	68-102	159-211						
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE SOUTH AFRICA)	12-78	163-211						
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	44-78	135-187						
PVP6_BT1V10	OUTER COAT PROTEIN P5	RICE DWARF VIRUS (RDV)	150-191	296-344	360-401					
PVP6_BT1V10	OUTER COAT PROTEIN P5	WOUND TUMOR VIRUS (WTV)	144-178	286-334	400-434					
PVP6_BT1V10	OUTER COAT PROTEIN P5	WOUND TUMOR VIRUS (STRAIN NJ) (WTV)	144-178	286-334						
PVP6_BT1V10	OUTER COAT PROTEIN P5	AUTOGRAFIA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS (C)	187-456							
PVP6_BT1V10	OUTER COAT PROTEIN P5	CHORISTHEURA FUNIFERANA NUCLEAR POLYIHDROSIS VIRUS (C)	183-453							
PVP6_BT1V10	OUTER COAT PROTEIN P5	HERPES VIRUS SAIMIRI (STRAIN 11)	50-99	163-211	911-984					
PVP6_BT1V10	OUTER COAT PROTEIN P5	AUTOGRAFIA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS (C)	44-78	363-397	400-440					
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA) (SEROTYPE 10)	201-235							
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	184-238							
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	184-238							
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE AUSTRALIA)	184-235							
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE SOUTH AFRICA)	184-228							
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	184-238							
PVP6_BT1V10	OUTER COAT PROTEIN P5	EPIDEMIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1) (EIDV)	16-50	134-178						
PVP6_BT1V10	OUTER COAT PROTEIN P5	RICE DWARF VIRUS (RDV)	47-95	172-235						
PVP6_BT1V10	OUTER COAT PROTEIN P5	WOUND TUMOR VIRUS (WTV)	47-84	195-243	451-495					
PVP6_BT1V10	OUTER COAT PROTEIN P5	AUTOGRAFIA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS (C)	75-51	99-142	150-204	221-298				
PVP6_BT1V10	OUTER COAT PROTEIN P5	ORGANIA PSEUDOSUGATA MULTICAPSID POLYIHDROSIS VIRUS (C)	80-162	410-451						
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	54-102	185-219						
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	54-102	185-219						
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	54-102	185-219						
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	54-102	185-219						
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE AUSTRALIA)	54-102	185-219						
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE SOUTH AFRICA)	54-102	185-219						
PVP6_BT1V10	OUTER COAT PROTEIN P5	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	54-102	185-219						
PVP6_BT1V10	OUTER COAT PROTEIN P5	FOXP2 VIRUS	191-245							
PVP6_BT1V10	OUTER COAT PROTEIN P5	RICE DWARF VIRUS (RDV)	13-47	186-226						
PVP6_BT1V10	OUTER COAT PROTEIN P5	WOUND TUMOR VIRUS (WTV)	140-212							
PVP6_BT1V10	OUTER COAT PROTEIN P5	WOUND TUMOR VIRUS (STRAIN NJ) (WTV)	140-212							
PVP6_BT1V10	OUTER COAT PROTEIN P5	BARLEY YELLOW DWARF VIRUS (ISOLATE MAV-PS1) (BYDV)	25-59							
PVP6_BT1V10	OUTER COAT PROTEIN P5	AUTOGRAFIA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS (C)	146-233							



GENE	ALLNOTIS	ALL VITRUS (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
GENE	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PV309_ROTIN1	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (STRAIN L-26)	1-35	282-320						
PV309_ROTIN2	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN N37)	2-43	282-320						
PV309_ROTIN3	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN MO AND STRAIN DJ)	2-43	282-320						
PV309_ROTIN4	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN P)	282-320							
PV309_ROTIN5	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN S3)	282-320							
PV309_ROTIN6	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST THOMAS J)	18-56	208-242	282-320					
PV309_ROTIN7	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN VA70)	18-56	208-242	282-320					
PV309_ROTIN8	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	2-43	282-320						
PV309_ROTIN9	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN AT76)	282-320							
PV309_ROTIN10	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN CRV-4)	282-320							
PV309_ROTIN11	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 4 / STRAIN OSU)	2-56	208-242	282-320					
PV309_ROTIN12	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 5 / STRAIN OSU)	282-320							
PV309_ROTIN13	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 5 / STRAIN TER-41)	282-320							
PV309_ROTIN14	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 4 / STRAIN BEN-144)	18-56	208-242	282-320					
PV309_ROTIN15	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE K)	18-56	208-242	282-320					
PV309_ROTIN16	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 4 / STRAIN BMH-1)	18-56	208-242	282-320					
PV309_ROTIN17	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (STRAIN YN)	1-35	282-320						
PV309_ROTIN18	GLYCOPROTEIN VP7	RUES ROTAVIRUS	282-320							
PV309_ROTIN19	GLYCOPROTEIN VP7	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	282-320							
PV309_ROTIN20	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN NCDV)	73-161							
PV309_ROTIN21	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (GROUP C / STRAIN SIINTOKU)	17-58							
PV309_ROTIN22	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN UK)	73-161							
PV309_ROTIN23	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (STRAIN A31)	73-162							
PV309_ROTIN24	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (STRAIN A67 CLONE 2)	73-162							
PV309_ROTIN25	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (STRAIN A64 / CLONE 6)	73-162							
PV309_ROTIN26	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (GROUP C / STRAIN BRISTOL)	121-158							
PV309_ROTIN27	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	73-136							
PV309_ROTIN28	GLYCOPROTEIN VP7	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	73-162							
PV309_ROTIN29	GLYCOPROTEIN VP7	ROTAVIRUS (GROUP B / STRAIN ADRV) (ADULT DIARRHEA ROTAVIRUS)	96-130							
PV309_ROTIN30	GLYCOPROTEIN VP7	ROTAVIRUS (GROUP B / STRAIN IDIR)	9-68							
PV309_ROTIN31	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN RV-3)	100-145							
PV309_ROTIN32	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 69A)	107-144							
PV309_ROTIN33	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE G / STRAIN D37)	107-144							
PV309_ROTIN34	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN DS1)	111-145							
PV309_ROTIN35	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	111-145							
PV309_ROTIN36	GLYCOPROTEIN VP7	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	111-145							
PV309_ROTIN37	GLYCOPROTEIN VP7	TONATO BLACK RING VIRUS (STRAIN C) (TBRV)	217-265							
PV309_ROTIN38	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN SBL-1) AND MUMPS VIRUS (STRAIN SBL)	9-46							
PV309_ROTIN39	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN EDINGBOUGH 2) AND (STRAIN EDINGBOUGH 4)	13-47							
PV309_ROTIN40	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN EDINGBOUGH 4)	13-47							
PV309_ROTIN41	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN MATSUYAMA)	13-51							
PV309_ROTIN42	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN BELFAST)	13-52							
PV309_ROTIN43	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN ENDERS)	9-46							
PV309_ROTIN44	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN ERLV-LYNN)	9-46							
PV309_ROTIN45	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN KILHAM)	9-51							
PV309_ROTIN46	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN BRISTOL 1)	13-55							
PV309_ROTIN47	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN NITAHARA VACCINE)	13-51							
PV309_ROTIN48	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN TAKAHASHI)	13-47							
PV309_ROTIN49	GLYCOPROTEIN VP7	MUMPS VIRUS (STRAIN URABE VACCINE A19)	13-47							
PV309_ROTIN50	GLYCOPROTEIN VP7	REOVIRUS (TYPE 2 / STRAIN DEARING)	8-122	127-175	222-259					
PV309_ROTIN51	GLYCOPROTEIN VP7	REOVIRUS (TYPE 2 / STRAIN D510N5)	1-178							

PGCENE	ALLIOTIS	ALLIOTIS (on bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
FILENAME	PROTEIN	VIRUS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
PIV21_REVD	SIGNA 1 PROTEIN PRECURSOR	PEOVIRUS (TYPE 1 / STRAIN LANG)	31-107	112-198						
PIV22_REVD	SIGNA 2 PROTEIN	REOVIRUS (TYPE 1 / STRAIN DEARING)	350-384							
PIV23_REVD	SIGNA 2 PROTEIN	REOVIRUS (TYPE 1 / STRAIN LANG)	350-384							
PIV24_REVD	SIGNA 1-3 PROTEIN	REOVIRUS (TYPE 1 / STRAIN DEARING)	85-119							
PIV25_REVD	SIGNA 1-3 PROTEIN	REOVIRUS (TYPE 1 / STRAIN DEARING)	7-45							
PIV26_REVD	STRUCTURAL PROTEIN 2 PRECURSOR	HEPATITIS E VIRUS (STRAIN DUBNA) (HEV)	318-332							
PIV27_REVD	STRUCTURAL PROTEIN 2 PRECURSOR	HEPATITIS E VIRUS (STRAIN NEXICO) (HEV)	317-331							
PIV28_REVD	STRUCTURAL PROTEIN 2 PRECURSOR	HEPATITIS E VIRUS (STRAIN NYANNAR) (HEV)	316-332							
PIV29_REVD	STRUCTURAL PROTEIN 2 PRECURSOR	HEPATITIS E VIRUS (STRAIN PAKISTAN) (HEV)	318-332							
PIV30_REVD	STRUCTURAL PROTEIN 2	HEPATITIS E VIRUS (ISOLATE RHESUS) (HEV)	186-220							
PIV31_REVD	PROTEIN T3A	CAPRIPOX VIRUS (STRAIN INS-1)	120-138							
PIV32_REVD	T4 PROTEIN	CAPRIPOX VIRUS (STRAIN INS-1)	86-120							
PIV33_REVD	T4 PROTEIN	CAPRIPOX VIRUS (STRAIN KS-1)	86-120							
PIV34_REVD	PROBABLE DNA PACKAGING PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)	215-290	595-629						
PIV35_REVD	PROBABLE DNA PACKAGING PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	417-451	617-658						
PIV36_REVD	PROBABLE DNA PACKAGING PROTEIN	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	468-502							
PIV37_REVD	PROBABLE DNA PACKAGING PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADAP) (EHV-1)	11-45							
PIV38_REVD	PROBABLE DNA PACKAGING PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	98-136	598-744						
PIV39_REVD	PROBABLE DNA PACKAGING PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	226-267							
PIV40_REVD	PROBABLE DNA PACKAGING PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS) (VZV)	588-622							
PIV41_REVD	PROBABLE DNA PACKAGING PROTEIN	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIBA) (PIV-4A)	4-38							
PIV42_REVD	Y1 PROTEIN	SENDAI VIRUS (STRAIN 694)	104-138							
PIV43_REVD	HYPOTHETICAL 10.1 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	16-80							
PIV44_REVD	HYPOTHETICAL 10.8 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	4-65							
PIV45_REVD	HYPOTHETICAL 11.0 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	35-59							
PIV46_REVD	HYPOTHETICAL 11.9 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	10-96							
PIV47_REVD	HYPOTHETICAL 11.7 KD PROTEIN	TORACO YELLOW DWARF VIRUS (STRAIN AUSTRALIA) (TYDV)	13-87							
PIV48_REVD	HYPOTHETICAL 12.3 KD PROTEIN IN COAT PROTEIN	FELINE CALCIVIRUS (STRAIN CF108 FV) (FCV)	4-38							
PIV49_REVD	HYPOTHETICAL 12.1 KD PROTEIN IN COAT PROTEIN	FELINE CALCIVIRUS (STRAIN F9) (FCV)	4-38							
PIV50_REVD	HYPOTHETICAL 12.7 KD PROTEIN IN COAT PROTEIN	RABBIT HEMORRHAGIC DISEASE VIRUS (HVDV)	13-50							
PIV51_REVD	HYPOTHETICAL 12.7 KD PROTEIN IN COAT PROTEIN	RABBIT HEMORRHAGIC DISEASE VIRUS (STRAIN V-333) (HVDV)	13-50							
PIV52_REVD	HYPOTHETICAL 13.1 KD PROTEIN	CASSAVA LATEX VIRUS (STRAIN WEST KENYA 844)	40-77							
PIV53_REVD	HYPOTHETICAL 13.1 KD PROTEIN	CASSAVA LATEX VIRUS (STRAIN NIGERIAN)	43-77							
PIV54_REVD	HYPOTHETICAL 14.1 KD PROTEIN IN 19 KD PROTEIN	ORGANIA PSEUDOTUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPV)	16-67							
PIV55_REVD	HYPOTHETICAL 13.3 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	2-36	62-96						
PIV56_REVD	HYPOTHETICAL 13.7 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	5-19							
PIV57_REVD	HYPOTHETICAL PROTEIN C-10A	HUMAN ADENOVIRUS TYPE 2	119-166							
PIV58_REVD	HYPOTHETICAL 15.8 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	1-35	77-111						
PIV59_REVD	HYPOTHETICAL 17.8 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	1-45	119-133						
PIV60_REVD	HYPOTHETICAL 18.0 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	102-136							
PIV61_REVD	HYPOTHETICAL 20.4 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	73-107							
PIV62_REVD	HYPOTHETICAL 28.5 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	171-180							
PIV63_REVD	HYPOTHETICAL PROTEIN 2	SOYBEAN CHLOROTIC NOTTLE VIRUS	117-154							
PIV64_REVD	HYPOTHETICAL 31.5 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	7-97	100-141						
PIV65_REVD	HYPOTHETICAL 31.7 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	210-278							
PIV66_REVD	HYPOTHETICAL 37.7 KD PROTEIN	AUTOGRAFIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (33-241)	115-149							
PIV67_REVD	HYPOTHETICAL PROTEIN 3	SOYBEAN CHLOROTIC NOTTLE VIRUS	1-51							
PIV68_REVD	HYPOTHETICAL 5.9 KD PROTEIN	SOYBEAN CHLOROTIC NOTTLE VIRUS	56-94							
PIV69_REVD	HYPOTHETICAL 5.7 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	81-123	503-537	546-587	638-700				
PIV70_REVD	HYPOTHETICAL PROTEIN 8	SOYBEAN CHLOROTIC NOTTLE VIRUS	46-83							
PIV71_REVD	HYPOTHETICAL BANGH-ORF1 PROTEIN	FOWLPOX VIRUS (ISOLATE HP-43) (FPOV) (H1N1)	74-115	184-221						

PGENE	ALL NOTIS	ALL VITRES (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
BUCLAME	PROTEIN	ALL VITRES (no bacteriophages)								
FOV01_FOVPM	HYPOTHETICAL BAHII-ORF4 PROTEIN	FOV01_FOVPM (ISOLATE IP-4) (HUNNICHI)	79-70							
FOV02_FOVPM	HYPOTHETICAL BAHII-ORF5 PROTEIN	FOV02_FOVPM (ISOLATE IP-4) (HUNNICHI)	1-37	61-95						
FOV03_FOVPM	HYPOTHETICAL BAHII-ORF6 PROTEIN	FOV03_FOVPM (ISOLATE IP-4) (HUNNICHI)	115-149							
FOV04_FOVPM	HYPOTHETICAL BAHII-ORF7 PROTEIN	FOV04_FOVPM (ISOLATE IP-4) (HUNNICHI)	144-178							
FOV05_FOVPM	HYPOTHETICAL BAHII-ORF8 PROTEIN	FOV05_FOVPM (ISOLATE IP-4) (HUNNICHI)	162-233							
FOV06_FOVPM	HYPOTHETICAL BAHII-ORF9 PROTEIN	FOV06_FOVPM (ISOLATE IP-4) (HUNNICHI)	4-47	117-153						
FOV07_FOVPM	HYPOTHETICAL BAHII-ORF10 PROTEIN	FOV07_FOVPM (ISOLATE IP-4) (HUNNICHI)	122-163							
FOV08_FOVPM	HYPOTHETICAL BAHII-ORF11 PROTEIN	FOV08_FOVPM (ISOLATE IP-4) (HUNNICHI)	458-506							
FOV09_FOVPM	HYPOTHETICAL BAHII-ORF12 PROTEIN	FOV09_FOVPM (ISOLATE IP-4) (HUNNICHI)	147-188							
FOV10_FOVPM	HYPOTHETICAL BAHII-ORF13 PROTEIN	FOV10_FOVPM (ISOLATE IP-4) (HUNNICHI)	160-204							
FOV11_FOVPM	HYPOTHETICAL BAHII-ORF14 PROTEIN	FOV11_FOVPM (ISOLATE IP-4) (HUNNICHI)	176-211							
FOV12_FOVPM	HYPOTHETICAL BAHII-ORF15 PROTEIN	FOV12_FOVPM (ISOLATE IP-4) (HUNNICHI)	176-211							
FOV13_FOVPM	HYPOTHETICAL BAHII-ORF16 PROTEIN	FOV13_FOVPM (ISOLATE IP-4) (HUNNICHI)	34-78	95-139						
FOV14_FOVPM	HYPOTHETICAL BAHII-ORF17 PROTEIN	FOV14_FOVPM (ISOLATE IP-4) (HUNNICHI)	24-58	181-222						
FOV15_FOVPM	HYPOTHETICAL BAHII-ORF18 PROTEIN	FOV15_FOVPM (ISOLATE IP-4) (HUNNICHI)	16-58							
FOV16_FOVPM	HYPOTHETICAL BAHII-ORF19 PROTEIN	FOV16_FOVPM (ISOLATE IP-4) (HUNNICHI)	39-81							
FOV17_FOVPM	HYPOTHETICAL BAHII-ORF20 PROTEIN	FOV17_FOVPM (ISOLATE IP-4) (HUNNICHI)	64-125							
FOV18_FOVPM	HYPOTHETICAL BAHII-ORF21 PROTEIN	FOV18_FOVPM (ISOLATE IP-4) (HUNNICHI)	94-147							
FOV19_FOVPM	HYPOTHETICAL BAHII-ORF22 PROTEIN	FOV19_FOVPM (ISOLATE IP-4) (HUNNICHI)	33-77							
FOV20_FOVPM	HYPOTHETICAL BAHII-ORF23 PROTEIN	FOV20_FOVPM (ISOLATE IP-4) (HUNNICHI)	100-134							
FOV21_FOVPM	HYPOTHETICAL BAHII-ORF24 PROTEIN	FOV21_FOVPM (ISOLATE IP-4) (HUNNICHI)	14-54							
FOV22_FOVPM	HYPOTHETICAL BAHII-ORF25 PROTEIN	FOV22_FOVPM (ISOLATE IP-4) (HUNNICHI)	70-127							
FOV23_FOVPM	HYPOTHETICAL BAHII-ORF26 PROTEIN	FOV23_FOVPM (ISOLATE IP-4) (HUNNICHI)	21-67							
FOV24_FOVPM	HYPOTHETICAL BAHII-ORF27 PROTEIN	FOV24_FOVPM (ISOLATE IP-4) (HUNNICHI)	6-51	89-130						
FOV25_FOVPM	HYPOTHETICAL BAHII-ORF28 PROTEIN	FOV25_FOVPM (ISOLATE IP-4) (HUNNICHI)	78-122							
FOV26_FOVPM	HYPOTHETICAL BAHII-ORF29 PROTEIN	FOV26_FOVPM (ISOLATE IP-4) (HUNNICHI)	1-45							
FOV27_FOVPM	HYPOTHETICAL BAHII-ORF30 PROTEIN	FOV27_FOVPM (ISOLATE IP-4) (HUNNICHI)	1-43							
FOV28_FOVPM	HYPOTHETICAL BAHII-ORF31 PROTEIN	FOV28_FOVPM (ISOLATE IP-4) (HUNNICHI)	4-38	281-315						
FOV29_FOVPM	HYPOTHETICAL BAHII-ORF32 PROTEIN	FOV29_FOVPM (ISOLATE IP-4) (HUNNICHI)	4-89							
FOV30_FOVPM	HYPOTHETICAL BAHII-ORF33 PROTEIN	FOV30_FOVPM (ISOLATE IP-4) (HUNNICHI)	33-72							
FOV31_FOVPM	HYPOTHETICAL BAHII-ORF34 PROTEIN	FOV31_FOVPM (ISOLATE IP-4) (HUNNICHI)	33-72							
FOV32_FOVPM	HYPOTHETICAL BAHII-ORF35 PROTEIN	FOV32_FOVPM (ISOLATE IP-4) (HUNNICHI)	51-101	106-157						
FOV33_FOVPM	HYPOTHETICAL BAHII-ORF36 PROTEIN	FOV33_FOVPM (ISOLATE IP-4) (HUNNICHI)	51-101	106-157						
FOV34_FOVPM	HYPOTHETICAL BAHII-ORF37 PROTEIN	FOV34_FOVPM (ISOLATE IP-4) (HUNNICHI)	49-111	197-231						
FOV35_FOVPM	HYPOTHETICAL BAHII-ORF38 PROTEIN	FOV35_FOVPM (ISOLATE IP-4) (HUNNICHI)	49-111	197-231						
FOV36_FOVPM	HYPOTHETICAL BAHII-ORF39 PROTEIN	FOV36_FOVPM (ISOLATE IP-4) (HUNNICHI)	1-63							
FOV37_FOVPM	HYPOTHETICAL BAHII-ORF40 PROTEIN	FOV37_FOVPM (ISOLATE IP-4) (HUNNICHI)	116-153							
FOV38_FOVPM	HYPOTHETICAL BAHII-ORF41 PROTEIN	FOV38_FOVPM (ISOLATE IP-4) (HUNNICHI)	25-66							
FOV39_FOVPM	HYPOTHETICAL BAHII-ORF42 PROTEIN	FOV39_FOVPM (ISOLATE IP-4) (HUNNICHI)	9-61							
FOV40_FOVPM	HYPOTHETICAL BAHII-ORF43 PROTEIN	FOV40_FOVPM (ISOLATE IP-4) (HUNNICHI)	1-57	62-96	149-183					
FOV41_FOVPM	HYPOTHETICAL BAHII-ORF44 PROTEIN	FOV41_FOVPM (ISOLATE IP-4) (HUNNICHI)	193-264							
FOV42_FOVPM	HYPOTHETICAL BAHII-ORF45 PROTEIN	FOV42_FOVPM (ISOLATE IP-4) (HUNNICHI)	134-175							
FOV43_FOVPM	HYPOTHETICAL BAHII-ORF46 PROTEIN	FOV43_FOVPM (ISOLATE IP-4) (HUNNICHI)	232-286	404-442						
FOV44_FOVPM	HYPOTHETICAL BAHII-ORF47 PROTEIN	FOV44_FOVPM (ISOLATE IP-4) (HUNNICHI)	1-45							
FOV45_FOVPM	HYPOTHETICAL BAHII-ORF48 PROTEIN	FOV45_FOVPM (ISOLATE IP-4) (HUNNICHI)	96-130							
FOV46_FOVPM	HYPOTHETICAL BAHII-ORF49 PROTEIN	FOV46_FOVPM (ISOLATE IP-4) (HUNNICHI)	96-130							
FOV47_FOVPM	HYPOTHETICAL BAHII-ORF50 PROTEIN	FOV47_FOVPM (ISOLATE IP-4) (HUNNICHI)	390-424							
FOV48_FOVPM	HYPOTHETICAL BAHII-ORF51 PROTEIN	FOV48_FOVPM (ISOLATE IP-4) (HUNNICHI)	170-204							
FOV49_FOVPM	HYPOTHETICAL BAHII-ORF52 PROTEIN	FOV49_FOVPM (ISOLATE IP-4) (HUNNICHI)	29-63							
FOV50_FOVPM	HYPOTHETICAL BAHII-ORF53 PROTEIN	FOV50_FOVPM (ISOLATE IP-4) (HUNNICHI)	3-37							
FOV51_FOVPM	HYPOTHETICAL BAHII-ORF54 PROTEIN	FOV51_FOVPM (ISOLATE IP-4) (HUNNICHI)	78-112							

PCGENE	ALLNOTIS	All Viruses (no bacteriophages)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
ELCNAJE	PROTEIN	VIRUS	AREA.1							
PYVBH_VACCC	HYPOTHETICAL 7.9 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	23-57							
PYVCC_VACCC	HYPOTHETICAL 7.4 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	5-39							
PYVDB_VACCC	HYPOTHETICAL 9.2 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	11-48							
PYVDB_VACCV	HYPOTHETICAL 8.3 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	29-80							
PYVDC_VACCV	HYPOTHETICAL 8.3 KD PROTEIN	VACCINIA VIRUS (STRAIN WR)	46-80							
PYVGB_VACCC	HYPOTHETICAL 7.3 KD PROTEIN	VACCINIA VIRUS (STRAIN WR)	7-41							
PYVTA_VACCC	HYPOTHETICAL 8.4 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	10-51							
	HYPOTHETICAL 8.1 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	9-53							

**TABLE VI**

**107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY**

**FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS**









PCGENE	1021784	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PENY HV1GB	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (STRAIN KIL-1-GP32)	274-301	535-596	637-677	776-824					
PENY HV1MA	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MAL ISOLATE)	547-595	633-707	794-826						
PENY HV1ME	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (AFA ISOLATE)	543-592	625-681	789-816						
PENY HV1MN	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (AN ISOLATE)	543-570	567-595	632-684	791-819					
PENY HV1NS	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NEW YORK-3 ISOLATE)	728-760								
PENY HV1ND	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE)	249-290	536-583	621-673	783-813					
PENY HV1OY	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (OVI ISOLATE)	544-593	610-704	789-820						
PENY HV1PV	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (PV22 ISOLATE)	545-594	631-683	791-818						
PENY HV1RH	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RHAT ISOLATE)	280-307	531-578	554-602	640-692					
PENY HV1SI	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (SF163 ISOLATE)	333-363	536-583	622-674	782-809					
PENY HV1SC	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (SF33 ISOLATE)	541-589	627-679	787-815						
PENY HV1SD	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (SC ISOLATE)	318-365	545-591	631-683						
PENY HV1W1	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (WNU1 ISOLATE)	338-365	545-591	631-683	791-818					
PENY HV1W2	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (WNU2 ISOLATE)	334-361	536-584	622-674	782-809					
PENY HV1Z1	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZC2C3C-234 ISOLATE)	235-296	542-591	628-640	790-820					
PENY HV1Z2	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE 3 ISOLATE)	231-292								
PENY HV1Z3	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE 6 ISOLATE)	256-297	543-593	630-682	792-822					
PENY HV1Z4	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE 8 ISOLATE)	266-307	573-601	634-678	797-828					
PENY HV1Z5	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE 10/21 ISOLATE)	545-594	627-666	791-823						
PENY HV1Z6	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE 10/21 ISOLATE)	61-88	532-591	621-648	653-697					
PENY HV1Z7	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE 10/21 ISOLATE)	334-393	623-650	655-690						
PENY HV1Z8	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE 10/21 ISOLATE)	61-88	523-530	555-582	644-688					
PENY HV1Z9	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE 10/21 ISOLATE)	60-87	524-551	556-583	613-640	645-693				
PENY HV1Z10	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE 10/21 ISOLATE)	61-88	524-551	556-583	613-640	662-689				
PENY HV1Z11	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE 10/21 ISOLATE)	58-85	533-592	632-698						
PENY HV1Z12	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE 10/21 ISOLATE)	42-476	523-554	556-586	648-682					
PENY HV1Z13	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE 10/21 ISOLATE)	537-584	614-673							
PENY HV1Z14	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ZAIRE 10/21 ISOLATE)	42-476	523-554	556-586	648-692					
PENY HV1Z15	ENV POLYPROTEIN	MINK CELL FOCUS-FORMING MURINE LEUKEMIA VIRUS (ISOLATE C1-1)	473-512								
PENY HV1Z16	ENV POLYPROTEIN	AKV MURINE LEUKEMIA VIRUS	408-515								
PENY HV1Z17	ENV POLYPROTEIN	CAS-BR-E MURINE LEUKEMIA VIRUS	517-544								
PENY HV1Z18	ENV POLYPROTEIN	FRIEND MURINE LEUKEMIA VIRUS (ISOLATE 37)	510-539								
PENY HV1Z19	ENV POLYPROTEIN	FRIEND MURINE LEUKEMIA VIRUS (ISOLATE FB29)	523-553								
PENY HV1Z20	ENV POLYPROTEIN	FRIEND MURINE LEUKEMIA VIRUS (ISOLATE FB29)	523-553								
PENY HV1Z21	ENV POLYPROTEIN	HONOLULU MURINE LEUKEMIA VIRUS	510-540								
PENY HV1Z22	ENV POLYPROTEIN	KIRSTEN MURINE LEUKEMIA VIRUS	40-81								
PENY HV1Z23	ENV POLYPROTEIN	MOLONEY MURINE LEUKEMIA VIRUS	502-543								
PENY HV1Z24	ENV POLYPROTEIN	RADIATION MURINE LEUKEMIA VIRUS	497-538								
PENY HV1Z25	ENV POLYPROTEIN	RADIATION MURINE LEUKEMIA VIRUS (STRAIN KAPLAN)	497-538								
PENY HV1Z26	ENV POLYPROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN DM6)	458-485	562-589							
PENY HV1Z27	ENV POLYPROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN GR)	458-485	562-589							
PENY HV1Z28	ENV POLYPROTEIN	SDJAN MASON-PFIZER VIRUS	422-470								
PENY HV1Z29	ENV POLYPROTEIN	FB1 MURINE OSTEOSARCOMA VIRUS	57-84								
PENY HV1Z30	ENV POLYPROTEIN	OVINE LENTIVIRUS (STRAIN SA-OM199)	42-69	196-222	780-807						
PENY HV1Z31	ENV POLYPROTEIN	RAUSCHER MINK CELL FOCUS-INDUCING VIRUS	487-517								
PENY HV1Z32	ENV POLYPROTEIN	SMAN FOAMY VIRUS (TYPE 1)	14-41	866-901							
PENY HV1Z33	ENV POLYPROTEIN	SMAN FOAMY VIRUS (TYPE 2 / STRAIN LK3)	18-45	319-357	673-700	863-908					
PENY HV1Z34	ENV POLYPROTEIN	SMAN IMMUNODEFICIENCY VIRUS (AGM153 ISOLATE)	269-310	561-588	597-619	652-679	697-724				
PENY HV1Z35	ENV POLYPROTEIN	SMAN IMMUNODEFICIENCY VIRUS (AGM153 ISOLATE)	270-301	566-593	597-624	658-685	703-730				
PENY HV1Z36	ENV POLYPROTEIN	SMAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM1 / CLONE GR1-1)	257-291	336-372	348-603	634-708					
PENY HV1Z37	ENV POLYPROTEIN	SMAN IMMUNODEFICIENCY VIRUS (TYO-1 ISOLATE)	3-10	268-298	596-617	651-678					
PENY HV1Z38	ENV POLYPROTEIN	CHIMPANZEE IMMUNODEFICIENCY VIRUS	160-187	233-289	316-366	526-584	627-654				
PENY HV1Z39	ENV POLYPROTEIN	SMAN IMMUNODEFICIENCY VIRUS (ISOLATE GB1)	8-35	158-185	389-650	784-816					
PENY HV1Z40	ENV POLYPROTEIN	SMAN IMMUNODEFICIENCY VIRUS (NM142-81 ISOLATE)	126-150	550-609	671-715						
PENY HV1Z41	ENV POLYPROTEIN	SMAN IMMUNODEFICIENCY VIRUS (NM231 ISOLATE)	156-215	277-289							
PENY HV1Z42	ENV POLYPROTEIN	SMAN IMMUNODEFICIENCY VIRUS (NM ISOLATE)	533-608								







FCGENE	10717164	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PROTEIN	PROTEIN	VIRUS	482-558								
PIEMA, INCKY	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CK YOTO/4182)	482-558								
PIEMA, INCM1	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CAISSISSI/PP/80)	482-558								
PIEMA, INCM2	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CNAR/482)	482-558								
PIEMA, INCP1	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN OPTIGBEIJING/1081)	483-559								
PIEMA, INCP2	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN OPTIGBEIJING/11581)	483-559								
PIEMA, INCP3	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN OPTIGBEIJING/43982)	483-559								
PIEMA, INCTA	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CTAYLOR/12147)	483-559								
PIEMA, INCTA	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CYAMAGATA/1081)	483-559								
PIEMA, NDVA	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA/37)	64-91								
PIEMA, NDVB	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE C45)	64-91								
PIEMA, NDVC	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN D8676)	64-91								
PIEMA, NDVD	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN B-HITCINER/47)	64-91								
PIEMA, NDVE	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN ITALIEN/45)	64-91								
PIEMA, NDVF	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN MITADICA/51)	64-91								
PIEMA, NDVG	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN QUEENSLAND/66)	64-91								
PIEMA, NDVH	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN TEXAS G.D./48)	64-91								
PIEMA, NDVI	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN ULSTER/67)	64-91								
PIEMA, NDVJ	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN WASHINGTON/1937)	64-91								
PIEMA, NDVK	HEMAGGLUTININ-NEURAMINIDASE	PHOCINE DISTEMPER VIRUS	39-66	46-73							
PIEMA, NDVL	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN WASHINGTON/1937)	79-110	366-393							
PIEMA, NDVM	HEMAGGLUTININ-NEURAMINIDASE	BOVINE PARAINFLUENZA 3 VIRUS	66-93								
PIEMA, NDVN	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 47885)	27-61								
PIEMA, NDVO	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN AUS/12483/474)	27-61								
PIEMA, NDVP	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TEX/345/80)	27-61								
PIEMA, NDVQ	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TEX/205/82)	27-61								
PIEMA, NDVR	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TEX/1267/83)	27-61								
PIEMA, NDVS	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN WASHU/51173)	27-61								
PIEMA, NDVT	HEMAGGLUTININ-NEURAMINIDASE	RACCOON POXVIRUS	166-214	236-283							
PIEMA, NDVU	HEMAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN 2, HOST MUTANTS)	79-106								
PIEMA, NDVW	HEMAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN FUSHIMI)	79-106								
PIEMA, NDVX	HEMAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN HAKUSI)	79-106								
PIEMA, NDVY	HEMAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN HVI)	79-106								
PIEMA, NDVZ	HEMAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN 2)	79-106								
PIEMA, SV41	HEMAGGLUTININ-NEURAMINIDASE	SEMIAN VIRUS 41	22-52	394-431							
PIEMA, VACC1	HEMAGGLUTININ PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	119-146	175-202	216-243						
PIEMA, VACC2	HEMAGGLUTININ PRECURSOR	VACCINIA VIRUS (STRAIN HD-3)	109-146	175-202	216-243						
PIEMA, VACC3	HEMAGGLUTININ PRECURSOR	VACCINIA VIRUS (STRAIN TIAN TAN)	119-146	175-202	216-243						
PIEMA, VACC4	HEMAGGLUTININ PRECURSOR	VACCINIA VIRUS (STRAIN WR)	109-146	175-202	216-243						
PIEMA, VARV	HEMAGGLUTININ PRECURSOR	VARIOLA VIRUS	111-148	177-211	214-244						
PIEX9, ADE02	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 2	100-134								
PIEX9, ADE03	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	100-134								
PIEX9, ADE07	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3 END 7	97-127								
PIEX9, ADE08	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	146-173	339-386	431-460						
PIEX9, ADE09	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	348-375								
PIEX9, ADE10	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 40	396-423								
PIEX9, ADE11	HEXON-ASSOCIATED PROTEIN	BOVINE ADENOVIRUS TYPE 3	305-338								
PIEX9, ADE12	HEXON-ASSOCIATED PROTEIN	COWPOX VIRUS	28-55								
PIEX9, ADE13	HEXON-ASSOCIATED PROTEIN	COWPOX VIRUS	462-489								
PIEX9, ADE14	HEXON-ASSOCIATED PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BATH)	12-43								
PIEX9, ADE15	HEXON-ASSOCIATED PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BATH)	113-147								
PIEX9, ADE16	HEXON-ASSOCIATED PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN D4)	17-44								
PIEX9, ADE17	HEXON-ASSOCIATED PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN D4)	17-44								
PIEX9, ADE18	HEXON-ASSOCIATED PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN PV147)	383-410								
PIEX9, ADE19	HEXON-ASSOCIATED PROTEIN	CARNATION ETCHED RING VIRUS	6-33								
PIEX9, ADE20	HEXON-ASSOCIATED PROTEIN	FIGWORT MOSAIC VIRUS (STRAIN DX5)	372-407								
PIEX9, ADE21	HEXON-ASSOCIATED PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	3-48	331-358							
PIEX9, ADE22	HEXON-ASSOCIATED PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	294-324								







FCGNAME	10711714	ALL Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	VIRUS	49-88								
PRAM1A1UE	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN ARUDDY TURNSTONE/NEW JERSEY/608/5)	49-88								
PRAM1A2UE	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN ATERN/ALSTRA/70C775)	49-88								
PRAM1A3UE	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/US/55R/0077)	50-81								
PRAM1A4UE	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/ITALY/194/4)	49-88								
PRAM1A5UE	NEURAMINIDASE	INFLUENZA A VIRUS (STRAIN A/WILSON-SMITH/10/33)	16-43								
PRAM1A6UE	NEURAMINIDASE	INFLUENZA B VIRUS (STRAIN B/LEED/40)	4-35								
PRAM1A7UE	NEURAMINIDASE	BOMBYX DENSONUCLEOSIS VIRUS	283-310								
PRAM1A8UE	PROB NONSTRUCT PRO PRECURSOR	BOMBYX DENSONUCLEOSIS VIRUS	42-69								
PRAM1A9UE	NON-STRUCTURAL PROTEIN	IMPATIENS NECROTIC SPOT VIRUS (STRAIN NL-07)	95-122								
PRAM1A10UE	NON-STRUCTURAL PROTEIN	TOMATO SPOTTED WILT VIRUS (IRAZILIAN ISOLATE C/NH/11/IR-01)	5-32	412-462							
PRAM1A11UE	NON-STRUCTURAL PROTEIN	TOMATO SPOTTED WILT VIRUS (STRAIN L)	5-32								
PRAM1A12UE	NUCLEOSIDE TRIPHOSPHATASE I	ANSACTA MOOREI ENTOMOPHILUS	28-49								
PRAM1A13UE	NUCLEOSIDE TRIPHOSPHATASE I	CHORISTONEURA BIENNIS ENTOMOPHILUS	122-166	347-374	524-551						
PRAM1A14UE	NUCLEOSIDE TRIPHOSPHATASE I	VACCINIA VIRUS (STRAIN COPENHAGEN)	65-92	394-421	514-587						
PRAM1A15UE	NUCLEOSIDE TRIPHOSPHATASE I	VACCINIA VIRUS (STRAIN WR)	65-92	394-421	514-587						
PRAM1A16UE	NUCLEOSIDE TRIPHOSPHATASE I	VARIOLA VIRUS	100-327	420-447	455-491						
PRAM1A17UE	NUCLEOSIDE TRIPHOSPHATASE I	HERPES SIMPLEX VIRUS (TYPE 6) (STRAIN UGANDA-1102)	81-108	189-216	688-715	785-812					
PRAM1A18UE	MAJOR ANTIGENIC STRUCTLCTL PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	88-115								
PRAM1A19UE	POLY(A) POL CATALYTIC SUBUNIT	VACCINIA VIRUS (STRAIN WR)	88-115								
PRAM1A20UE	POLY(A) POL CATALYTIC SUBUNIT	VARIOLA VIRUS	88-115								
PRAM1A21UE	POLY(A) POL REG SUBUNIT	CAPRIPOX VIRUS (STRAIN KS-1)	118-145								
PRAM1A22UE	POLY(A) POL REG SUBUNIT	FOWLPOX VIRUS	27-54								
PRAM1A23UE	121 KD PROTEIN IN PE SREGION	AUTOGRAHA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS	61-105								
PRAM1A24UE	11.3 KD PROTEIN IN P26 SREGION	ORGIA PSEUDOTSUGATA MULTICAPSID POLYIHDROSIS VIRUS	61-95								
PRAM1A25UE	MAJOR IMMEDIATE EARLY PROTEIN	AUTOGRAHA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS	204-248								
PRAM1A26UE	MAJOR IMMEDIATE EARLY PROTEIN	AUTOGRAHA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS	4-38	51-78							
PRAM1A27UE	PENTON PROTEIN	AVIAN ADENOVIRUS GALLO (STRAIN 5A2)	96-123								
PRAM1A28UE	GENOME POLYPROTEIN 1	BARLEY YELLOW MOSAIC VIRUS (GERMAN ISOLATE)	1772-1299	1773-1802	2226-2263						
PRAM1A29UE	GENOME POLYPROTEIN 1	BARLEY YELLOW MOSAIC VIRUS (JAPANESE STRAIN II-1)	1774-1801	2214-2261							
PRAM1A30UE	RNA1 POLYPROTEIN	HUNGARIAN GRAPEVINE CHROME MOSAIC VIRUS	481-508	1909-1941							
PRAM1A31UE	RNA1 POLYPROTEIN	GRAPEVINE FANLEAF VIRUS	170-197	635-677	938-985	1161-1195					
PRAM1A32UE	RNA1 POLYPROTEIN	TOMATO BLACK RING VIRUS (STRAIN 5)	1096-1123								
PRAM1A33UE	GENOME POLYPROTEIN 2	BARLEY YELLOW MOSAIC VIRUS (GERMAN ISOLATE)	240-281	801-878							
PRAM1A34UE	GENOME POLYPROTEIN 2	BARLEY YELLOW MOSAIC VIRUS (JAPANESE STRAIN II-1)	240-267	801-878							
PRAM1A35UE	RNA3 POLYPROTEIN	HUNGARIAN GRAPEVINE CHROME MOSAIC VIRUS	11-38								
PRAM1A36UE	RNA3 POLYPROTEIN	GRAPEVINE FANLEAF VIRUS	549-576								
PRAM1A37UE	RNA3 POLYPROTEIN	TOMATO RINGSPOT VIRUS (ISOLATE RASPIERY)	982-1009								
PRAM1A38UE	GENOME POLYPROTEIN	BOVINE ENTEROVIRUS (STRAIN VG-5-27)	17-44	1010-1037	1145-1172						
PRAM1A39UE	GENOME POLYPROTEIN	BOVINE VIRAL DIARRHEA VIRUS (ISOLATE NADL)	629-660	1082-1112	1301-1310	2211-2261	2476-2503	2609-2636	3613-3642		
PRAM1A40UE	GENOME POLYPROTEIN	BOVINE VIRAL DIARRHEA VIRUS (STRAIN SD-1)	1301-1331	2143-2171	2519-2546	2802-2829	3323-3350				
PRAM1A41UE	GENOME POLYPROTEIN	BEAN YELLOW MOSAIC VIRUS	96-123								
PRAM1A42UE	GENOME POLYPROTEIN	COXSACKIEVIRUS A21 (STRAIN COE)	7-34	664-694	1062-1099	1900-1930					
PRAM1A43UE	GENOME POLYPROTEIN	COXSACKIEVIRUS A9 (STRAIN GRIGGS)	1040-1076								
PRAM1A44UE	GENOME POLYPROTEIN	COXSACKIEVIRUS B1	645-672	841-868	1021-1057						
PRAM1A45UE	GENOME POLYPROTEIN	COXSACKIEVIRUS B3	1024-1060	1881-1908							
PRAM1A46UE	GENOME POLYPROTEIN	COXSACKIEVIRUS B4	644-673	1022-1058							
PRAM1A47UE	GENOME POLYPROTEIN	COXSACKIEVIRUS B5	1024-1060								
PRAM1A48UE	GENOME POLYPROTEIN	CLOVER YELLOW VEIN VIRUS	130-154								
PRAM1A49UE	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 1 (STRAIN SINGAPORE S13190)	1838-1885	2890-2935	2989-3016						
PRAM1A50UE	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN 16681)	1344-1371	1858-1885	2908-2935	2982-3016	3117-3147				
PRAM1A51UE	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 3 (STRAIN JAMAICA-PDK31)	1344-1371	1858-1885	2485-2519	2908-2935	3117-3147				
PRAM1A52UE	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 4 (STRAIN PR15951)	1344-1371	1858-1885	2908-2935	3117-3147	3146-3373				
PRAM1A53UE	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN TONGA 1924)	1344-1371	1858-1885	2903-2932	3076-3013	3114-3144	3143-3370			
PRAM1A54UE	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 3	1134-1161	1448-1475							
PRAM1A55UE	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 4	837-864	1342-1369	1857-1884	2494-2521	2980-3014	3145-3372			
PRAM1A56UE	GENOME POLYPROTEIN	ECHOVIRUS 11 (STRAIN GREGORY)	2885-2910	2977-3011	3142-3169						
PRAM1A57UE	GENOME POLYPROTEIN		213-249								

PCGENE	1071784	All Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PPOLG EMCV	GENOME POLYPROTEIN	ENCEPHALOMYOCARDITIS VIRUS	70-108	1484-1518	1522-1563							
PPOLG EMCVB	GENOME POLYPROTEIN	ENCEPHALOMYOCARDITIS VIRUS (STRAIN ENIC-B NONDIABETIC)	70-97	1486-1520	1524-1563							
PPOLG EMCVB	GENOME POLYPROTEIN	ENCEPHALOMYOCARDITIS VIRUS (STRAIN ENIC-D DIABETIC)	70-97	1486-1520	1524-1563							
PPOLG EMCVB	GENOME POLYPROTEIN	MENGO ENCEPHALOMYOCARDITIS VIRUS (STRAIN 17A)	70-108	1486-1520	1524-1563							
PPOLG EMCVB	GENOME POLYPROTEIN	MENGO ENCEPHALOMYOCARDITIS VIRUS	3-41									
PPOLG EMCVB	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A10-41)	302-329	1119-1146								
PPOLG EMCVB	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A12)	301-328	1119-1146								
PPOLG EMCVB	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAINS OIK AND OIHIS)	1119-1146									
PPOLG EMCVB	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN CI-SANTA PAU (C-S1))	101-128									
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE 1)	702-729									
PPOLG EMCVB	GENOME POLYPROTEIN	HOG CHOLERA VIRUS (STRAIN ALFORT)	699-726	1193-1232	1301-1333	1434-1461	1068-1095	1406-1440				
PPOLG EMCVB	GENOME POLYPROTEIN	HOG CHOLERA VIRUS (STRAIN BRESIA)	699-726	1193-1232	1301-1333	1434-1461	1068-1095	1406-1440	1512-1559			
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE BK)	702-729	1045-1072								
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE II)	702-729	1045-1072								
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IIC-16)	314-401	2089-2116								
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IIC-18)	1049-1076	2089-2116								
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE JAPANESE)	378-405	702-729	1045-1072							
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE IIC-17)	702-729	1045-1072								
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE TAIWAN)	702-729	1045-1072								
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN 2A)	202-237	1021-1048	1117-1149	1454-1481						
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN 41C)	202-237	1021-1048	1117-1149	1454-1481						
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN 1B5)	202-237	1021-1048	1117-1149	1454-1481						
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN CR26)	202-237	1021-1048								
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN GA 16)	182-216									
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN IN-175)	202-237	1021-1048	1103-1149							
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN LA)	202-237	1021-1048	1103-1149							
PPOLG EMCVB	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STRAIN NIBB)	202-237	1021-1048	1103-1149							
PPOLG EMCVB	GENOME POLYPROTEIN	SIMIAN HEPATITIS A VIRUS (STRAIN AGM-27)	207-241	1025-1032	1115-1192							
PPOLG EMCVB	GENOME POLYPROTEIN	SIMIAN HEPATITIS A VIRUS (STRAIN CY-145)	201-237									
PPOLG EMCVB	GENOME POLYPROTEIN	HUMAN RHINOVIRUS 14	17-44	559-586	652-679	1877-1904						
PPOLG EMCVB	GENOME POLYPROTEIN	HUMAN RHINOVIRUS 18	1132-1159	1855-1882								
PPOLG EMCVB	GENOME POLYPROTEIN	HUMAN RHINOVIRUS 2	1135-1152	1552-1593								
PPOLG EMCVB	GENOME POLYPROTEIN	HUMAN RHINOVIRUS 89	883-910	1141-1168	1566-1607	1862-1889						
PPOLG EMCVB	GENOME POLYPROTEIN	HUMAN ENTEROVIRUS 70 (STRAIN 167071)	876-910									
PPOLG EMCVB	STRUCTURAL POLYPROTEIN	AVIAN INFECTIONOUS BURSAL DISEASE VIRUS (STRAIN OH)	231-277									
PPOLG EMCVB	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN SA-14)	214-248	983-1010	2796-2823							
PPOLG EMCVB	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN SA(V))	214-248	983-1010	2796-2823							
PPOLG EMCVB	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN JAOA5912)	214-248	983-1010	2796-2823							
PPOLG EMCVB	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN NAKAYAMA)	141-175	911-938								
PPOLG EMCVB	GENOME POLYPROTEIN	KUNIN VIRUS (STRAIN M8461C)	980-1007									
PPOLG EMCVB	GENOME POLYPROTEIN	LANGAT VIRUS (STRAIN TP21)	431-463	1634-1661								
PPOLG EMCVB	GENOME POLYPROTEIN	LANGAT VIRUS (STRAIN YELANSEV)	431-463									
PPOLG EMCVB	GENOME POLYPROTEIN	LOUPING ILL VIRUS	41-465									
PPOLG EMCVB	GENOME POLYPROTEIN	LOUPING ILL VIRUS (STRAIN SB 26)	151-185									
PPOLG EMCVB	GENOME POLYPROTEIN	MOSQUITO CELL FUSING AGENT	671-698	3036-3083	3103-3130							
PPOLG EMCVB	GENOME POLYPROTEIN	MAIZE DWARF MOSAIC VIRUS	10-37									
PPOLG EMCVB	GENOME POLYPROTEIN	MURRAY VALLEY ENCEPHALITIS VIRUS	312-236									
PPOLG EMCVB	GENOME POLYPROTEIN	ORANTHOGALUM MOSAIC VIRUS	24-51	946-973								
PPOLG EMCVB	GENOME POLYPROTEIN	PEPPER MOTTLE VIRUS (CALIFORNIA ISOLATE)	377-404	704-738	831-858	900-927	1167-1201	1485-1512	1787-1814	2433-2464		
PPOLG EMCVB	GENOME POLYPROTEIN	POLIOVIRUS TYPE 1 (STRAIN MATHONEY)	1060-1100	1901-1931								
PPOLG EMCVB	GENOME POLYPROTEIN	POLIOVIRUS TYPE 1 (STRAIN SABIN)	670-697	1063-1101	1901-1931							
PPOLG EMCVB	GENOME POLYPROTEIN	POLIOVIRUS TYPE 2 (STRAIN LANSING)	1061-1099	1901-1931								
PPOLG EMCVB	GENOME POLYPROTEIN	POLIOVIRUS TYPE 2 (STRAIN W-2)	1061-1099	1901-1931								
PPOLG EMCVB	GENOME POLYPROTEIN	POLIOVIRUS TYPE 3 (STRAIN 21127)	1060-1098	1900-1930								
PPOLG EMCVB	GENOME POLYPROTEIN	POLIOVIRUS TYPE 3 (STRAINS PILEON37 AND PILEON 12A(J))	1060-1098	1900-1930								
PPOLG EMCVB	GENOME POLYPROTEIN	PLUM POX VIRUS (STRAIN D)	921-948	1498-1523	2771-2798							
PPOLG EMCVB	GENOME POLYPROTEIN	PLUM POX VIRUS (STRAIN EL AMAR)	1146-1187									









PCGENE	1071784	PROTEIN	All Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
CILNAME													
PRAPL SENDZ		RNA POLYMERASE BETA SUBUNIT	SENDAI VIRUS (STRAIN Z)	629-636	1082-1116	1759-1756	2145-2180						
PRAPL SENDI		RNA-DIRECTED RNA POLYMERASE	SEOL VIRUS (STRAIN 80-19)	461-488	564-591	731-758	905-932						
PRAPL SENDR		RNA POLYMERASE BETA SUBUNIT	SIMIAN VIRUS 2 (STRAIN 21004-WR)	1096-1123	1230-1277	1686-1710	2120-2147						
PRAPL SENDS		RNA POLYMERASE BETA SUBUNIT	SOMCHUS YELLOW NET VIRUS	825-859	1092-1119	1490-1520	1973-2000	2080-2107					
PRAPL SENDT		RNA-DIRECTED RNA POLYMERASE	TOMATO SPOTTED WILT VIRUS (BRASILIAN ISOLATE CPNH10R-01)	477-504	542-573	1119-1150	1193-1229	1330-1357	1415-1442	1671-1698	1857-1884	2083-2110	
PRAPL SENDU		RNA POLYMERASE	UUKUNIEMI VIRUS	2166-2193	2324-2368	2771-2798							
PRAPL SENDV		RNA POLYMERASE BETA SUBUNIT	VEESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN IIAZELI)	142-187	1037-1071	1304-1331							
PRAPL SENDW		RNA POLYMERASE BETA SUBUNIT	VEESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN OGDEN)	1510-1557	1809-1836								
PRAPL SENDX		RNA POLYMERASE BETA SUBUNIT	VEESICULAR STOMATITIS VIRUS (STRAIN SAN JUAN)	1205-1232	1809-1836								
PRAPL SENDY		RNA-DIRECTED RNA POLYMERASE	APPLE CHLOROTIC LEAF SPOT VIRUS	1500-1567	1788-1798								
PRAPL SENDZ		PUTATIVE RNA-DIR RNA POL	BEET WESTERN YELLOW VIRUS (ISOLATE FL-1)	238-264	364-391								
PRAPL SENDA		PUTATIVE RNA-DIR RNA POL	BARLEY YELLOW DWARF VIRUS (ISOLATE MAY-PS1)	316-383									
PRAPL SENDB		PUTATIVE RNA-DIR RNA POL	BARLEY YELLOW DWARF VIRUS (ISOLATE MAY-PS2)	772-799									
PRAPL SENDC		PUTATIVE RNA-DIR RNA POL	BARLEY YELLOW DWARF VIRUS (ISOLATE P-PAV)	772-799									
PRAPL SENDD		PUTATIVE RNA-DIR RNA POL	CARNATION MOTTLE VIRUS	772-799									
PRAPL SENDE		PUTATIVE RNA-DIR RNA POL	CUCUMBER GREEN MOTTLE MOSAIC VIRUS (WATERMELON STRAIN S11)	91-127	272-304	667-694							
PRAPL SENDF		PUTATIVE RNA-DIR RNA POL	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN 5270)	387-414	1040-1067								
PRAPL SENDG		PUTATIVE RNA-DIR RNA POL	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN AUSTRALIAN 002-73)	316-363	392-419								
PRAPL SENDH		PUTATIVE RNA-DIR RNA POL	INFECTIOUS PANCREATIC NECROSIS VIRUS (SEROTYPE JASPER)	661-688	717-744								
PRAPL SENDI		PUTATIVE RNA-DIR RNA POL	INFECTIOUS PANCREATIC NECROSIS VIRUS (SEROTYPE SP)	773-800									
PRAPL SENDJ		RNA POLYMERASE	LYMPHOCYTIC CHORIOENCEPHALITIS VIRUS (STRAIN ARASTRONG)	773-800	1032-1079								
PRAPL SENDK		PUTATIVE RNA-DIR RNA POL	PEPPER MILD MOTTLE VIRUS (STRAIN SPAIN)	814-886	1032-1079								
PRAPL SENDL		RNA-DIRECTED RNA POLYMERASE	REOVIRUS (TYPE 1 / STRAIN LANG)	402-429	769-736	1072-1099							
PRAPL SENDM		RNA-DIRECTED RNA POLYMERASE	REOVIRUS (TYPE 1 / STRAIN LANG)	61-88									
PRAPL SENDN		RNA-DIR RNA POL SUBUNIT VP1	BOVINE ROTAVIRUS (STRAIN U)	68-95	218-245	791-818							
PRAPL SENDO		RNA-DIR RNA POL SUBUNIT VP1	BOVINE ROTAVIRUS (STRAIN U)	65-95	218-245	791-818	975-1002						
PRAPL SENDP		RNA-DIR RNA POL SUBUNIT VP1	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	3-44	75-102	363-390	543-583						
PRAPL SENDQ		RNA-DIR RNA POL SUBUNIT VP1	PORCINE ROTAVIRUS (STRAIN GOTTFRIED)	65-95	102-129	791-839	975-1002						
PRAPL SENDR		RNA-DIR RNA POL SUBUNIT VP1	SIMIAN 11 ROTAVIRUS (STRAIN SAI1)	65-95	791-839	975-1002							
PRAPL SENDS		RNA-DIRECTED RNA POLYMERASE	SACCHAROMYCES CEREVISIAE VIRUS L-A	147-188									
PRAPL SENDT		RNA POLYMERASE	TACARUBE VIRUS	163-204	241-271	1107-1134	1978-2008						
PRAPL SENDU		PUTATIVE RNA-DIR RNA POL	TOBACCO MILD GREEN MOSAIC VIRUS (TMV STRAIN U2)	230-257	1316-1343	1397-1424							
PRAPL SENDV		RNA POLYMERASE ALPHA SUBUNIT	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A31908)	99-133									
PRAPL SENDW		RNA POLYMERASE ALPHA SUBUNIT	CANINE DISTEMPER VIRUS (STRAIN ONDERSTEEPOORT)	315-370									
PRAPL SENDX		RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS	99-141									
PRAPL SENDY		RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN 18337)	99-141									
PRAPL SENDZ		RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A3)	99-141									
PRAPL SENDA		RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP A / STRAIN LONG)	315-370									
PRAPL SENDB		RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN EDMONSTON)	315-370									
PRAPL SENDC		RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN IP-1-CA)	315-370									
PRAPL SENDD		RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN YAMAGATA-1)	315-370									
PRAPL SENDE		RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C3)	84-111	234-261	375-416							
PRAPL SENDF		RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C3)	84-111	234-261	375-416							
PRAPL SENDG		RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C1-573)	84-111	232-262	375-416							
PRAPL SENDH		RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C1-573)	84-111	232-262	375-416							
PRAPL SENDI		RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN C14083)	84-111	244-271	375-416							
PRAPL SENDJ		RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS	167-194	222-256								
PRAPL SENDK		RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIDA)	167-194	222-256								
PRAPL SENDL		RNA POLYMERASE ALPHA SUBUNIT	BOVINE PARAINFLUENZA 3 VIRUS	34-91	255-282	285-314							
PRAPL SENDM		RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 47883)	114-144	269-299								
PRAPL SENDN		RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIDA)	4-38									
PRAPL SENDO		RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN PV)	93-127									
PRAPL SENDP		RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN Z / HOST MUTANTS)	310-357	379-420								
PRAPL SENDQ		RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN 694)	310-357	379-420								
PRAPL SENDR		RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN FUSHIDA)	310-357	379-420								
PRAPL SENDS		RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN HARRIS)	310-357	379-420								
PRAPL SENDT		RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN Z)	310-357	379-420								



PCGENE	107117s.4	All Viruses (no bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
FILENAME	PROTEIN	VIRUS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
PRPT SVS	RNA POLYMERASE ALPHA SUBUNIT	SIMIAN VIRUS 7 (STRAIN W3)	305-232	216-261						
PSDC VACCV	SUPEROXIDE DISMUTASE LIKE PROTEIN	VACCINIA VIRUS (STRAIN W8)	72-99							
PSDC VARY	SUPEROXIDE DISMUTASE LIKE PROTEIN	VARIOLA VIRUS	72-99							
PSHR AMEPV	SPHEROIDIN	ANISACTA MOOREI ENTOMOPHOX VIRUS	91-118	140-167	227-261	361-390				
PSH1 MTXXL	SERPIN 1	MYXOMA VIRUS (STRAIN LAUSANNE)	286-313							
PSH2 VACCV	SERINE PROTEINASE INHIBITOR 2	VACCINIA VIRUS (STRAIN W8)	59-86							
PSH3 VACCV	SERINE PROTEINASE INH 1 HOMOLOG	VACCINIA VIRUS (STRAIN CPENHAGEN)	18-45							
PTC2 CHVPI	TYPE II RESTRICTION ENZYME CVI11	PARAMECIUM BURSARIA CHLORELLA VIRUS 1	16-43							
PTA2 VACCV	TRANS-ACTIVATOR PROTEIN A3	VACCINIA VIRUS	95-113							
PTAG FOWPV	TRANS-ACTIVATOR PROTEIN FPO	FOWLPOX VIRUS	3-51							
PTAG VACCV	TRANS-ACTIVATOR PROTEIN GK1	VACCINIA VIRUS	3-30							
PTAG VARY	TRANS-ACTIVATOR PROTEIN GK1	VARIOLA VIRUS	3-30							
PTAL BFV	LARGE T ANTIGEN	BUDGERIGAR FLEDGLING DISEASE VIRUS	291-318							
PTAL POVBO	LARGE T ANTIGEN	BOVINE POLYOMAVIRUS	502-537							
PTAL POVIA	LARGE T ANTIGEN	HAMSTER POLYOMAVIRUS	387-621							
PTAL POVY	LARGE T ANTIGEN	LYMPHOTROPIC POLYOMAVIRUS	224-238	616-684						
PTAL POVMJ	LARGE T ANTIGEN	MOUSE POLYOMAVIRUS (STRAIN 3)	513-540							
PTAL POVMA	LARGE T ANTIGEN	MOUSE POLYOMAVIRUS (STRAIN A2)	511-538							
PTAL POVMC	LARGE T ANTIGEN	MOUSE POLYOMAVIRUS (STRAIN CRAWFORD SMALL-PLAQUE)	508-535							
PTAT NPVAC	TRANS-ACT TRANS REG PROTEIN	AUTOGRAHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	407-434	489-523	532-559					
PTAT NPVBM	TRANS-ACT TRANS REG PROTEIN	BOMBYX MORI NUCLEAR POLYHEDROSIS VIRUS	412-439	494-528	537-564					
PTAT NPVOP	TRANS-ACT TRANS REG PROTEIN	ORGANIA PSEUDOTISUGATA MULTICAPSID POLYHEDROSIS VIRUS	512-534							
PTGU EBV	LARGE TEGUMENT PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-1)	145-172	1215-1242	1344-1371	1876-1902				
PTGU HCVVA	PROBABLE LARGE TEGUMENT PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	1251-1281	2202-2229						
PTGU HSV1	LARGE TEGUMENT PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 STRAIN 17)	667-694	1673-1710						
PTGU HSV6	LARGE TEGUMENT PROTEIN	HERPES SIMPLEX VIRUS (TYPE 6 STRAIN GS)	102-129	228-262	367-611	962-993	1098-1181	1661-1688	1884-1911	
PTGU HSVB	LARGE TEGUMENT PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	328-256	366-593	1205-1232					
PTGU HSVS	PROBABLE LARGE TEGUMENT PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	328-256	366-593	1205-1232					
PTGU VZVDO	LARGE TEGUMENT PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	524-607	673-700	777-814	846-898	940-986	990-1017	1467-1497	2102-2135
PTGU ADE07	DNA TERMINAL PROTEIN	HUMAN ADENOVIRUS TYPE 7	1121-1138	1579-1609						
PTMAF AVISA	TRANSFORMING PROTEIN MAF	AVIAN MUSCULOPONEUROTIC FIBROSARCOMA VIRUS AS42	302-336							
PTOP1 SFVKA	DNA TOPOISOMERASE I	SHOPE FIBROMA VIRUS (STRAIN KASZA)	38-65	132-176						
PTOP1 VACCV	DNA TOPOISOMERASE I	VACCINIA VIRUS	38-65							
PTOP1 VARY	DNA TOPOISOMERASE I	VARIOLA VIRUS	38-65							
PTOP2 AFM2	DNA TOPOISOMERASE II	AFRICAN SWINE FEVER VIRUS (ISOLATE MALAWI LIL 201)	902-936							
PTYSV HSVAT	THYMIDYLATE SYNTHASE	HERPESVIRUS ATELES	116-143							
PTYSV HSVS	THYMIDYLATE SYNTHASE	HERPESVIRUS SAIMIRI (STRAIN 11)	126-147							
PUL06 EBV	VIRION PROTEIN UL3	EPSTEIN-BARR VIRUS (STRAIN B95-1)	115-142	313-340	342-369					
PUL06 HSV1	VIRION PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 STRAIN 17)	586-613							
PUL06 HSVB	VIRION GENE 43 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	640-667							
PUL06 HSVS	VIRION GENE 43 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	15-42	302-338	368-402					
PUL08 HCMVA	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-47							
PUL11 EBV	HYPOTHETICAL PROTEIN BBLF1	EPSTEIN-BARR VIRUS (STRAIN B95-1)	15-42							
PUL13 HCMVA	HYPOTHETICAL PROTEIN UL13	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	347-374							
PUL14 HSVB	HYPOTHETICAL GENE 48 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	247-286							
PUL14 VZVDO	HYPOTHETICAL GENE 44 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	64-101							
PUL16 HCMVA	HYPOTHETICAL PROTEIN UL16	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	81-112							
PUL30 HCMVA	HYPOTH PRO UL30 PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	34-61							
PUL31 HSVB	GENE 40 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	44-71							
PUL31 VZVDO	GENE 38 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	380-407							
PUL33 HSVS	VIRION GENE 19 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	34-61	304-321	362-389					
PUL31 HCMVA	HYPOTHETICAL PROTEIN UL31	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	167-194							
PUL33 HSVB	MAJOR ENVELOPE GLYCOPROTEIN 300	EQUINE HERPESVIRUS TYPE 1	345-375							
PUL34 HSV1	VIRION PROTEIN UL34	HERPES SIMPLEX VIRUS (TYPE 1 STRAIN 17)	116-143							
PUL34 HSVS	GENE 67 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	208-235							
PUL34 VZVDO	VIRION GENE 44 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	112-139							
PUL35 HCMVA	HYPOTHETICAL PROTEIN UL35	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	535-562							

PCGENE	10717144	All Virus (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	EXOTIN	VIRUS									
PUL37 HSV11	PROTEIN UL37	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	470-497	831-884							
PUL37 HSV11	PROTEIN UL37	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD49)	715-749	987-1014							
PUL37 HSV11	GENE 33 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	311-65	683-737							
PUL37 HSV11	GENE 21 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	107-134	976-1003							
PUL41 VZV0	HOST SHUTOFF VIRION PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	330-364								
PUL41 VZV0	DNA-BINDING PROTEIN UL42	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	231-258								
PUL41 VZV0	GENE 13 MEMBRANE PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	129-156								
PUL41 VZV0	PROTEIN UL47	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	114-148	312-349							
PUL47 HSV11	VIRION PROTEIN UL47	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	488-515	488-515							
PUL47 HSV11	VIRION PROTEIN UL47	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN F)	190-217								
PUL47 HSV11	97 KD ALPHA TRANS-INDUCING PROTEIN	EQUINE HERPESVIRUS TYPE 4	159-186								
PUL50 HCMVA	PROTEIN UL49	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	185-212	787-814							
PUL50 HCMVA	PROB DNA REPLICATION PROTEIN BSLF1	EPSTEIN-BARR VIRUS (STRAIN B95-8)	191-220	943-970							
PUL53 HSVB	DNA REPLICATION PROTEIN UL52	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD49)	300-337								
PUL53 HSVB	PROB DNA REP GENE 34 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	74-101								
PUL53 HSVB	PROB DNA REP GENE 34 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	65-92								
PUL59 HCMVA	HYPOTHETICAL PROTEIN UL59	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	5-71								
PUL70 HCMVA	PROB DNA REP PROTEIN UL70	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	9-36								
PUL73 HCMVA	UL73 GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	45-79								
PUL73 HSVB	HYPOTHETICAL GENE 53 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	409-436								
PUL74 HCMVA	HYPOTHETICAL PROTEIN UL74	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	516-563	729-768							
PUL77 HSVB	HYPOTHETICAL PROTEIN BICRF1	EPSTEIN-BARR VIRUS (STRAIN B95-8)	582-609								
PUL87 HSVB	HYPOTHETICAL PROTEIN 3R	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	107-144	168-196							
PUL92 EBV	HYPOTHETICAL PROTEIN BDLF4	EPSTEIN-BARR VIRUS (STRAIN B95-8)	92-122								
PUL92 HSVB	HYPOTHETICAL GENE 31 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	26-53	314-381							
PUL93 HCMVA	PROTEIN UL93	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	37-71								
PUL93 HCMVA	HYPOTHETICAL PROTEIN UL93	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	73-100	105-134							
PUL93 HCMVA	HYPOTHETICAL PROTEIN 13R	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	4-31	443-477							
PUL94 HCMVA	VIRION PROTEIN UL104	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	90-124								
PUL99 HCMVA	HYPOTHETICAL PROTEIN UL119	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	135-176								
PUL00 HCMVA	HYPOTHETICAL PROTEIN UL130	HERPESVIRUS SAIMIRI (STRAIN 11)	81-115								
PUL00 HCMVA	URACIL-DNA GLYCOSYLASE	SHOPE FIBROMA VIRUS (STRAIN KASZA)	85-116	129-156							
PUL00 HCMVA	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	85-116	129-156							
PUL00 HCMVA	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN WR)	85-116								
PUL00 HCMVA	URACIL-DNA GLYCOSYLASE	VARIOLA VIRUS	85-116								
PUL00 HCMVA	HYPOTHETICAL PROTEIN HVL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	20-47								
PUL00 HCMVA	HYPOTHETICAL PROTEIN HVL4	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	273-308								
PUL00 HCMVA	MEMBRANE PROTEIN HVL5	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	191-218								
PUL00 HCMVA	LIS 121-1 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS57)	2-29								
PUL00 HCMVA	LIS 137 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS57)	2-29								
PUL00 HCMVA	LIS 137 PROTEIN	AFRICAN SWINE FEVER VIRUS (ISOLATE LEIDEN)	2-29								
PUL00 HCMVA	LIS 137 PROTEIN	TOBACCO RATTLE VIRUS (STRAIN PLB3)	39-86								
PUL00 HCMVA	HELICASE	TOBACCO RATTLE VIRUS (STRAIN PLB3)	496-560								
PUL00 HCMVA	16 KD PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	79-113	945-972							
PUL00 HCMVA	16 KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN PSG)	23-54	710-737	840-868						
PUL00 HCMVA	16 KD PROTEIN	BROAD BEAN MOTTLE VIRUS	22-58	384-411	836-863	892-919					
PUL00 HCMVA	16 KD PROTEIN	BROME MOSAIC VIRUS	249-276								
PUL00 HCMVA	16 KD PROTEIN	COWPEA CHLOROTIC MOTTLE VIRUS	11-38								
PUL00 HCMVA	16 KD PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	11-38	864-902							
PUL00 HCMVA	16 KD PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN O)	11-38								
PUL00 HCMVA	16 KD PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN Q)	11-38								
PUL00 HCMVA	16 KD PROTEIN	PEANUT STUNT VIRUS (STRAIN J)	4-38	372-399							
PUL00 HCMVA	16 KD PROTEIN	TOMATO ASPERM VIRUS	11-38	271-298	376-403	857-884					
PUL00 HCMVA	16 KD PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	4-31								
PUL00 HCMVA	16 KD PROTEIN	PEA EARLY BROWNING VIRUS	140-170								
PUL00 HCMVA	16 KD PROTEIN	TOBACCO RATTLE VIRUS	170-197								

PCGENE	107178.4	All Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILENAME	PROTEIN	VIRUS	48-75									
PV3K TRVC	39 KD MAJOR EARLY PROTEIN	TOBACCO RATTLE VIRUS (STRAIN TCN)										
PV3A BDMV	2A PROTEIN	BROAD BEAN MOTTLE VIRUS	101-124									
PV3A CCMV	2A PROTEIN	COWPEA CHLOROTIC MOTTLE VIRUS	178-205									
PV3A CMVN	2A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	792-819									
PV3A PSV1	2A PROTEIN	PEANUT STUNT VIRUS (STRAIN I)	325-352	712-751								
PV3A TAV	2A PROTEIN	TOMATO ASPERMY VIRUS	313-340	722-756								
PV3K HCMVE	30 KD MAJOR EARLY PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN EISENHART)	194-221									
PV3K TRVC	29.1 KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN TCN)	130-160									
PV3P ADE41	31 KD PHOSPHOPROTEIN	HUMAN ADENOVIRUS TYPE 41	15-42									
PV3B ASF87	K162 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	35-102									
PV3B ASF87	D363 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	3-30	172-199								
PV3A BNV	3A PROTEIN	BROME MOSAIC VIRUS	11-38									
PV3A CMVN	3A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	222-252									
PV3A CMVN	3A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN I)	212-252									
PV3A CMVO	3A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN O)	222-252									
PV3A CMVY	3A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN Y)	222-252									
PV3A BV8	3A PROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN HEALING 1 F)	25-57									
PV3A BV8	3A PROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN ESC/18 V66)	29-56									
PV3B BV8	3B PROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUJETTE)	6-33									
PV3K BYDVP	50 KD PROTEIN	BARLEY YELLOW DWARF VIRUS (ISOLATE PAV)	119-146									
PV3K BWYF	51 KD PROTEIN	BEEF WESTERN YELLOW VIRUS (ISOLATE FL-1)	113-147	424-451								
PV3K BWYF	51 KD PROTEIN	BEEF WESTERN YELLOW VIRUS (ISOLATE GR1)	113-147	424-451								
PV3K PLV1	56 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN I)	124-151	438-472								
PV3K PLVW	56 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	124-151	438-477								
PV3K BSMV	51 KD PROTEIN	BARLEY STRIPE MOSAIC VIRUS	128-155									
PV3K PLV1	60.7 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN I)	110-140									
PV3K PLVW	60.7 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	110-140									
PV3K AMYLE	90 KD PROTEIN	ALFALFA MOSAIC VIRUS (STRAIN 425/7 ISOLATE LEIDEN)	107-114									
PV3K VACC	PROTEIN A6	VACCINIA VIRUS (STRAIN COPENHAGEN)	157-216	250-277	283-310	314-355						
PV3K VACC	PROTEIN A6	VACCINIA VIRUS (STRAIN WR)	156-215	249-276	282-309	313-354						
PV3K VACC	PROTEIN A6	VARIOLA VIRUS	157-216	250-277	283-310	314-355						
PV3K VACC	PROTEIN A6	VACCINIA VIRUS (STRAIN COPENHAGEN)	176-208									
PV3K VACC	PROTEIN A8	VARIOLA VIRUS	176-208									
PV3K VACC	PROTEIN A8	VARIOLA VIRUS	60-95									
PV3K VACC	PROTEIN A9	VACCINIA VIRUS (STRAIN COPENHAGEN)	219-283									
PV3K VACC	PROTEIN A11	VARIOLA VIRUS	220-284									
PV3K VACC	PROTEIN A11	VARIOLA VIRUS	440-467									
PV3K VACC	36 KD ABORTIVE LATE PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	8-67	330-357								
PV3K VACC	PROTEIN A20	VARIOLA VIRUS	8-67	330-357								
PV3K VACC	PROTEIN A20	VARIOLA VIRUS	45-72									
PV3K VACC	PROTEIN A22	VARIOLA VIRUS	56-83									
PV3K VACC	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	95-144									
PV3K VACC	PROTEIN A23	VARIOLA VIRUS	95-144									
PV3K VACC	PROTEIN A23	VACCINIA VIRUS (STRAIN WR)	22-49									
PV3K VACC	PROTEIN A28	VARIOLA VIRUS	22-49									
PV3K VACC	PROTEIN A30	VACCINIA VIRUS (STRAIN WR)	12-55									
PV3K VACC	PROTEIN A31	VACCINIA VIRUS (STRAIN COPENHAGEN)	88-115									
PV3K VACC	PROTEIN A31	VARIOLA VIRUS	88-122									
PV3K VACC	PROTEIN A34	VACCINIA VIRUS (STRAIN COPENHAGEN)	87-114									
PV3K VACC	PROTEIN A34	VACCINIA VIRUS (STRAIN WR)	87-114									
PV3K VACC	PROTEIN A34	VARIOLA VIRUS	87-114									
PV3K VACC	PROTEIN A36 PRECURSOR	VACCINIA VIRUS (STRAIN WR)	120-155									
PV3K VACC	PROTEIN A36 PRECURSOR	VARIOLA VIRUS	122-154									
PV3K VACC	PROTEIN A38	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV3K VACC	PROTEIN A38	VACCINIA VIRUS (STRAIN WR)	44-81									
PV3K VACC	PROTEIN A38	VARIOLA VIRUS	44-91									
PV3K VACC	PROTEIN A39	VACCINIA VIRUS (STRAIN COPENHAGEN)	37-71	155-182								

PCGENE	1021784	All Viruses (no bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
FILENAME	PROTEIN	VIRUS	75-109	193-220							
PVA39 VACCV	PROTEIN A39	VACCINIA VIRUS (STRAIN WR)									
PVA43 VACCC	PROTEIN A43	VACCINIA VIRUS (STRAIN COPIENHAGEN)									
PVA43 VACCV	PROTEIN A43	VACCINIA VIRUS (STRAIN WR)	145-172								
PVA43 VARV	PROTEIN A43	VARIOLA VIRUS	146-173								
PVA47 VACCC	PROTEIN A47	VACCINIA VIRUS (STRAIN COPIENHAGEN)	143-184								
PVA47 VACCV	PROTEIN A47	VACCINIA VIRUS (STRAIN WR)									
PVA47 VARV	PROTEIN A47	VARIOLA VIRUS	142-184								
PVA49 VACCC	PROTEIN A49	VACCINIA VIRUS (STRAIN COPIENHAGEN)	61-91								
PVA49 VACCV	PROTEIN A49	VACCINIA VIRUS (STRAIN WR)									
PVA49 VARV	PROTEIN A49	VARIOLA VIRUS	61-91								
PVA53 VACCC	PROTEIN A53	VACCINIA VIRUS (STRAIN COPIENHAGEN)	55-82	126-156	415-462						
PVA53 VACCV	PROTEIN A53	VACCINIA VIRUS (STRAIN WR)	55-82	126-156	415-462						
PVAL1 BICTV	ALI PROTEIN	BEEF CURLY TOP VIRUS	22-49								
PVAL3 CLVK	ALI PROTEIN	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 844)	79-106								
PVAL3 CLVN	ALI PROTEIN	CASSAVA LATENT VIRUS (STRAIN NIGERIAN)	79-106								
PVAL3 SLCV	ALI PROTEIN	SQUASH LEAF CURL VIRUS	101-128								
PVAL3 TFLCV	ALI PROTEIN	TOMATO YELLOW LEAF CURL VIRUS	79-129								
PVAL3 TFLCV	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CN-1841)	22-70	91-129							
PVAL3 TFLCV	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DAI)	22-70								
PVAL3 TFLCV	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN BIC)	22-70	91-129							
PVAL3 TFLCV	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN NY133)	22-70	91-129							
PVAL3 TFLCV	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN NY147)	22-70	91-129							
PVAL3 TFLCV	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN W260)	22-70	91-130							
PVAL3 TFLCV	APHID TRANSMISSION PROTEIN	GARNATION ETCHED BING VIRUS	102-138								
PVAL3 TFLCV	APHID TRANSMISSION PROTEIN	FIGWORT MOSAIC VIRUS (STRAIN DXS)	52-82	101-130							
PVAL3 TFLCV	PROTEIN B1	VACCINIA VIRUS (STRAIN WR)	108-135								
PVB04 VACCC	PROTEIN B4	VACCINIA VIRUS (STRAIN COPIENHAGEN)	92-123	182-211	286-313	324-361					
PVB04 VACCV	PROTEIN B4	VACCINIA VIRUS (STRAIN WR)	92-123	182-211	286-313	324-361					
PVB04 VARV	PROTEIN B4	VARIOLA VIRUS	89-127	182-211	286-313	324-361					
PVB04 VACCC	PLAQUE-SIZE / HOST RANGE PRO PREC	VACCINIA VIRUS (STRAIN LC16M0)	234-284								
PVB05 VACCC	PLAQUE-SIZE / HOST RANGE PRO PREC	VACCINIA VIRUS (STRAIN COPIENHAGEN)	234-284								
PVB05 VACCV	PLAQUE-SIZE / HOST RANGE PRO PREC	VACCINIA VIRUS (STRAIN LISTER)	234-284								
PVB05 VACCC	PLAQUE-SIZE / HOST RANGE PRO PREC	VACCINIA VIRUS (STRAIN WR)	234-284								
PVB07 VACCV	PROTEIN B7 PRECURSOR	VACCINIA VIRUS (STRAIN WR)	28-62								
PVB08 VACCC	PROTEIN B8 PRECURSOR	VACCINIA VIRUS (STRAIN COPIENHAGEN)	26-53								
PVB08 VACCV	PROTEIN B8 PRECURSOR	VACCINIA VIRUS (STRAIN WR)	26-53								
PVB11 VACCC	PROTEIN B11	VACCINIA VIRUS (STRAIN COPIENHAGEN)	21-34								
PVB11 VACCV	PROTEIN B11	VACCINIA VIRUS (STRAIN WR)	5-31								
PVB15 COMPX	IL-1 BIND PRO PRECURSOR	GOVPOX VIRUS	113-140								
PVB17 VACCC	PROTEIN B17	VACCINIA VIRUS (STRAIN COPIENHAGEN)	238-285								
PVB17 VACCV	PROTEIN B17	VACCINIA VIRUS (STRAIN WR)	238-285								
PVB18 VACCC	PROTEIN B18	VACCINIA VIRUS (STRAIN COPIENHAGEN)	337-375								
PVB18 VACCV	PROTEIN B18	VACCINIA VIRUS (STRAIN WR)	337-375								
PVB18 VARV	PROTEIN B18	VARIOLA VIRUS	337-375								
PVB19 VACCC	SURFACE ANTIGEN S PRECURSOR	VACCINIA VIRUS (STRAIN COPIENHAGEN)	182-212								
PVB19 VACCV	SURFACE ANTIGEN S PRECURSOR	VACCINIA VIRUS (STRAIN DAIREN 1)	180-210								
PVB19 VACCV	SURFACE ANTIGEN S PRECURSOR	VACCINIA VIRUS (STRAIN WR)	180-210								
PVB19 VARV	SURFACE ANTIGEN S PRECURSOR	VARIOLA VIRUS	180-210								
PVB20 VACCC	PROTEIN B20	VACCINIA VIRUS (STRAIN COPIENHAGEN)	48-82								
PVB21 VACCV	PROTEIN B21	VACCINIA VIRUS (STRAIN WR)	64-91								
PVB21 BGMV	BLI PROTEIN	BEAN GOLDEN MOSAIC VIRUS	120-147	248-273							
PVB21 CLVK	BLI PROTEIN	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 844)	118-145								
PVB21 CLVN	BLI PROTEIN	CASSAVA LATENT VIRUS (STRAIN NIGERIAN)	118-145								
PVB21 PYMVV	BLI PROTEIN	POTATO YELLOW MOSAIC VIRUS (ISOLATE VENEZUELA)	120-147								
PVB22 VACCC	PROTEIN C3	VACCINIA VIRUS (STRAIN COPIENHAGEN)	405-432								
PVB22 VACCV	PROTEIN C3	VACCINIA VIRUS (STRAIN WR)	41-71	405-432							

PCGENE	101st/784	All Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ELKNAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PVC04 SFVKA	PROTEIN C4	SHOPE FIBROMA VIRUS (STRAIN KASZA)	209-216	484-515							
PVC04 VACCC	PROTEIN C4	VACCINIA VIRUS (STRAIN COPENHAGEN)	12-46								
PVC04 VACCV	PROTEIN C4	VACCINIA VIRUS (STRAIN WR)	12-46								
PVC04 VARV	PROTEIN C4	VARIOLA VIRUS	12-46								
PVC03 SFVKA	HYPOTHEICAL PROTEIN C3	SHOPE FIBROMA VIRUS (STRAIN KASZA)	85-123	152-179							
PVC03 VACCC	PROTEIN C3	VACCINIA VIRUS (STRAIN COPENHAGEN)	38-63								
PVC03 VACCV	PROTEIN C3	VACCINIA VIRUS (STRAIN WR)	38-63								
PVC03 VARV	PROTEIN C3	VARIOLA VIRUS	36-66								
PVC01 VACCV	PROTEIN C7	VACCINIA VIRUS (STRAIN WR)	80-111								
PVC01 VARV	PROTEIN C7	VARIOLA VIRUS	80-111								
PVC09 VACCC	PROTEIN C9	VACCINIA VIRUS (STRAIN COPENHAGEN)	42-69	82-116	178-205	232-279	289-333	373-605			
PVC09 VACCV	PROTEIN C9	VACCINIA VIRUS (STRAIN WR)	42-69	82-116	178-205	232-279	289-333	373-605			
PVC09 VACCV	PROTEIN C9	VACCINIA VIRUS (STRAIN WR)	42-69	82-116	178-205	232-279	289-333	373-605			
PVC10 VACCC	PROTEIN C10	VACCINIA VIRUS (STRAIN COPENHAGEN)	136-180								
PVC10 VACCV	PROTEIN C10	VACCINIA VIRUS (STRAIN WR)	136-180								
PVC10 VARV	PROTEIN C10	VARIOLA VIRUS	136-163								
PVC11 SFVKA	PROTEIN C11	SHOPE FIBROMA VIRUS (STRAIN KASZA)	3-30	19-66	137-182	206-240					
PVC11 VACCC	PROTEIN C11	VACCINIA VIRUS (STRAIN COPENHAGEN)	111-152								
PVC11 VACCV	PROTEIN C11	VACCINIA VIRUS (STRAIN WR)	40-74								
PVC11 VARV	PROTEIN C11	VARIOLA VIRUS	36-97								
PVC12 VACCC	PROTEIN C12	SHOPE FIBROMA VIRUS (STRAIN KASZA)	72-99								
PVC12 VACCV	PROTEIN C12	VACCINIA VIRUS (STRAIN COPENHAGEN)	399-126								
PVC12 VARV	PROTEIN C12	VARIOLA VIRUS	847-874								
PVCAP EBY	MAJOR CAPSID PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-1)	136-170	335-382							
PVCAP HSVAU	MAJOR CAPSID PROTEIN	HERPES SIMPLEX VIRUS (TYPE 67 STRAIN UGANDA-1102)	769-799								
PVCAP HSVAU	MAJOR CAPSID PROTEIN	HERPES VIRUS SAMIRI (STRAIN 11)	88-115	199-248							
PVCAP NPVAC	DNA-BINDING PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS	133-165								
PVC0M ADE02	MINOR CORE PROTEIN	HUMAN ADENOVIRUS TYPE 2	88-115								
PVC0M ADE03	MINOR CORE PROTEIN	HUMAN ADENOVIRUS TYPE 3	87-114								
PVC05 FOWP1	92.6 KD PROTEIN	FOWLPOX VIRUS (STRAIN FP-1)	6-33	184-211	321-348						
PVC05 VACCC	PROTEIN D5	VACCINIA VIRUS (STRAIN COPENHAGEN)	240-267	333-360							
PVC05 VACCV	PROTEIN D5	VACCINIA VIRUS (STRAIN WR)	240-267								
PVC05 VARV	PROTEIN D5	VARIOLA VIRUS	240-267								
PVC09 VACCC	PROTEIN D9	VACCINIA VIRUS (STRAIN COPENHAGEN)	123-150								
PVC09 VACCV	PROTEIN D9	VACCINIA VIRUS (STRAIN WR)	123-150								
PVC09 VARV	PROTEIN D9	VARIOLA VIRUS	123-160								
PVC10 SFVKA	PROTEIN D10	SHOPE FIBROMA VIRUS (STRAIN KASZA)	18-33								
PVC10 VACCC	DNA-BINDING PROTEIN	CARNATION ETCHED RING VIRUS	2-35								
PVC10 VACCV	PROTEIN E2	VARIOLA VIRUS	287-322								
PVC10 VARV	PROTEIN E2	VACCINIA VIRUS (STRAIN COPENHAGEN)	89-116	437-464							
PVC06 VACCC	PROTEIN E6	VACCINIA VIRUS (STRAIN WR)	89-116	437-464							
PVC06 VACCV	PROTEIN E6	VARIOLA VIRUS	89-116	367-394	437-464						
PVC06 VARV	PROTEIN E6	HUMAN PAPILLOMAVIRUS TYPE 18	60-87								
PVE1 HPV18	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 18	21-48								
PVE1 HPV2A	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 2A	180-207								
PVE1 HPV33	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	103-130								
PVE1 HPV39	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 39	55-89								
PVE1 HPV41	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	25-59								
PVE1 HPV42	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 42	146-173								
PVE1 HPV47	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	21-48								
PVE1 HPV57	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 57	72-113								
PVE3 NPVAC	EARLY 21.9 KD PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS	5-34								
PVE3 CRPVK	PROBABLE E3 PROTEIN	COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN KANSAS)	17-51								
PVE3 HPV05	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 5	157-184	314-361							
PVE3 HPV13	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 13	61-105	312-342							
PVE3 HPV16	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 16	313-340								
PVE3 HPV18	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 18	159-186								
PVE3 HPV1A	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 1A	159-193								
PVE3 HPV2A	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 2A	306-331								
PVE3 HPV33	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33									

PCGENE	10717144	All Viruses (no bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILENAME	PROTEIN	VIRUS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PVE1 HPV33	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	158-192	327-334							
PVE2 HPV39	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 39	7-34	323-337							
PVE3 HPV47	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	17-51	148-175	276-303						
PVE4 HPV51	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 51	137-184								
PVE5 HPV57	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 57	166-193								
PVE6 HPV58	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 58	2-36	309-336							
PVE7 HPV59	PROBABLE E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 59	17-51								
PVE8 PAPV6	PROBABLE E2 PROTEIN	EUROPEAN ELK PAPILLOMAVIRUS	120-150								
PVE9 PCPV1	E2 PROTEIN	PYGMY CHIMPANZEE PAPILLOMAVIRUS TYPE 1	267-294	327-361							
PVEA HPV63	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 3	202-229								
PVEB HPV11	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 11	81-108								
PVEA HPV16	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 16	66-93								
PVEA HPV18	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 18	59-86								
PVEA HPV21	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 21	75-102								
PVEA HPV41	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	63-97								
PVEA HPV58	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 58	202-229								
PVEA HPV11	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 11	30-60								
PVEA HPV68	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 68	30-60								
PVEA HPV6C	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 6C	30-60								
PVE3 HPV33	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	27-54								
PVE3 HPV38	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 38	11-41								
PVE4 PCPV1	PROBABLE E4 PROTEIN	PYGMY CHIMPANZEE PAPILLOMAVIRUS TYPE 1	33-62								
PVE5 HPV18	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 18	75-102								
PVEA HPV31	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 31	69-96								
PVEA HPV39	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 39	71-102								
PVEA HPV41	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	119-146								
PVEA HPV43	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 43	75-102								
PVEA HPV51	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 51	71-99								
PVEA HPVME	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE ME10	71-102								
PVEA HPVAC	EARLY M KD PROTEIN	AUTOGRAFIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	630-647								
PVEV GYTN	VIRAL ENHANCING FACTOR	TRICHOPLUSIA NI GRANULOSIS VIRUS	411-418								
PVEV DRY11	ENVELOPE GLYCOPROTEIN PRECURSOR	DHOB1 VIRUS (STRAIN INDIAN/11/0/1)	318-366								
PVEV EAV	ENVELOPE GLYCOPROTEIN	EQUINE ARTERITIS VIRUS	120-147								
PVEV THOGV	ENVELOPE GLYCOPROTEIN PRECURSOR	THOGOTO VIRUS	313-347								
PVE70 VACC	PROTEIN F3	VACCINIA VIRUS (STRAIN COPENHAGEN)	71-110	185-212							
PVE70 VACC	PROTEIN F3	VACCINIA VIRUS (STRAIN WR)	71-110	185-212							
PVE70 VACC	36 KD MAJOR MEMBRANE PRO PRECURSOR	VACCINIA VIRUS (STRAIN L-1VP)	33-60								
PVE76 VACC	36 KD MAJOR MEMBRANE PRO PRECURSOR	VACCINIA VIRUS (STRAIN WR)	33-60								
PVE76 VACC	PROTEIN F6	VARIOLA VIRUS	10-44								
PVE11 VACC	PROTEIN F11	VACCINIA VIRUS (STRAIN COPENHAGEN)	274-321								
PVE11 VACC	PROTEIN F11	VACCINIA VIRUS (STRAIN L-1VP)	270-317								
PVE11 VACC	PROTEIN F11	VARIOLA VIRUS	274-321								
PVE12 VACC	PROTEIN F12	VACCINIA VIRUS (STRAIN COPENHAGEN)	10-37	113-140	354-381						
PVE12 VACC	PROTEIN F12	VACCINIA VIRUS (STRAIN L-1VP)	10-37	113-140	354-381						
PVE13 VACC	PROTEIN F13	VARIOLA VIRUS	10-37	202-216	354-381						
PVE13 VACC	PROTEIN F13	VARIOLA VIRUS	10-37	202-216	354-381						
PVE16 VACC	PROTEIN F16	VACCINIA VIRUS (STRAIN COPENHAGEN)	35-62	132-179							
PVE16 VACC	PROTEIN F16	VACCINIA VIRUS (STRAIN L-1VP)	35-62	132-179							
PVE16 VACC	PROTEIN F16	VARIOLA VIRUS	33-62	149-179							
PVE16 VACC	PROTEIN F16	VARIOLA VIRUS	146-173								
PVE16 VACC	PROTEIN F16	FOWLPOX VIRUS	59-86								
PVE16 VACC	10 KD FUSION PROTEIN	ORF VIRUS (STRAIN NZ2)	37-64								
PVE16 VACC	14 KD FUSION PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	37-64								
PVE16 VACC	KD FUSION PROTEIN	VACCINIA VIRUS (STRAIN WR)	37-64								
PVE16 VACC	PROTEIN G1	VACCINIA VIRUS (STRAIN COPENHAGEN)	225-232	301-315							
PVE16 VACC	PROTEIN G1	VACCINIA VIRUS (STRAIN WR)	164-191	240-274							
PVE16 VACC	PROTEIN G1	VARIOLA VIRUS	235-232	301-315							
PVE16 VACC	ISATIN-B-TSC DEF PROTEIN	VACCINIA VIRUS (STRAIN WR)	96-123								
PVE16 VACC	ISATIN-B-TSC DEF PROTEIN	VARIOLA VIRUS	96-123								







FCGGENE	1071178.4	All Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	VIRUS	151-178	426-512	109-136					
PVGLF_NDVU	FUSION GLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN ULSTER/69)	151-178	426-512	109-136					
PVGLF_PHDV	FUSION GLYCOPROTEIN PRECURSOR	PHOCINE DISTEMPER VIRUS	36-40	221-202	109-136					
PVGLF_PTHC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C19)	147-174	210-266						
PVGLF_P2H	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 2 VIRUS	90-117	141-175	238-266	483-528				
PVGLF_P2HG	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN GREER)	90-117	141-175	238-266	483-528				
PVGLF_P2HT	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIDA)	90-117	141-175	238-266	483-528				
PVGLF_P2HB	FUSION GLYCOPROTEIN PRECURSOR	BOVINE PARAINFLUENZA 3 VIRUS	115-182	207-241	459-497					
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIII 47885)	115-182	207-241	459-497					
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	RINDERPEST VIRUS (STRAIN KABETE O)	224-265	458-495						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	RINDERPEST VIRUS (STRAIN L)	224-265	458-495						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN Z/HOST MUTANTS)	122-149	211-245	480-507					
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN FUSHIMI)	122-149	211-245	480-507					
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN HARBIS)	122-149	211-245	480-507					
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN HV)	122-149	211-245	480-507					
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN Z)	122-149	211-245	480-507					
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	SIMIAN VIRUS 41	144-185	241-269	459-496					
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	SIMIAN VIRUS 5 (STRAIN W)	137-171	417-444						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	TURKEY RHINOTRACHEITIS VIRUS	124-161	193-200	457-484					
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	BOVINE EPHEMERAL FEVER VIRUS	523-557							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COPENHAGEN)	92-123							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN 18317)	61-91							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RS11857)	66-107							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RS16190)	243-273							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN 8/60)	66-93							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 4	271-298							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	383-410							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRAIN STREET)	489-519							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	VEICULAR STOMATITIS VIRUS (GEROTYPE INDIANA / STRAIN GLASCOV)	472-499							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	EPSTEIN-BARR VIRUS (STRAIN B95-8)	349-376	619-648						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	107-136	270-297						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN TOWNE)	106-135							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN G5)	62-89	360-403						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	HERPES VIRUS SAIMIRI (STRAIN 11)	388-415							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	47-111							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	BUNYAVIRUS GERMISTON	512-546	914-941	1128-1255					
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	BUNYAVIRUS LA CROSSE (ISOLATE L74)	912-950							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	BUNYAVIRUS LA CROSSE (ISOLATE L74)	940-974	504-535	682-709					
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	DUGBE VIRUS	71-100	693-720						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN B-1)	71-100	693-720						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN HO10)	71-100	693-720						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN LEE)	71-100	693-720						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN 76-118)	71-100	693-720						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	IMPATIENS NECROTIC SPOT VIRUS	628-655	1069-1101						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	PROSPECT HILL VIRUS	69-96							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	PUNJALA VIRUS (STRAIN HALLNAS B1)	72-110							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	PUNJALA VIRUS (STRAIN SOTKANON)	72-110							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	SEOL VIRUS (STRAIN B0-39)	513-540	693-720						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	SEOL VIRUS (STRAIN B2)	513-540	693-720						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	SEOL VIRUS (STRAIN SR-11)	513-540	693-720						
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	BOVINE EPHEMERAL FEVER VIRUS	523-564							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	BERNE VIRUS	48-82	1145-1179	1184-1211	1305-1332				
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	GLYCOPROTEIN POLYPYPTHEIN PRECURSOR	14-41							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	GLYCOPROTEIN POLYPYPTHEIN PRECURSOR	86-113							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	GLYCOPROTEIN POLYPYPTHEIN PRECURSOR	86-113							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	GLYCOPROTEIN POLYPYPTHEIN PRECURSOR	334-375							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	GLYCOPROTEIN POLYPYPTHEIN PRECURSOR	109-136							
PVGLF_P3H4	FUSION GLYCOPROTEIN PRECURSOR	GLYCOPROTEIN POLYPYPTHEIN PRECURSOR	303-331							









PGENE	1071784	All Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	VIRUS									
PVP10 RGDV	NONSTRUCTURAL PROTEIN PMS10	RICE GALL DWARF VIRUS	205-232								
PVP10 WTV	NONSTRUCTURAL PROTEIN PMS10	WOUND TUMOR VIRUS	151-181	227-254							
PVP11 RDV	NONSTRUCTURAL PROTEIN PMS11	RICE DWARF VIRUS	53-80								
PVP11 WTV	NONSTRUCTURAL PROTEIN PMS12	WOUND TUMOR VIRUS	81-108								
PVP12 WTV	NONSTRUCTURAL PROTEIN PMS12	WOUND TUMOR VIRUS	81-108								
PVP19 ANCV	CORE PROTEIN P19	ARTICHOKE MOTTLED CRINKLE VIRUS	71-100								
PVP19 TBVC	CORE PROTEIN P19	TOMATO BUSHY STUNT VIRUS (STRAIN CHERRY)	71-100								
PVP21 HSYSA	PROBABLE CAPSID PROTEIN VP21	HERPESVIRUS SAIMIRI (STRAIN 11)	2-20								
PVP26 HSYED	CAPSID PROTEIN VP26	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB41)	36-63								
PVP26 HSYSA	CAPSID PROTEIN VP26	HERPESVIRUS SAIMIRI (STRAIN 11)	48-75								
PVP28 HSYSA	OUTER CAPSID PROTEIN VP28	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4 / STRAIN VACCINE)	277-304	410-437	632-662	907-934					
PVP2 BTY1J	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	815-846								
PVP2 BTY1A	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 1 / ISOLATE AUSTRALIA)	808-825								
PVP2 BTY1S	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEROTYPE 1 / ISOLATE SOUTH AFRICA)	119-146								
PVP2 BTY1V	OUTER CAPSID PROTEIN VP2	EPIZOOTIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1)	72-103	415-453							
PVP2 ROTBR	RNA-BINDING PROTEIN VP2	BOVINE ROTAVIRUS (STRAIN RF)	19-94	524-554							
PVP2 ROTBU	RNA-BINDING PROTEIN VP2	BOVINE ROTAVIRUS (STRAIN UK)	70-101	533-567							
PVP2 ROTHW	RNA-BINDING PROTEIN VP2	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	36-96	128-156	518-545	705-746					
PVP2 ROTPC	RNA-BINDING PROTEIN VP2	PORCINE ROTAVIRUS GROUP C (STRAIN COWDEN)	19-75								
PVP2 ROTSI	RNA-BINDING PROTEIN VP2	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	81-119								
PVP20 ASFE7	PHOSPHOPROTEIN P20	AFRICAN SWINE FEVER VIRUS (STRAIN E-75)	80-107	231-258							
PVP21 ASFB7	PHOSPHOPROTEIN P21	AFRICAN SWINE FEVER VIRUS (STRAIN RA715)	80-107	231-258							
PVP31 EBOV	POLYMERASE COMPLEX PROTEIN VP31	EBOLA VIRUS	270-297								
PVP31 MABVM	POLYMERASE COMPLEX PROTEIN VP31	MARBURG VIRUS (STRAIN MUSKOE)	68-102								
PVP31 MABVP	POLYMERASE COMPLEX PROTEIN VP31	MARBURG VIRUS (STRAIN POPP)	178-205								
PVP31 NPVAC	EARLY 31 KD PROTEIN	AUTOGRAHA CALIFORNICA NUCLEAR POLYOMEDROSIS VIRUS	264-291								
PVP31 NPVBM	EARLY 31 KD PROTEIN	BOVINE MORBID NUCLEAR POLYOMEDROSIS VIRUS	134-161								
PVP31 VACCV	ORIGININOM ENV PRO P31	VACCINIA VIRUS (STRAIN WR)	263-290								
PVP39 NPVOP	MAJOR CAPSID PROTEIN	ORGYIA PSEUDOTUGATA MULTICAPSID POLYOMEDROSIS VIRUS	132-159								
PVP3 HSYV4	VP3 CORE PROTEIN	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4 / STRAIN VACCINE)	214-232								
PVP3 BTY1D	VP3 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	214-232								
PVP3 BTY1J	VP3 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	214-232								
PVP3 BTY1A	VP3 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE AUSTRALIA)	209-243	798-832							
PVP3 EHDV1	VP3 CORE PROTEIN	EPIZOOTIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1)	99-133								
PVP3 EHDV4	VP3 CORE PROTEIN	EPIZOOTIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 2 / STRAIN AUSTRALIA)	39-66	379-384							
PVP3 GELV	P1 PROTEIN	GRAPEVINE FANLEAF VIRUS	26-67	350-377	451-497	619-692					
PVP3 ROTFC	INNER CORE PROTEIN VP3	PORCINE ROTAVIRUS GROUP C / STRAIN COWDEN	440-470								
PVP3 ROTSI	INNER CORE PROTEIN VP3	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	205-232								
PVP40 EBY	CAPSID PROTEIN P40	EPSTEIN-BARR VIRUS (STRAIN B91-4)	515-549								
PVP40 HSYSA	CAPSID PROTEIN P40	HERPESVIRUS SAIMIRI (STRAIN 11)	174-208	495-522							
PVP40 BTY1T	CAPSID PROTEIN P40	INFECTIOUS LARYNGITIS VIRUS (STRAIN THORNE V882)	8-35	589-619							
PVP40 VZVD	CAPSID PROTEIN P40	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	8-35	584-622							
PVP41 ROTSI	OUTER CAPSID PROTEIN VP4	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	48-75								
PVP41 ROTSI	OUTER CAPSID PROTEIN VP4	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	48-75								
PVP44 VACCC	MAJOR CORE PROTEIN P44 PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	80-110								
PVP44 VACCV	MAJOR CORE PROTEIN P44 PRECURSOR	VACCINIA VIRUS (STRAIN WR)	7-37								
PVP44 VACV	MAJOR CORE PROTEIN P44 PRECURSOR	VARIOLA VIRUS	7-37								
PVP48 FOWPV	MAJOR CORE PROTEIN P48 PRECURSOR	FOWLPOX VIRUS	34-61	576-603							
PVP48 VACCC	MAJOR CORE PROTEIN P48 PRECURSOR	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	34-61	576-603							
PVP48 VACCV	MAJOR CORE PROTEIN P48 PRECURSOR	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	34-61	576-603							
PVP48 VACV	MAJOR CORE PROTEIN P48 PRECURSOR	NEBRASKA CALF DIARRHEA VIRUS (STRAIN NCDV-LINCOLN)	555-632								
PVP4 BTY1D	VP4 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	595-639								
PVP4 BTY1J	VP4 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)									
PVP4 BTY1V	VP4 CORE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 1 / ISOLATE SOUTH AFRICA)									
PVP4 BTY1S	VP4 CORE PROTEIN	EPIZOOTIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1)									
PVP4 BTY1A	VP4 CORE PROTEIN	EPIZOOTIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 2 / STRAIN AUSTRALIA)									
PVP4 BTY1D	OUTER CAPSID PROTEIN VP4	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)									
PVP4 BTY1J	OUTER CAPSID PROTEIN VP4	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)									
PVP4 BTY1S	OUTER CAPSID PROTEIN VP4	BLUETONGUE VIRUS (SEROTYPE 1 / ISOLATE SOUTH AFRICA)									
PVP4 BTY1A	OUTER CAPSID PROTEIN VP4	EPIZOOTIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1)									
PVP4 BTY1D	OUTER CAPSID PROTEIN VP4	EPIZOOTIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 2 / STRAIN AUSTRALIA)									

PCGENE	1011/184	All Viruses (no bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
FILE NAME	PROTEIN	VIRUS									
VP4 ROTB	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVIRUS (STRAIN C46)	8-35	584-622							
VP4 ROTBC	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVIRUS (STRAIN UK)	595-629								
VP4 ROTBU	OUTER CAPSID PROTEIN VP4	EQUINE ROTAVIRUS (STRAIN H-2)	112-146	235-269	552-629						
VP4 ROTBI	OUTER CAPSID PROTEIN VP4	ROTAVIRUS (GROUP B / STRAIN IDIR)	5-32								
VP4 ROTGI	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 076)	8-35	572-628							
VP4 ROTHI	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN RV-5)	8-35	279-306	565-621						
VP4 ROTJ	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 694)	8-35	112-139	584-629						
VP4 ROTK	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 694)	8-35	279-306	565-621						
VP4 ROTL	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN US1)	8-35	279-306	565-621						
VP4 ROTM	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN K8)	8-35	111-138							
VP4 ROTN	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN KU)	8-35	77-104	279-306	577-621					
VP4 ROTL	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN L26)	8-35	279-306	565-621						
VP4 ROTM	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN K37)	8-35	572-610							
VP4 ROTN	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN MCN1)	8-35	573-628							
VP4 ROTP	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN P)	8-35	577-621							
VP4 ROTR	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN RV)	8-35	105-135	235-262						
VP4 ROTI	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST. THOMAS 3)	8-35	572-627							
VP4 ROTJ	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN VA10)	8-35	279-306	590-617						
VP4 ROTK	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	8-35	577-621							
VP4 ROTL	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN OSU)	112-146	584-625							
VP4 ROTM	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	5-33	115-161	293-310						
VP4 ROTN	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN GOTTFRIED)	8-35	572-628	584-625						
VP4 ROTP	OUTER CAPSID PROTEIN VP4	RHESUS ROTAVIRUS	8-35	584-622							
VP4 ROTQ	OUTER CAPSID PROTEIN VP4	SIMIAN 11 ROTAVIRUS (STRAIN SA11-FEM)	8-35	589-619							
VP4 ROTR	OUTER CAPSID PROTEIN VP4	SIMIAN 11 ROTAVIRUS (STRAIN SA11-SEM)	8-35	130-157	584-622						
VP4 ROTS	OUTER CAPSID PROTEIN VP4	AFRICAN TUMOR VIRUS	28-62								
VP4 ROTV	NONSTRUCTURAL PROTEIN PNS4	WOUND TUMOR VIRUS	113-183	191-218							
VP4 ROTW	OUTER CAPSID PROTEIN VP5	WOUND TUMOR VIRUS (SEROTYPE 4 / STRAIN VACCINE)	51-80	99-126							
VP4 ROTX	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	51-80	92-126							
VP4 ROTY	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	51-80	89-126							
VP4 ROTZ	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 13 / ISOLATE USA)	51-80	89-126							
VP4 ROT1	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE AUSTRALIA)	51-80	92-126	148-182						
VP4 ROT2	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE SOUTH AFRICA)	51-80	89-126							
VP4 ROT3	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	51-80	89-126							
VP4 ROT4	OUTER CAPSID PROTEIN VP5	EPIDEMIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1)	31-80	191-218	399-426						
VP4 ROT5	OUTER COAT PROTEIN P5	WOUND TUMOR VIRUS	64-8-63								
VP4 ROT6	VP6 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	161-193								
VP4 ROT7	PROB NONSTRUCT 41.0 KD PRO	MAIZE ROUGH DWARF VIRUS	153-202								
VP4 ROT8	61 KD PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	36-63								
VP4 ROT9	VP6 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	157-189								
VP4 ROT10	MAJOR ENY GLYCOPRO PRECURSOR	ORGANIA PSEUDOTISUGATA MULTICAPSID POLYEDROSIS VIRUS	45-72								
VP4 ROT11	MAJOR ENY GLYCOPRO PRECURSOR	AUTOGRAPIA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	44-81								
VP4 ROT12	VP6 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	157-189								
VP4 ROT13	VP6 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	157-189								
VP4 ROT14	VP6 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	157-189								
VP4 ROT15	VP6 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	157-189								
VP4 ROT16	VP6 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE SOUTH AFRICA)	161-193								
VP4 ROT17	VP6 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	133-172								
VP4 ROT18	STRUCTURAL PROTEIN P6	RICE DWARF VIRUS	10-37	314-381							
VP4 ROT19	VP4 PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	413-440								
VP4 ROT20	PROBABLE MEMBRANE ANTIGEN 75	HERPESVIRUS SAMIRI (STRAIN 11)	181-208	929-977							
VP4 ROT21	79 KD PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	44-78	370-397							
VP4 ROT22	VP7 CORE PROTEIN	EPIDEMIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1)	16-43								
VP4 ROT23	NONSTRUCTURAL PROTEIN PMS7	WOUND TUMOR VIRUS	458-485								
VP4 ROT24	CAPSID PROTEIN P6	AUTOGRAPIA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	101-142	200-298							
VP4 ROT25	CAPSID PROTEIN P7	ORGANIA PSEUDOTISUGATA MULTICAPSID POLYEDROSIS VIRUS	132-159								
VP4 ROT26	NONSTRUCTURAL PROTEIN P8	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	105-132								
VP4 ROT27	STRUCTURAL PROTEIN VP8 PRECURSOR	FOWLPOX VIRUS	211-238								





GENE	1071784	All Viruses (no bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PROTEIN	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PROTEIN	PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN RV-5)	13-40	111-145						
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN DS1)	13-40	111-145						
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	111-145							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	RABBIT ROTAVIRUS (STRAIN ALABAMA)	111-145							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	111-146							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS	9-46							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN MATSUJIMA)	12-41							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN BELFAST)	9-41							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN ENDERS)	9-46							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN JER-L-1YN)	9-46							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN KILIAN)	9-46							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN BRISTOL 1)	9-46							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN MTH AHARA VACCINE)	12-41							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN RV)	9-41							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MUMPS VIRUS (STRAIN URABE VACCINE A49)	12-41							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 1 / STRAIN DEARING)	26-63	71-122	127-168	222-239				
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 2 / STRAIN D510N1S)	4-104	130-193						
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 1 / STRAIN LANG)	4-52	35-104	112-160					
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 1 / STRAIN DEARING)	350-384							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 2 / STRAIN D510N1S)	289-316							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 1 / STRAIN DEARING)	90-117							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	REOVIRUS (TYPE 1 / STRAIN LANG)	50-77							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	CAPRIPOX VIRUS (STRAIN INS-1)	124-158							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SHOPE FIBROMA VIRUS (STRAIN KASZA)	250-277							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	234-290							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	417-451							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	HERPES SIMPLEX VIRUS (TYPE 8 / STRAIN LGANIDA-1 [n])	176-203							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	ICTALURID HERPESVIRUS 1	310-377							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	394-421							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN VT1)	169-196							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN KKA1)	169-196							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIIBA)	4-38							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	35-65							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	4-61							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	30-78							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	TOBACCO YELLOW DWARF VIRUS (STRAIN AUSTRALIA)	53-87							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	85-112							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	59-86							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	AUTOGRAFIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	80-107							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	5-39							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	77-111							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	9-36	119-153						
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MAIZE STREAK VIRUS (NIGERIAN ISOLATE)	34-61							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	MAIZE STREAK VIRUS (SOUTH-AFRICAN ISOLATE)	34-61							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	76-103							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	93-164							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	118-148							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	24-97							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	231-267							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	AUTOGRAFIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	133-184							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	122-149							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	56-94							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	81-121	546-573	658-700					
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	13-40							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	FOWLPOX VIRUS (ISOLATE HP-318[MUNICH])	74-108	152-179	184-218					
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	FOWLPOX VIRUS (ISOLATE HP-318[MUNICH])	62-89							
PVS11 ROTIS	MINOR OUTER CAPSID PROTEIN	FOWLPOX VIRUS (ISOLATE HP-318[MUNICH])	162-197	214-241						

PCGENE	1021/7814	FILENAME	PROTEIN	ALL Viruses (no bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PYB12_FOWPM		HYPOTHETICAL BAMB1-ORF12 PROTEIN		VIRUS	11-38								
PYB13_FOWPM		HYPOTHETICAL BAMB1-ORF13 PROTEIN		FOWLPOX VIRUS (ISOLATE HP-418(MUNICH))	128-167								
PYBL3_FOAMV		BEL-3 PROTEIN		HUMAN SPONDAEVIROVIRUS	87-116								
PYDHI_HSV57		HYPOTH 21.1 KD IN DIFER 3 REGION		HERPESVIRUS SAIMIRI (STRAIN 484-77)	161-188								
PYDHI_HSV58		HYPOTH 22.2 KD IN DIFER 3 REGION		HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 484)	52-82								
PYDHI_HSV59		HYPOTH 23.3 KD IN DIFER 3 REGION		HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 488)	53-83								
PYF36_FOWP1		HYPOTHETICAL 23.5 KD PROTEIN		FOWLPOX VIRUS (STRAIN F6-1)	8-35								
PYF30_FOWP1		HYPOTHETICAL 30.5 KD PROTEIN		FOWLPOX VIRUS (STRAIN F6-1)	170-204								
PYH22_VACCV		HYPOTH 21.7 KD IN DIFER 3 PRO		VACCINIA VIRUS (STRAIN WR)	37-64	95-126	144-171						
PYH23_VACCV		HYPOTH HOST RANGE 27.4 KD PRO		VACCINIA VIRUS (STRAIN WR)	31-58	179-206							
PYK83_EBV		HYPOTHETICAL BKRF2 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN B95-8)	90-121								
PYK84_EBV		HYPOTHETICAL BKRF4 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN B95-8)	19-53								
PYL15_ADE41		HYPOTH 12.4 KD IN 31 KD REGION		HUMAN ADENOVIRUS TYPE 41	47-86								
PYLO3_EBV		HYPOTHETICAL BLRF3 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN B95-8)	27-54								
PYORI_COTMV		HYPOTHETICAL 23 KD PROTEIN		COMELINA YELLOW MOTTLE VIRUS	94-143								
PYOR2_COTMV		HYPOTHETICAL 13 KD PROTEIN		COMELINA YELLOW MOTTLE VIRUS	35-76								
PYOR3_WCMVM		HYPOTHETICAL 13 KD PROTEIN		WHITE CLOVER MOSAIC VIRUS (STRAIN M)	64-94								
PYOR3_WCMVO		HYPOTHETICAL 13 KD PROTEIN		WHITE CLOVER MOSAIC VIRUS (STRAIN O)	65-95								
PYOR3_ADEG1		HYPOTHETICAL 31.3 KD PROTEIN		AVIAN ADENOVIRUS GALI (STRAIN PHELP5)	92-119								
PYORA_TTV1		HYPOTHETICAL 8.1 KD PROTEIN		THERMOPROTEUS TENAX VIRUS I (STRAIN KRA1)	23-57								
PYOR4_TTV1		HYPOTHETICAL 26.8 KD PROTEIN		THERMOPROTEUS TENAX VIRUS I (STRAIN KRA1)	15-42								
PYORQ_TTV1		HYPOTHETICAL 7.3 KD PROTEIN		THERMOPROTEUS TENAX VIRUS I (STRAIN KRA1)	3-21								
PYORW_TTV1		HYPOTHETICAL 12.1 KD PROTEIN		THERMOPROTEUS TENAX VIRUS I (STRAIN KRA1)	4-40								
PYP12_RTBV		HYPOTHETICAL P12 PROTEIN		RICE TUNGRO BACILLIFORM VIRUS	44-71								
PYP12_RTBVP		HYPOTHETICAL P12 PROTEIN		RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES)	44-71								
PYP24_RTBV		HYPOTHETICAL P24 PROTEIN		RICE TUNGRO BACILLIFORM VIRUS	59-101	106-157							
PYP24_RTBVP		HYPOTHETICAL P24 PROTEIN		RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES)	51-101	106-157							
PYP46_RTBV		HYPOTHETICAL P46 PROTEIN		RICE TUNGRO BACILLIFORM VIRUS	58-107	197-231							
PYP46_RTBVP		HYPOTHETICAL P46 PROTEIN		RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES)	58-107	197-231							
PYP63_NPVAC		HYPOTH PRO P6.3 5 REGION		AUTOGRAPIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	44-71								
PYP63_NPVOP		HYPOTH 40.0 KD IN P6.3 5 REGION		ORGANIA PSEUDOTISUGATA MULTICAPSID POLYHEDROSIS VIRUS	325-352								
PYP6H_NPVAC		HYPOTH 23.6 KD IN POLYHEDRIN 5 REGION		AUTOGRAPIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	116-153								
PYPOL_IPNYN		HYPOTHETICAL 17.0 KD PROTEIN		INFECTIOUS PANCREATIC NECROSIS VIRUS (STRAIN NI)	5-32	59-96	156-183						
PYQJ_AMEPV		HYPOTHETICAL PROTEIN IN TK 3 REGION		HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN GS)	208-235								
PYRF1_HSV60		HYPOTHETICAL PROTEIN RF1		HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN GS)	233-257	268-299							
PYRF2_HSV60		HYPOTHETICAL PROTEIN RF2		HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN GS)	141-168								
PYRF3_HSV60		HYPOTHETICAL PROTEIN RF3		HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN GS)	404-441								
PYRF4_HSV60		HYPOTHETICAL PROTEIN RF4		HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN GS)	10-45								
PYRF2_IRV6		REPETITIVE PROTEIN ORF2		CHILLO RUDESCENT VIRUS	7-34								
PYVAG_VACCV		HYPOTHETICAL 9.3 KD PROTEIN		VACCINIA VIRUS (STRAIN COPENHAGEN)	81-112								
PYVAH_VACCV		HYPOTHETICAL 14.5 KD PROTEIN		VACCINIA VIRUS (STRAIN COPENHAGEN)	29-77								
PYVDB_VACCV		HYPOTHETICAL 1.3 KD PROTEIN		VACCINIA VIRUS (STRAIN COPENHAGEN)	46-77								
PYVDB_VACCV		HYPOTHETICAL 8.3 KD PROTEIN		VACCINIA VIRUS (STRAIN WR)	20-50								
PYVDB_VACCV		HYPOTHETICAL 7.3 KD PROTEIN		VACCINIA VIRUS (STRAIN WR)	10-44								
PYVGB_VACCV		HYPOTHETICAL 8.4 KD PROTEIN		VACCINIA VIRUS (STRAIN COPENHAGEN)	132-179								
PYZL2_EBV		HYPOTHETICAL BZL27 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN B95-8)									

TABLE VII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

(PREFERRED VIRAL SEQUENCES)

2

ECCE LINE	10711714	All Viruses (no better description)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
BLK NAME	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
POL MLVAX	POL POLYPROTEIN	AKA MURINE LEUKEMIA VIRUS	453-460								
PENY MLVAV	ENV POLYPROTEIN	AKY MURINE LEUKEMIA VIRUS	517-544								
POL MLVAV	POL POLYPROTEIN	AKY MURINE LEUKEMIA VIRUS	805-832								
PATYC AVIM2	MYC TRANSFORMING PROTEIN	AVIAN MYELOCTYOMATOSIS VIRUS CHII	232-266	375-402							
PATYC AVIM0	MYC TRANSFORMING PROTEIN	AVIAN MYELOCTYOMATOSIS VIRUS HBI	233-267	376-403							
PATYC AVIMC	MYC TRANSFORMING PROTEIN	AVIAN MYELOCTYOMATOSIS VIRUS NC19	233-267	376-403							
VLI EPVL	PROBABLE LI PROTEIN	AVIAN PAPILLOMA VIRUS EPV-L	38-65								
PVGLB HSVB1	GLYCOPROTEIN 1 PRECURSOR	BOVINE HERPESVIRUS TYPE 1	427-454								
PURQ HSVB3	RIBONUC-DIPHOSPH REDUCT SMALL CHA	BOVINE HERPESVIRUS TYPE 1 (STRAIN 34)	90-117								
PVGLB HSVB2	GLYCOPROTEIN B-1 PRECURSOR	BOVINE HERPESVIRUS TYPE 2 (STRAIN BMV)	447-474								
PENY BLV06	ENV POLYPROTEIN	BOVINE IMMUNODEFICIENCY VIRUS (ISOLATE 106)	17-44	344-603	631-693						
PENY BLV71	ENV POLYPROTEIN	BOVINE IMMUNODEFICIENCY VIRUS (ISOLATE 127)	17-44	573-632	660-724						
PENY BLVAF	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (AMERICAN ISOLATE FLK)	304-377								
PENY BLVAV	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (AMERICAN ISOLATE VDM)	304-377								
PENY BLVAU	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (AUSTRALIAN ISOLATE)	304-377								
PENY BLVB2	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (BELGIUM ISOLATE LID35)	304-377								
PENY BLVB5	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (JAPANESE ISOLATE BLV-1)	304-377								
PHEMA PJIB	HEMAGGLUTININ-NEURAMINIDASE	BOVINE PARAINFLUENZA 3 VIRUS	66-93								
PRAP PJIB	RNA POLYMERASE ALPHA SUBUNIT	BOVINE PARAINFLUENZA 3 VIRUS	34-91	255-282	283-314						
PVGLF PJIB	FUSION GLYCOPROTEIN PRECURSOR	BOVINE PARAINFLUENZA 3 VIRUS	115-182	207-241	459-497						
PYMAT PJIB	MATRIX PROTEIN	BOVINE PARAINFLUENZA 3 VIRUS	201-231								
PRPP BRSA	RNA POLYMERASE ALPHA SUBUNIT	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A1908)	99-133								
PVGLF BRSA	FUSION GLYCOPROTEIN PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A1908)	38-65	154-202	216-243	441-469	486-531				
PVMA2 BRSA	MATRIX GLYCOPROTEIN M2	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A1908)	124-152								
PYMAT BRSA	MATRIX PROTEIN	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A1908)	219-246								
PVGLF BRSC	FUSION GLYCOPROTEIN PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COPENHAGEN)	38-65	154-202	216-243	441-471	488-533				
PVGL2 BRSC	MAJOR SURFACE GLYCOPROTEIN O	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COPENHAGEN)	92-123								
PVGLF BRSVR	FUSION GLYCOPROTEIN PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COPENHAGEN)	38-65	154-202	216-243	441-471	488-533				
PENY MLVCB	ENV POLYPROTEIN	CAS-BK-E MURINE LEUKEMIA VIRUS	510-539								
PENY SVICZ	ENV POLYPROTEIN	CHIMPANZEE IMMUNODEFICIENCY VIRUS	160-187	253-289	316-366	526-584	637-654				
PVPU SVICZ	VPU PROTEIN	CHIMPANZEE IMMUNODEFICIENCY VIRUS	51-78								
PVCL SVICZ	POL POLYPROTEIN	CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIVCP21)	242-269								
PVEA CPVK	PROBABLE E1 PROTEIN	COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN KANSAS)	5-34								
VLI CPVK	PROBABLE L1 PROTEIN	COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN KANSAS)	331-383								
PPOL DEN15	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 1 (STRAIN SINGAPORE 575/90)	1858-1885	2890-2933	2989-3016						
PPOL DEN16	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN 16681)	1544-1571	1858-1885	2908-2935	2912-3016	3117-3147				
PPOL DEN17	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 3 (STRAIN 16681-PDK53)	1544-1571	1858-1885	2883-2939	2908-2935	2982-3016	3117-3147			
PPOL DEN18	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 4 (STRAIN JAMAICA)	1544-1571	1858-1885	2908-2935	3117-3147	3386-3373				
PPOL DEN19	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN PR13951)	1544-1571	1858-1885	2903-2932	2979-3013	3114-3144	3341-3370			
PPOL DEN1	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 3	1134-1161	1448-1473							
PPOL DEN4	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 4	872-884	1542-1569	1857-1884	2404-2521	2980-3014	3345-3372			
PPOL HPB00	DNA POLYMERASE	DUCK HEPATITIS B VIRUS (BROWN SHANGHAI DUCK ISOLATE S3)	2883-2930	2977-3011	3342-3369						
PPOL HPB0C	DNA POLYMERASE	DUCK HEPATITIS B VIRUS (STRAIN CHINA)	5-39								
PPOL HPB0W	DNA POLYMERASE	DUCK HEPATITIS B VIRUS (WHITE SHANGHAI DUCK ISOLATE S31)	5-39	304-331							
PTEGU EBV	LARGE TEGUMENT PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)	145-172	1215-1242	1344-1371	1876-1903					
PULAK EBV	VIRION PROTEIN BB9F1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	115-142	313-340	542-569						
PULL1 EBV	HYPOTHETICAL PROTEIN BBLF1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	15-42								
PUL31 EBV	PROB DNA REPLICATION PROTEIN BSLF1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	185-212	987-814							
PUL37 EBV	HYPOTHETICAL PROTEIN BICRF1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	409-436								
PUL39 EBV	HYPOTHETICAL PROTEIN BDLF4	EPSTEIN-BARR VIRUS (STRAIN B95-4)	107-144	168-196							
PVCP EBV	MAJOR CAPSID PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)	847-874								
PVGL2 EBV	PROBABLE MEMBRANE GLYCOPROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)	68-102								
PVGLB EBV	GLYCOPROTEIN GP110 PRECURSOR	EPSTEIN-BARR VIRUS (STRAIN B95-4)	95-122	631-658							
PVGLH EBV	GLYCOPROTEIN GP45 PRECURSOR	EPSTEIN-BARR VIRUS (STRAIN B95-4)	349-376	619-648							
PVGPB EBV	PROBABLE MEMBRANE ANTIGEN GP45	EPSTEIN-BARR VIRUS (STRAIN B95-4)	104-149								

PCGENE	10711214	All Virus (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PYV00 EBV	CAPSID PROTEIN P40	EPSTEIN-BARR VIRUS (STRAIN 195-8)	400-470								
PYV01 EBV	PROBABLE DNA PACKAGING PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	314-290								
PYV02 EBV	HYPOTHEICAL BKRF1 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	90-121								
PYV03 EBV	HYPOTHEICAL BKRF4 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	19-53								
PYV04 EBV	HYPOTHEICAL BLRF1 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	27-54								
PYV05 EBV	HYPOTHEICAL BLRF2 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	132-179								
PZL1 EBV	BLRF1 TRANS-ACTIVATOR PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	193-220								
PZL2 EBV	EARLY ANTIGEN PROTEIN R	EPSTEIN-BARR VIRUS (STRAIN 195-8)	977-1004								
PZL3 EBV	EARLY ANTIGEN PROTEIN I	EPSTEIN-BARR VIRUS (STRAIN 195-8)	55-82								
PZL4 EBV	GENE TERMINAL PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 195-8)	148-175								
PZL5 EBV	LATENT MEMBRANE PROTEIN 1	EPSTEIN-BARR VIRUS (STRAIN 195-8)	294-321								
PZL6 EBV	LATENT MEMBRANE PROTEIN 2	EPSTEIN-BARR VIRUS (STRAIN 195-8)	148-175								
PZL7 EBV	LATENT MEMBRANE PROTEIN 3	EPSTEIN-BARR VIRUS (STRAIN 195-8)	145-175								
PZL8 EBV	MAJOR ENVELOPE GLYCOPROTEIN 300	EQUINE HERPESVIRUS TYPE 1	124-151								
PZL9 EBV	GLYCOPROTEIN C PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (ISOLATE 115521A)	463-470	934-961							
PZL10 EBV	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB1)	463-470	934-961							
PZL11 EBV	ALPHA TRANS-IND FACTOR #2 KD PRO	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	294-321								
PZL12 EBV	PROBABLE HELICASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	255-289								
PZL13 EBV	RIBONUCLEOPROTEIN REDUCT LARGE CHA	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	184-211	321-348							
PZL14 EBV	LARGE TEGUMENT PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	75-102								
PZL15 EBV	VIRION GENE 56 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	239-256	566-593	1205-1232						
PZL16 EBV	HYPOTHEICAL GENE 48 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	600-667								
PZL17 EBV	GENE 40 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	247-266								
PZL18 EBV	GENE 21 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	44-71								
PZL19 EBV	DNA REPLICATION PROTEIN UL32	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	715-749	987-1014							
PZL20 EBV	GENE 3 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	193-220	943-970							
PZL21 EBV	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	146-176								
PZL22 EBV	GLYCOPROTEIN G PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	433-470	934-961							
PZL23 EBV	PROB INTEGRAL MEMBRANE PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	383-410								
PZL24 EBV	CAPSID PROTEIN VP26	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	167-174								
PZL25 EBV	GENE 3 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	36-63								
PZL26 EBV	CELL FUSION PROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN KENTUCKY A)	146-176								
PZL27 EBV	97 KD ALPHA TRANS-INDUCING PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAINS AB4P and KY A)	433-470	933-960							
PZL28 EBV	GLYCOPROTEIN G PRECURSOR	EQUINE HERPESVIRUS TYPE 4	312-339								
PZL29 EBV	DEOXY 5'-TRIPHOSPH NUCLEOTIDASE	EQUINE HERPESVIRUS TYPE 4	190-217	616-643							
PZL30 EBV	PROBABLE E3 PROTEIN	EUROPEAN ELK PAPILLOMAVIRUS	271-298								
PZL31 EBV	ENT POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALUNA)	170-190								
PZL32 EBV	ENT POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALUNA)	650-680	722-749							
PZL33 EBV	ENT POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO)	442-473								
PZL34 EBV	ENT POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE T42)	639-668	720-747							
PZL35 EBV	MYC TRANSFORMING PROTEIN	FELINE LEUKEMIA PROVIRUS (CLONE CFE-6)	640-679	721-748							
PZL36 EBV	MYC TRANSFORMING PROTEIN	FELINE LEUKEMIA VIRUS	509-538								
PZL37 EBV	ENT POLYPROTEIN	FELINE LEUKEMIA VIRUS (STRAIN AG15GOW-1)	391-420								
PZL38 EBV	ENT POLYPROTEIN	FELINE LEUKEMIA VIRUS (STRAIN LAMBDA-01)	490-519								
PZL39 EBV	ENT POLYPROTEIN	FELINE LEUKEMIA VIRUS (STRAIN SARNA)	510-539								
PZL40 EBV	ENT POLYPROTEIN	FRIEND MURINE LEUKEMIA VIRUS (ISOLATE 57)	482-516								
PZL41 EBV	ENT POLYPROTEIN	FRIEND MURINE LEUKEMIA VIRUS (ISOLATE F829)	523-557								
PZL42 EBV	ENT POLYPROTEIN	FRIEND MURINE LEUKEMIA VIRUS (ISOLATE PVC-211)	523-557								
PZL43 EBV	ENT POLYPROTEIN	GIBBON APE LEUKEMIA VIRUS	176-203	523-564							
PZL44 EBV	ENT POLYPROTEIN	GIBBON APE LEUKEMIA VIRUS	396-443	447-474							
PZL45 EBV	ENT POLYPROTEIN	GROUND SQUIRREL HEPATITIS VIRUS	535-582	676-703							
PZL46 EBV	DNA POLYMERASE		271-333								



PCGENE	10717184	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PCPOL_HSV5A	PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	621-632								
PDUT_HSV5A	DNA POLYMERASE	HERPESVIRUS SAIMIRI (STRAIN 11)	179-213								
PHL1_HSV5A	DEOXYU-5'-TRIPHOSPH NUCOTIDYLASE	HERPESVIRUS SAIMIRI (STRAIN 11)	418-449								
PIC1_HSV5A	PROBABLE HELICASE	HERPESVIRUS SAIMIRI (STRAIN 11)	518-83	482-532							
PIC2_HSV5A	PROBABLE PROC & TRANSPORT PRO	HERPESVIRUS SAIMIRI (STRAIN 11)	48-78								
PK18_HSV5A	IMMEDIATE-EARLY PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	340-386								
PK19_HSV5A	THYMIDINE KINASE	HERPESVIRUS SAIMIRI (STRAIN 11)	324-351								
PR1_HSV5A	RIBONUC-DIPHOSPH REDUCT LARGE CHA	HERPESVIRUS SAIMIRI (STRAIN 11)	524-607	672-700	777-814	846-898	949-986	990-1017	1467-1497	2102-2113	
PT53_HSV5A	PROBABLE LARGE TEGUMENT PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	120-147								
PT55_HSV5A	THYMIDYLATE SYNTHASE	HERPESVIRUS SAIMIRI (STRAIN 11)	15-42	302-358	368-402						
PUL6_HSV5A	VIRION GENE 43 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	34-61	204-231	367-389						
PUL13_HSV5A	VIRION GENE 19 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	208-235								
PUL14_HSV5A	GENE 67 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	31-65	685-737							
PUL17_HSV5A	GENE 63 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	120-157								
PUL32_HSV5A	PROB DNA REP GENE 56 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	9-36								
PUL11_HSV5A	HYPOTHETICAL GENE 53 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	582-609								
PUL19_HSV5A	HYPOTHETICAL GENE 24 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	92-122								
PUL93_HSV5A	HYPOTHETICAL GENE 31 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	135-176								
PUNG_HSV5A	URACIL-DNA GLYCOSYLASE	HERPESVIRUS SAIMIRI (STRAIN 11)	769-799								
PVCAP_HSV5A	MAJOR CAPSID PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	138-165								
PVC41_HSV5A	HYPOTHETICAL GENE 43 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	360-394								
PVC48_HSV5A	HYPOTHETICAL GENE 44 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	47-74								
PVG32_HSV5A	HYPOTHETICAL GENE 52 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	388-413								
PVLGH_HSV5A	GLYCOPROTEIN H PRECURSOR	HERPESVIRUS SAIMIRI (STRAIN 11)	80-107								
VNCP_HSV5A	INTEGRAL MEMBRANE PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	2-29								
VP22_HSV5A	PROBABLE CAPSID PROTEIN VP22	HERPESVIRUS SAIMIRI (STRAIN 11)	48-75								
VP26_HSV5A	CAPSID PROTEIN VP26	HERPESVIRUS SAIMIRI (STRAIN 11)	205-232	344-372							
VP28_HSV5A	CAPSID PROTEIN P40	HERPESVIRUS SAIMIRI (STRAIN 11)	181-208	929-977							
VP231_HSV5A	PROBABLE MEMBRANE ANTIGEN 75	HERPESVIRUS SAIMIRI (STRAIN 11)	333-368	512-539							
PDN81_HSV5A	MAJOR DNA-BINDING PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	127-154								
PCG82_HSV5A	CYCLIN HOMOLOG	HERPESVIRUS SAIMIRI (STRAIN 11)	161-188								
PDYH1_HSV57	HYPOTH 24.1 KD IN DHFR 3 REGION	HERPESVIRUS SAIMIRI (STRAIN 484-77)	52-82								
PDYH1_HSV5C	HYPOTH 24.7 KD IN DHFR 3 REGION	HERPESVIRUS SAIMIRI (STRAIN 484-77)	51-83								
PDYH4_HSV5C	HYPOTH 9.9 KD IN DHFR 3 REGION	HERPESVIRUS SAIMIRI (STRAIN 484-77)	510-540								
PERV_MLVH0	ENV POLYMERASE	HOMULY MORINE LEUKEMIA VIRUS	733-760								
PDPOL_HCMVA	DNA POLYMERASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	294-324								
PIC18_HCMVA	PROB PROC & TRANSPORT PRO UL36	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	32-49								
PIR03_HCMVA	HYPOTHETICAL PROTEIN IRL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	74-162								
PIR12_HCMVA	HYPOTHETICAL PROTEIN IRL12	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	31-82								
PIR17_HCMVA	HYPOTHETICAL PROTEIN IRL17	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	623-649								
PR1_HCMVA	RIBONUC-DIPHOSPH REDUCT LARGE CHA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	1251-1281	2202-2239							
PTEGU_HCMVA	PROBABLE LARGE TEGUMENT PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-47								
PUL08_HCMVA	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	347-374								
PUL13_HCMVA	HYPOTHETICAL PROTEIN UL13	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	81-112								
PUL16_HCMVA	HYPOTHETICAL PROTEIN UL16	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	14-61								
PUL20_HCMVA	HYPOTH PRO UL20 PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	623-649								
PUL31_HCMVA	HYPOTHETICAL PROTEIN UL31	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	114-148								
PUL33_HCMVA	HYPOTHETICAL PROTEIN UL33	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	114-148								
PUL47_HCMVA	PROTEIN UL47	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	159-166								
PUL50_HCMVA	PROTEIN UL50	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	74-101								
PUL59_HCMVA	HYPOTHETICAL PROTEIN UL59	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	65-92								
PUL70_HCMVA	PROB DNA REP PROTEIN UL70	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	5-73								
PUL73_HCMVA	UL73 GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	45-79								
PUL74_HCMVA	HYPOTHETICAL PROTEIN UL74	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	26-53								
PUL91_HCMVA	PROTEIN UL91	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	37-71								
PUL93_HCMVA	HYPOTHETICAL PROTEIN UL93	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	4-31								
PUL44_HCMVA	VIRION PROTEIN UL104	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	13-78								
PUL89_HCMVA	HYPOTHETICAL PROTEIN UL119	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)									

FCG CODE	10711784	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PULD1 HCMVA	PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	90-124									
PUS09 HCMVA	HYPOTHETICAL PROTEIN UL110	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	20-47									
PUS14 HCMVA	HYPOTHETICAL PROTEIN HOLF3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	277-308									
PUS18 HCMVA	MEMBRANE PROTEIN HWL5	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	101-218									
PVGLB HCMVA	GLYCOPROTEIN B PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	35-88	397-424	440-467	451-478						
PVGLH HCMVA	GLYCOPROTEIN H PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	107-136	270-297								
PVGLI HCMVA	IE GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	47-111									
PVTEK HCMVA	PROBABLE DNA PACKAGING PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	417-431									
PVNB1 HCMVA	MAJOR DNA-BINDING PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	437-464									
PVOK HCMVE	JO K DNA-BINDING PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN EISENHAUT)	194-221									
PVGLB HCMVT	GLYCOPROTEIN B PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN TOWNE)	50-88	397-424	413-462	452-479						
PVGLH HCMVT	GLYCOPROTEIN H PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN TOWNE)	106-135									
PENV HVIA2	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ARV2/SF2 ISOLATE)	544-592	630-682	790-835							
PGAG HVIA2	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ARV2/SF2 ISOLATE)	97-118									
POL HVIA2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ARV2/SF2 ISOLATE)	218-245	620-661								
PVPU HVIA2	VPU PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ARV2/SF2 ISOLATE)	3-31									
PENV HVIB1	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 AND RHX3 ISOLATES)	5-48									
PPOL HVIB1	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	545-594	631-683	791-818							
PENV HVIB5	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	230-237	637-673								
PENV HVIB8	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	230-237	637-673								
PENV HVIB8	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	540-589	636-678	786-813							
PENV HVIB8	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	21-48									
PENV HVIB8	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	267-294	331-365	567-590	674-679	787-813					
PVPU HVIB8	VPU PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	22-49									
PENV HVIB8	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	550-599	636-688	796-823							
PENV HVIB8	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	230-237	637-673								
PENV HVIB8	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	5-48									
PENV HVIC4	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	397-474	557-606	843-893	1007-1035						
PVPU HVIC4	VPU PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CDC-451 ISOLATE)	3-30									
PENV HVIEL	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ELI ISOLATE)	255-296	386-413	543-591	628-680						
PENV HVIEL	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ELI ISOLATE)	81-119									
PENV HVIEL	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ELI ISOLATE)	217-244	624-660								
PVPU HVIEL	VPU PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ELI ISOLATE)	6-33									
PENV HVIH2	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RDXB2 ISOLATE)	545-594	631-683	791-818							
PPOL HVIH2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RDXB2 ISOLATE)	218-245	620-661	921-951							
PVPU HVIH2	VPU PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RDXB2 ISOLATE)	5-48									
PENV HVIH3	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RDXD3 ISOLATE)	545-594	631-683	791-818							
PENV HVIJ3	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RDXD3 ISOLATE)	350-377	556-605	842-894	1002-1029						
PGAG HVIJ3	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RDXD3 ISOLATE)	91-118									
PVPU HVIJ3	VPU PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RDXD3 ISOLATE)	2-29									
PENV HVIJR	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RCSF ISOLATE)	336-363	627-675	783-811							
PPOL HVIJR	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RCSF ISOLATE)	222-249	624-665								
PVPU HVIJR	VPU PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RCSF ISOLATE)	22-49									
PENV HVIMA	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MAL ISOLATE)	547-595	633-707	794-826							
PPOL HVIMA	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MAL ISOLATE)	217-244	476-510	619-660							
PVPU HVIMA	VPU PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MAL ISOLATE)	5-32									
PENV HVIMG	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MFA ISOLATE)	543-592	629-681	789-816							
PGAG HVIMG	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MFA ISOLATE)	343-370	567-595	632-684	791-819						
PVPU HVIMG	VPU PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MFA ISOLATE)	82-118									
PPOL HVIMN	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NN ISOLATE)	231-248	621-664								
PENV HVIND	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE)	249-290	536-583	621-673	783-813						
PENV HVIND	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE)	81-119									
PPOL HVIND	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE)	217-244	624-660								
PENV HVIND	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE)	6-33									
PENV HVIND	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NEW YORK-3 ISOLATE)	376-360									
PPOL HVIND	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NEW YORK-3 ISOLATE)	218-245	622-661								
PENV HVIOY	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (OVI ISOLATE)	544-593	630-674	789-820							



PCGENE	10717144	All Virus (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
POL_HV10Y	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (OVI ISOLATE)	218-243	620-661										
PENY_HV10Y	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (PV2 ISOLATE)	545-594	631-683	791-818									
POL_HV1PV	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (PV2 ISOLATE)	200-237	637-673										
PVPU_HV1PV	VP1 PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (PV2 ISOLATE)	5-48											
PENY_HV1RH	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (R/HA1 ISOLATE)	280-307	331-378	534-602	640-692	800-832							
PPOL_HV1RH	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (R/HA1 ISOLATE)	217-244	619-660										
VIF_HV1RH	VIRION INTEGRITY FACTOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (R/HA1 ISOLATE)	62-89											
PENY_HV1SC	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (SC ISOLATE)	318-365	545-593										
PENY_HV1ST	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (SF162 ISOLATE)	313-363	536-585	622-674	782-809								
PVPU_HV1ST	VP1 PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (SF162 ISOLATE)	22-49											
PENY_HV1S3	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (SF13 ISOLATE)	541-589	637-679	787-815									
PENY_HV1K8	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (STRAIN KD-1-OP22)	274-301	555-596	637-677	776-824								
POL_HV1U4	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (STRAIN UGANDAN/ISOLATE U)	217-244	513-540	619-660									
PENY_HV1W1	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (WM1 ISOLATE)	318-365	545-593	631-683	791-818								
PENY_HV1W2	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (WM2 ISOLATE)	314-361	536-584	622-674	782-809								
PENY_HV1Z4	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z44 ISOLATE)	266-307	571-601	634-678	797-828								
PENY_HV1Z2	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-234 ISOLATE)	255-296	542-591	628-680	790-820								
PPOL_HV1Z2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-234 ISOLATE)	217-244	619-660										
PENY_HV1Z3	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z3/ARE 3 ISOLATE)	251-292											
PENY_HV1Z6	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z6/ARE 6 ISOLATE)	256-297	545-593	630-682	792-822								
NEGATIVE FACTOR			86-174											
PENY_HV1Z1	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z1/ARE 1 ISOLATE)	545-594	627-666	791-823									
PENY_HV1Z8	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE BEN)	61-88	532-591	621-648	653-697								
PGAG_HV1Z8	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE BEN)	88-115											
POL_HV1Z8	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE BEN)	491-582											
PENY_HV1ZC	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE CAN)	534-593	623-650	655-699									
POL_HV1ZC	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE CAN)	471-562											
PENY_HV2D1	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194)	61-88	532-550	555-582	644-688								
PGAG_HV2D1	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194)	88-115											
POL_HV2D1	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194)	509-600											
PENY_HV2D2	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194)	491-568											
PENY_HV2D1	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194)	60-87	574-551	556-583	613-640	644-693							
PENY_HV2B2	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE GHANA-1)	471-562											
PGAG_HV2B2	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE GHANA-1)	61-88	574-551	556-583	613-640	662-689							
POL_HV2B2	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE GHANA-1)	88-115											
PENY_HV2B3	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE N111-2)	471-529											
POL_HV2B3	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE N111-2)	58-85	533-592	632-698									
PENY_HV2B4	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	537-584	614-673										
POL_HV2B4	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	473-562											
PENY_HV2B5	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	442-476	537-554	559-586	648-692								
PGAG_HV2B5	GAG POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	88-115											
POL_HV2B5	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	491-582											
PENY_HV2B6	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	442-476	537-554	559-586	648-692								
POL_HV2B6	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	81-108											
PENY_HV2B7	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	30-60											
POL_HV2B7	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	157-184	334-361										
PENY_HV2B8	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	61-105	312-342										
POL_HV2B8	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	66-93											
PENY_HV2B9	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	60-87											
POL_HV2B9	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	310-340											
PENY_HV2B10	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	59-86											
POL_HV2B10	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	75-102											
PENY_HV2B11	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	183-210											
POL_HV2B11	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	159-186											
PENY_HV2B12	ENV POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	407-445											
POL_HV2B12	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE S111SY)	21-48											

PCGENE	10711314	All Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PVE2 HPV2A	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 2A	158-191									
PVE4 HPV31	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 31	75-102									
PVE6 HPV31	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 31	69-96									
PVE1 HPV33	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	180-207									
PVE2 HPV33	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	204-231									
VL1 HPV33	PROBABLE L1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	19-46									
PVE3 HPV33	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	158-192	327-354								
PVE5 HPV33	PROBABLE E5 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	27-54									
PVE1 HPV39	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 39	103-130									
PVE2 HPV39	E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 39	7-34	323-357								
PVE6 HPV39	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 39	71-102									
PVE1 HPV41	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	55-89									
PVE4 HPV41	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	63-97									
PVE6 HPV41	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	119-146									
VL1 HPV41	PROBABLE L1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	345-372									
PVE1 HPV42	PROBABLE L2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 42	415-442									
PVE6 HPV42	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 42	25-59									
PVE1 HPV47	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	75-102									
PVE3 HPV47	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	146-173									
PVE2 HPV47	PROBABLE E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	17-51	148-175	276-303							
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	17-51									
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	202-229									
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	137-184									
PVE6 HPV47	E6 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	72-99									
VL1 HPV47	PROBABLE L1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	19-46									
PVE1 HPV47	E1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	21-48									
PVE3 HPV47	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	166-193									
PVE2 HPV47	PROBABLE E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	2-36	309-336								
VL1 HPV47	PROBABLE L1 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	45-72									
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	17-51									
PVE2 HPV47	PROBABLE E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	202-229									
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	11-41									
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	30-60									
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	30-60									
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	354-392									
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	71-102									
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	84-111	234-261	373-416							
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	372-404	455-482								
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	84-111	234-261	373-416							
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	147-174	210-266								
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	84-111	244-271	373-416							
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	41-75									
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	84-111	232-262	373-416							
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	79-110	366-393								
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	377-404	444-488								
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	167-194	232-256								
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	90-117	141-175	218-266	483-528						
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	90-117	141-175	218-266	483-528						
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	322-349	1564-1598	1687-1721	1901-1946						
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	167-194	232-256								
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	90-117	141-175	218-266	483-528						
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	96-123									
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	27-61									
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	376-403									
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	27-61									
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	52-86	136-163	608-638	1081-1133	1994-2036	2115-2142				
PVE4 HPV47	PROBABLE E4 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	114-144	269-299								









PCGCODE	10717814	FILENAME	PROTEIN	All Yrater (no bacteriophage3)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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PCGENE	10717184	All Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PENY MLVX1	ENV POLYPROTEIN	KIRSTEN MURINE LEUKEMIA VIRUS	40-81								
PENY MLVX2	ENV POLYPROTEIN	KIRSTEN MURINE LEUKEMIA VIRUS	93-120	332-379							
PENY MLVX3	GLYCOPROTEIN B PRECURSOR	MAKER'S DISEASE HERPESVIRUS (STRAIN RB-1B)	471-512								
PENY MLVX4	ENV POLYPROTEIN	MINK CELL FOCUS-FORMING MURINE LEUKEMIA VIRUS	488-515								
PENY MLVX5	ENV POLYPROTEIN	MINK CELL FOCUS-FORMING MURINE LEUKEMIA VIRUS (ISOLATE CL-3)	502-543								
PENY MLVX6	MAJOR DNA-BINDING PROTEIN	MOLONEY MURINE LEUKEMIA VIRUS	584-618								
PENY MLVX7	PROB PRO C & TRANSPORT PRO	MURINE CYTOMEGALOVIRUS (STRAIN SMITH)	661-691								
PENY MLVX8	GLYCOPROTEIN B PRECURSOR	MURINE CYTOMEGALOVIRUS (STRAIN SMITH)	381-408	441-475							
PENY MLVX9	ENV POLYPROTEIN	MURINE CYTOMEGALOVIRUS (STRAIN SMITH)	267-294	327-361							
PENY MLVX10	IMMEDIATE-EARLY PROTEIN I	PYGMY CHIMPANZEE PAPILLONAVIRUS TYPE I	15-62								
PENY MLVX11	PROBABLE E3 PROTEIN	PYGMY CHIMPANZEE PAPILLONAVIRUS TYPE I	497-538								
PENY MLVX12	ENV POLYPROTEIN	RADIATION MURINE LEUKEMIA VIRUS	716-743	805-832							
PENY MLVX13	ENV POLYPROTEIN	RADIATION MURINE LEUKEMIA VIRUS	497-538								
PENY MLVX14	POL POLYPROTEIN	RADIATION MURINE LEUKEMIA VIRUS (STRAIN KAPLAN)	101-128	190-217							
PENY MLVX15	MAJOR DNA-BINDING PROTEIN	RADIATION MURINE LEUKEMIA VIRUS (STRAIN KAPLAN)	435-462	532-559							
PENY MLVX16	GENOME POLYPROTEIN	SIMIAN CYTOMEGALOVIRUS (STRAIN COLBURN)	207-241	1025-1052	1115-1192						
PENY MLVX17	ENV POLYPROTEIN	SIMIAN HEPATITIS A VIRUS (STRAIN AGM-27)	203-237								
PENY MLVX18	POL POLYPROTEIN	SIMIAN HEPATITIS A VIRUS (STRAIN CY-145)	269-310	561-588	592-619	652-679	697-724				
PENY MLVX19	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGN155 ISOLATE)	431-458	547-574	637-671						
PENY MLVX20	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGN155 ISOLATE)	45-72								
PENY MLVX21	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGN155 ISOLATE)	270-301	566-593	597-624	658-685	703-730				
PENY MLVX22	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGN155 ISOLATE)	71-98	432-516	642-669						
PENY MLVX23	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGN155 ISOLATE)	281-308	553-612	642-669	691-718					
PENY MLVX24	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (F236/S3014 ISOLATE)	88-115								
PENY MLVX25	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (F236/S3014 ISOLATE)	496-523								
PENY MLVX26	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM1/CLONE GRI-1)	252-291	1116-122	1548-603	634-708					
PENY MLVX27	GAO POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM1/CLONE GRI-1)	431-507								
PENY MLVX28	NEGATIVE FACTOR	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM1/CLONE GRI-1)	76-137								
PENY MLVX29	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM1/CLONE GRI-1)	478-515								
PENY MLVX30	VIRION INFECTIVITY FACTOR	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGM1/CLONE GRI-1)	2-36								
PENY MLVX31	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE GRI1)	8-35	158-185	589-650	784-816					
PENY MLVX32	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE GRI1)	232-254	636-670							
PENY MLVX33	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (KAW ISOLATE)	553-608								
PENY MLVX34	GAO POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (KAW ISOLATE)	88-115								
PENY MLVX35	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (KAW ISOLATE)	533-560								
PENY MLVX36	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	349-608								
PENY MLVX37	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	120-150	550-609	671-715						
PENY MLVX38	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	533-560								
PENY MLVX39	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	156-215	277-289							
PENY MLVX40	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	286-313	554-593	646-722						
PENY MLVX41	GAO POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	88-115								
PENY MLVX42	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	499-526								
PENY MLVX43	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	88-115								
PENY MLVX44	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (TYO-1 ISOLATE)	2-30	264-298	590-617	651-678					
PENY MLVX45	REV PROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (TYO-1 ISOLATE)	657-691								
PENY MLVX46	ENV POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (TYO-1 ISOLATE)	41-68								
PENY MLVX47	POL POLYPROTEIN	SIMIAN MASON-PFIZER VIRUS	427-470								
PENY MLVX48	GAO POLYPROTEIN	SIMIAN MASON-PFIZER VIRUS	374-612	670-697							
PENY MLVX49	ALKALINE EXONUCLEASE	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	322-260								
PENY MLVX50	PROBABLE HELICASE	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	109-139								
PENY MLVX51	RBONUC-DIPHOSPH REDUCT LARGE CHA	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	490-517	701-728							
PENY MLVX52	LARGE TEGUMENT PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	119-146								
PENY MLVX53	HYPOTHETICAL GENE 46 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	1121-1158	1579-1609							
PENY MLVX54	GENE 31 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	64-101								
PENY MLVX55			380-407								

CCGNE	1011714	All Viruses (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	VIRUS	117-119								
PULJ4 VZVD	YINON GENE 24 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	107-114	485-512	719-746	976-1003					
PULJ7 VZVD	GENE 21 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	310-364								
PUL41 VZVD	HOST SHUTOFF VIRION PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	176-156	312-349							
PUL41 VZVD	GENE 15 MEMBRANE PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	301-337								
PUL33 VZVD	PROB DNA REP GENE 6 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	295-322								
PVGLC VZVD	GLYCOPROTEIN GPV	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	174-208	495-522							
PYP40 VZVD	CAPSID PROTEIN P40	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	394-421								
PYTER VZVD	PROBABLE DNA PACKAGING PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	285-326								
PVGLC VZVS	GLYCOPROTEIN GPV	VARICELLA-ZOSTER VIRUS (STRAIN SCOTT)	295-322								
PDOL WHV1	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 1	290-311								
PDOL WHV39	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 39	212-242								
PDOL WHV7	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 7	211-241	290-331							
PDOL WHV8	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 8	212-242	289-330							
PDOL WHV81	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 8	212-242	290-331							

**TABLE VIII**

**107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY**

**FOR ALL PROCARYOTIC PROTEINS**

PCGENE	10711714	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
P120K_RICKI	120 KD SURFACE-EXPOSED PROTEIN	RICKETTSIA RICKETTSII	81-110	240-298	335-382	638-672	746-818	1168-1202			
P17K_RICTY	17 KD ANTIGEN PRECURSOR	RICKETTSIA TYPHI	67-94								
P190K_RICKI	190 KD ANTIGEN PRECURSOR (CELL SURFACE)	RICKETTSIA RICKETTSII	241-268	460-487	607-634	734-781	829-836	904-931	1220-1234	1344-1371	1723-1730
P22KD_DESMO	22.6 KD PROTEIN	DESULFOCOCCUS MOBILIS	2065-2096	2131-2168							
P40KD_VIBAN	40 KD PROTEIN PRECURSOR	VIBRIO ANGUILLARUM	35-52	59-89	120-147						
P60IM_ECOLI	60 KD INNER-MEMBRANE PROTEIN	ESCHERICHIA COLI	153-196								
P60IM_PROMI	60 KD INNER-MEMBRANE PROTEIN	PROTEUS MIRABILIS	511-538								
P63KD_ZYMO	63 KD PROTEIN	ZYMONOMAS MOBILIS	14-41								
P6PGD_BACSU	PROB 6-PHOSPHOGLUCONATE DEHYDROGENASE	BACILLUS SUBTILIS	95-122	444-524							
P6PGD_ECOLI	6-PHOSPHOGLUCONATE DEHYDROGENASE	ESCHERICHIA COLI	24-51	218-246							
P6PGD_SALTY	6-PHOSPHOGLUCONATE DEHYDROGENASE	SALMONELLA TYPHIMURIUM	205-232								
P6ACA_STAAT	6-AMINOGLYCOSIDE N-ACETYLTRANSFERASE	STAPHYLOCOCCUS AUREUS	203-232								
P6AT1_BAGSP	ASPARTATE AMINOTRANSFERASE	BACILLUS SP	450-477								
P6AT1_ECOLI	ASPARTATE AMINOTRANSFERASE	ESCHERICHIA COLI	146-173	185-212							
P6B1_ECOLI	ABC PROTEIN	ESCHERICHIA COLI	351-378								
P6B1C_ECOLI	ABORTIVE PHAGE RESISTANCE PROTEIN ABIC	LACTOCOCCUS LACTIS	176-203								
P6CCR_AGRTU	TRANSCRIPTIONAL REPRESSOR ACCR	AGROBACTERIUM TUMEFACIENS	85-126	170-204	209-223						
P6CEA_ECOLI	ISOCITRATE LYASE	ESCHERICHIA COLI	127-154								
P6CON_BACSU	ACONITATE HYDRATASE	BACILLUS SUBTILIS	398-432								
P6COR_ECOLI	ACONITATE HYDRATASE	ESCHERICHIA COLI	48-75								
P6CPL_ECOLI	ACETOLIN CATABOLISM REG PRO	ALCALIGENES EUTROPHUS	41-68	613-640							
P6CRA_ECOLI	ACRYL CARRIER PROTEIN	ESCHERICHIA COLI	85-112								
P6CRA_ECOLI	ACRYLAVIN RESISTANCE PROTEIN A PRECURSOR	ESCHERICHIA COLI	4-31								
P6CRA_ECOLI	ACRYLAVIN RESISTANCE PROTEIN B	ESCHERICHIA COLI	313-247								
P6CRF_ECOLI	ACRYLAVIN RESISTANCE PROTEIN F	ESCHERICHIA COLI	520-551								
P6CT1_STRO	PUTATIVE KETOACYL REDUCTASE	STREPTOMYCES COELICOLOR	512-550	726-753							
P6CT1_LISMO	ACTIN-ASSEMBLY INDUCING PROTEIN PRECURSOR	LISTERIA MONOCYTOGENES	153-184	516-601							
P6CYS_NOCLO	ACYL SYNTHETASE	NOCAOIA LACTANDURANS	217-264	516-601							
P6DAX_BACSU	METHYLTRANSFERASE	BACILLUS SUBTILIS	3129-3163								
P6DDA_BACSU	ATP-DEPENDENT NUCLEASE SUBUNIT A	BACILLUS SUBTILIS	136-170								
P6DDB_BACSU	ATP-DEPENDENT NUCLEASE SUBUNIT B	BACILLUS SUBTILIS	398-425	454-481	532-556	1095-1032					
P6DHI_CLOAB	NADPH-DEPENDENT BUTANOL DEHYDROGENASE	CLOSTRIDIUM ACETOBUTYLICUM	337-284	870-901	943-977						
P6DHI_CLOAB	NADPH-DEPENDENT BUTANOL DEHYDROGENASE A	CLOSTRIDIUM ACETOBUTYLICUM	284-311								
P6DHB_CLOAB	NADH-DEPENDENT BUTANOL DEHYDROGENASE B	CLOSTRIDIUM ACETOBUTYLICUM	298-325								
P6DHE_CLOAB	ALCOHOL DEHYDROGENASE	ESCHERICHIA COLI	598-625								
P6DIE_ECOLI	ALCOHOL DEHYDROGENASE	ESCHERICHIA COLI	651-680	775-806							
P6DIY_ECOLI	PUTATIVE REGULATORY PROTEIN ADIY	ESCHERICHIA COLI	271-298								
P6DPT_MYCOE	140 KD ADHESIN PRECURSOR	MYCOPLASMA GENITALIUM	45-72								
P6DPT_MYCPN	ADHESIN P1 PRECURSOR	MYCOPLASMA PNEUMONIAE	90-131	697-724	923-950	990-1017	1169-1199	1387-1414			
P6DPT_RICPR	ADP-ATP CARRIER PROTEIN	RICKETTSIA PROVAZEKII	357-384								
P6ERA_AERYH	AEROXYLASE PRECURSOR	AEROMONAS HYDROPHILA	276-307								
P6GAL_STRAU	ALPHA-GALACTOSIDASE	STREPTOCOCCUS MUTANS	278-305								
P6GAR_PSEAT	BETA-AARASE PRECURSOR	PSEUDOMONAS ATLANTICA	419-483	597-633							
P6GR_STAAT	ACCESSORY GENE REGULATORY PROTEIN	STAPHYLOCOCCUS AUREUS	26-53								
P6L_YEREN	ATTACH INVAS LOCUS PROTEIN PRECURSOR	YERSINIA ENTEROCOLITICA	139-159	165-192							
P6KIH_ECOLI	ASPARTOKINASE I	ESCHERICHIA COLI	19-46								
P6KIH_ECOLI	ASPARTOKINASE II	ESCHERICHIA COLI	3-30	468-493	503-530						
P6K3_BACSU	ASPARTATE KINASE II ALPHA AND BETA SUBUNITS	BACILLUS SUBTILIS	51-78	608-635							
P6KAB_CORG	ASPARTATE KINASE ALPHA AND BETA SUBUNITS	CORYNEBACTERIUM GLUTAMICUM	266-312								
P6LF_ECOLI	FRUCTOSE-BISPHOSPHATE ALDOLASE	ESCHERICHIA COLI	5-32								
P6LGE_PSEAE	ALGNATE BIOSYN TRANS REG PROTEIN ALGP	PSEUDOMONAS AERUGINOSA	286-316								
P6LGE_PSEAE	ALGNATE PRODUCTION PROTEIN ALGE PRECURSOR	PSEUDOMONAS AERUGINOSA	160-194								
P6LGE_PSEAE	TRANSCRIPTIONAL REGULATORY PROTEIN ALGP	PSEUDOMONAS AERUGINOSA	149-376								
P6LGE_PSEOL	ALKANE-1 MONOOXYGENASE	PSEUDOMONAS AERUGINOSA	81-115								
P6LKT_PSEOL	KUBREDOXIN-NADH REDUCTASE	PSEUDOMONAS OLEOVORANS	115-142								
P6LKS_ECOLI	ALANINE RACEMASE, CATABOLIC PRECURSOR	ESCHERICHIA COLI	138-172	338-365							
			9-16								

PCGENE	10117844	Prokaryotic Sequences	AMPA.1	AMPA.2	AMPA.3	AMPA.4	AMPA.5	AMPA.6	AMPA.7	AMPA.8	AMPA.9
FILENAME	PROTEIN	ORGANISMI	AMPA.1	AMPA.2	AMPA.3	AMPA.4	AMPA.5	AMPA.6	AMPA.7	AMPA.8	AMPA.9
PALR_BACST	ALANINE RACEMASE	BACILLUS STEAROTHERMOPHILUS	126-151								
PALR_BACSU	ALS OPERON REGULATORY PROTEIN	BACILLUS SUBTILIS	119-146								
PALYS_BACSP	AUTOLYSIN PRECURSOR	BACILLUS SP	151-187								
PALYS_BACSU	AUTOLYSIN PRECURSOR	BACILLUS SUBTILIS	147-191								
PALYS_STAAU	AUTOLYSIN	STAPHYLOCOCCUS AUREUS	244-271								
PAMIA_STRN	AMIA PROTEIN PRECURSOR	STREPTOCOCCUS PNEUMONIAE	221-264	146-473							
PAMD_PSECL	AMIDASE	PSEUDOMONAS CILICORAPIUS	72-99								
PAMIE_STRN	OLIGOPEPTIDE TRANSPORT PROTEIN AMIE	STREPTOCOCCUS PNEUMONIAE	182-214								
PAMPA_ECOLI	AMINOPEPTIDASE A1	ESCHERICHIA COLI	111-138	199-226							
PAMPC_SERMA	BETA-LACTAMASE PRECURSOR	SERRATIA MARCESCENS	231-258								
PAMPL_BICPR	CYTOSOL AMINOPEPTIDASE	RICKETTSIA PROWAZEKII	3-47	72-99							
PAMPP_ECOLI	X-PRO AMINOPEPTIDASE	ESCHERICHIA COLI	655-682								
PAMPT_TIEAO	AMINOPEPTIDASE T	ESCHERICHIA COLI	110-137								
PAMV1_DICTH	ALPHA-AMYLASE 1	THERMUS AQUATICUS	281-308								
PAMV2_DICTH	ALPHA-AMYLASE 2	DICTYOGLOMUS THERMOPHILUM	307-534								
PAMV3_DICTH	CYTOSOL AMYLASE	DICTYOGLOMUS THERMOPHILUM	151-178	307-534							
PAMV4_DICTH	ALPHA-AMYLASE 3	SALMONELLA TYPHIMURUM	70-104								
PAMV5_DICTH	ALPHA-AMYLASE 4	DICTYOGLOMUS THERMOPHILUM	280-307								
PAMV6_DICTH	BETA-AMYLASE PRECURSOR	BACILLUS CIRCULANS	61-88								
PAMV7_DICTH	BETA-AMYLASE	BACILLUS POLYMYXA	60-87	266-293	1143-1184						
PAMV8_DICTH	BETA-AMYLASE	CLOSTRIDIUM THERMOSULFUROGENES	269-296	178-405	459-486						
PAMV9_DICTH	GLUCOAMYLASE PRECURSOR	CLOSTRIDIUM SP	103-148	480-510							
PAMV10_DICTH	MALTOGENIC ALPHA-AMYLASE PRECURSOR	BACILLUS STEAROTHERMOPHILUS	426-453								
PAMV11_DICTH	RAW-STARCH-DIGESTING AMYLASE	BACILLUS SP	210-237	435-465	615-642						
PAMV12_DICTH	ALPHA-AMYLASE PRECURSOR	AEROMONAS HYDROPHILA	415-453								
PAMV13_DICTH	ALPHA-AMYLASE PRECURSOR	ALTEROMONAS HALOPLANKTIS	166-193								
PAMV14_DICTH	ALPHA-AMYLASE PRECURSOR	BACILLUS AMYLOLIQUEFACIENS	102-136								
PAMV15_DICTH	ALPHA-AMYLASE PRECURSOR	BACILLUS CIRCULANS	437-474								
PAMV16_DICTH	ALPHA-AMYLASE PRECURSOR	BACILLUS MEGATERIUM	212-239								
PAMV17_DICTH	ALPHA-AMYLASE PRECURSOR	BACILLUS SUBTILIS	61-88	441-482							
PAMV18_DICTH	ALPHA-AMYLASE PRECURSOR	BACILLUS SUBTILIS	165-203	281-308							
PAMV19_DICTH	ALPHA-AMYLASE PRECURSOR	BUTYRIVIBRIO FIBRISOLVENS	372-418	546-571	579-606	793-822					
PAMV20_DICTH	PUTATIVE ALPHA-AMYLASE	CLOSTRIDIUM ACETOBYTILICUM	283-310								
PAMV21_DICTH	ALPHA-AMYLASE PRECURSOR	CLOSTRIDIUM THERMOSULFUROGENES	431-468	612-642							
PAMV22_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	173-200								
PAMV23_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV24_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV25_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV26_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV27_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV28_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV29_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV30_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV31_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV32_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV33_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV34_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV35_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV36_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV37_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV38_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV39_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV40_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV41_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV42_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV43_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV44_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV45_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV46_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV47_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV48_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV49_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV50_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV51_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV52_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV53_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV54_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV55_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV56_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV57_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV58_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV59_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV60_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV61_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV62_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV63_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV64_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV65_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV66_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV67_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV68_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV69_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV70_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV71_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV72_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV73_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV74_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV75_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV76_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV77_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV78_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV79_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV80_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV81_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV82_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV83_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV84_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV85_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV86_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV87_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV88_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV89_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV90_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV91_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV92_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV93_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV94_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV95_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV96_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV97_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV98_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV99_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								
PAMV100_DICTH	ALPHA-AMYLASE PRECURSOR	STREPTOMYCES LIMOSUS	232-259								

PGENE	1071714.4	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PAPK1 ECOLI	SHIKIMATE KINASE I	ESCHERICHIA COLI	84-118								
PAPM1 STRYP	IGA RECEPTOR PRECURSOR	STREPTOCOCCUS PYOGENES	12-46	127-137	266-324						
PAPF1 ECOLI	ADP PROTEIN	ESCHERICHIA COLI	255-282								
PAPSA ECOLI	ARSENICAL PUMP-DRIVING ATPASE	ESCHERICHIA COLI	201-238								
PASB1 ECOLI	ARSENICAL PUMP MEMBRANE PROTEIN	ESCHERICHIA COLI	291-318								
PASB1 STAAU	ARSENICAL PUMP MEMBRANE PROTEIN	STAPHYLOCOCCUS AUREUS	27-71	295-322							
PASB1 STAXY	ARSENICAL PUMP MEMBRANE PROTEIN	STAPHYLOCOCCUS AUREUS	27-71	295-322							
PASR1 STAAU	ARSENICAL RESIST OPERON REPRESSOR PROTEIN	STAPHYLOCOCCUS AUREUS	56-93								
PART1 ECOLI	ARTA PROTEIN	ESCHERICHIA COLI	3-30								
PART1 ECOLI	TRANSPORT SYSTEM PROTEIN ART1	ESCHERICHIA COLI	105-132	213-240							
PART1 ECOLI	TRANSPORT SYSTEM PROTEIN ART2	ESCHERICHIA COLI	176-206								
PASAT1 ENTITA	AGGREGATION SUBSTANCE PRECURSOR	ENTEROCOCCUS FAECALIS	193-234	478-505	799-826	859-896					
PASNA ECOLI	ASPARTATE-AMMONIA LIGASE	ESCHERICHIA COLI	127-158								
PASNB ECOLI	ASPARAGINE SYNTHETASE II	ESCHERICHIA COLI	460-477								
PASNC1 UCOLI	REGULATORY PROTEIN ASNC	ESCHERICHIA COLI	116-141								
PASPA ECOLI	ASPARTATE AMMONIA-LYASE	BACILLUS SUBTILIS	7-34								
PASPA ECOLI	ASPARTATE AMMONIA-LYASE	ESCHERICHIA COLI	204-236								
PASPA SERMA	ASPARTATE AMMONIA-LYASE	SERRATIA MARCESCENS	204-231								
PASPD1 BACLI	L-ASPARAGINASE	BACILLUS LICHENIFORMIS	353-288								
PASPD1 ERWCHI	L-ASPARAGINASE PRECURSOR	ERWINIA CHIRYSANTHEMI	188-218								
PASPD1 ACIGL	GLUTAMINASE-ASPARAGINASE	ACINETOBACTER GLUTAMINIFICANS	46-80								
PASPY ECOLI	ARGININOSUCCINATE SYNTHASE	ESCHERICHIA COLI	334-381								
PASPY METBA	ARGININOSUCCINATE SYNTHASE	METHANOSARCINA BARKEII	287-314								
PATPA STAAU	POTENTIAL ATP-BINDING PROTEIN	STAPHYLOCOCCUS AUREUS	201-245								
PATPA ENTITA	POTASSIUMCOPPER-TRANSPORTING ATPASE A	ENTEROCOCCUS FAECALIS	41-68	201-245							
PATPB ENTITA	POTASSIUMCOPPER-TRANSPORTING ATPASE B	ENTEROCOCCUS FAECALIS	41-68	347-374							
PATPB SALTU	MGE(2+) TRANSPORT ATPASE P-TYPE	SALMONELLA TYPHIMURUM	280-310	450-477							
PATPB SYN76	ATP SYNTHASE A CHAIN	SYNECHOCOCCUS SP	501-530								
PATPB VIBAL	ATP SYNTHASE A CHAIN	VIBRIO ALGINOLYTICUS	233-260								
PATPA ANASP	ATP SYNTHASE ALPHA CHAIN	ANABAENA SP	11-38	96-130							
PATPA BACME	ATP SYNTHASE ALPHA CHAIN	BACILLUS MEGATERIUM	4-36	453-480							
PATPA ECOLI	ATP SYNTHASE ALPHA CHAIN	ESCHERICHIA COLI	486-513								
PATPA ENTITA	ATP SYNTHASE ALPHA CHAIN	ENTEROCOCCUS FAECALIS	4-36	484-518							
PATPA MYCGA	ATP SYNTHASE ALPHA CHAIN	MYCOPLASMA GALLISEPTICUM	362-409								
PATPA PROMO	ATP SYNTHASE ALPHA CHAIN	PROFIBRILLUM MODESTUM	6-36								
PATPA RHORU	ATP SYNTHASE ALPHA CHAIN	RHODOSPIRILLUM RUBRUM	165-200	459-486							
PATPA SULAC	ATP SYNTHASE ALPHA CHAIN	SULFOLOBUS ACIDOCALDARIUS	318-345	562-589							
PATPA SYN71	ATP SYNTHASE ALPHA CHAIN	SYNECHOCOCCUS SP	7-44								
PATPA SYN76	ATP SYNTHASE ALPHA CHAIN	SYNECHOCOCCUS SP	8-45	362-389							
PATPA SYN73	ATP SYNTHASE ALPHA CHAIN	SYNECHOCYSTIS SP	8-37	454-500							
PATPA THEP3	ATP SYNTHASE ALPHA CHAIN	THERMOPHILIC BACTERIUM PS-3	9-36								
PATPA VIBAL	ATP SYNTHASE ALPHA CHAIN	VIBRIO ALGINOLYTICUS	444-513								
PATPB ANASP	ATP SYNTHASE BETA CHAIN	ANABAENA SP	280-307	370-397							
PATPB BACFI	ATP SYNTHASE BETA CHAIN	BACILLUS FIRMIUS	163-190	358-385							
PATPB MYCGA	ATP SYNTHASE BETA CHAIN	MYCOPLASMA GALLISEPTICUM	373-402								
PATPB RHORU	ATP SYNTHASE BETA CHAIN	RHODOSPIRILLUM RUBRUM	339-386								
PATPB SULAC	ATP SYNTHASE BETA CHAIN	SULFOLOBUS ACIDOCALDARIUS	164-191								
PATPB SYN71	ATP SYNTHASE BETA CHAIN	SYNECHOCOCCUS SP	381-408								
PATPB SYN76	ATP SYNTHASE BETA CHAIN	SYNECHOCOCCUS SP	291-318	381-408							
PATPB SYN73	ATP SYNTHASE BETA CHAIN	SYNECHOCYSTIS SP	381-408								
PATPD ANASP	ATP SYNTHASE DELTA CHAIN	ANABAENA SP	109-139	143-170							
PATPD BACFI	ATP SYNTHASE DELTA CHAIN	BACILLUS FIRMIUS	63-90	133-160							
PATPD BACME	ATP SYNTHASE DELTA CHAIN	BACILLUS MEGATERIUM	132-159								
PATPD ENTITA	ATP SYNTHASE DELTA CHAIN	ENTEROCOCCUS FAECALIS	14-41								
PATPD PROMO	ATP SYNTHASE DELTA CHAIN	PROFIBRILLUM MODESTUM	79-116	118-149							
PATPD RHORU	ATP SYNTHASE DELTA CHAIN	RHODOSPIRILLUM RUBRUM	125-152								
PATPD RHORU	ATP SYNTHASE DELTA CHAIN	RHODOSPIRILLUM RUBRUM	119-146								







PGENE	1071784	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILENAME	PROTEIN	ORGANISM	86-113	314-341	730-773	798-825	830-892				
PBX1 CLOBO	CLOSTRIDIUM NEUROTOXIN TYPE C1 PRECURSOR	CLOSTRIDIUM BOTULINUM	86-113	314-341	730-773	798-825	830-892				
PBX2 CLOBO	CLOSTRIDIUM NEUROTOXIN TYPE D PRECURSOR	CLOSTRIDIUM BOTULINUM	471-500	526-576	721-770	804-831	847-892	906-963	1060-1087		
PBX3 CLOBO	CLOSTRIDIUM NEUROTOXIN TYPE E PRECURSOR	CLOSTRIDIUM BOTULINUM	234-291	350-381	704-733	773-811	890-917	992-1019	1115-1149		
PBX4 CLOBO	CLOSTRIDIUM NEUROTOXIN TYPE F PRECURSOR	CLOSTRIDIUM BOTULINUM	234-291	350-381	704-733	773-811	890-917	992-1019	1115-1149		
PBX5 CLOBO	CLOSTRIDIUM NEUROTOXIN TYPE F PRECURSOR	CLOSTRIDIUM BOTULINUM	669-710	735-772	892-919	1013-1040	1095-1122	1183-1210			
PC50 MICAE	CYTCHROME C50	MICROCYSTIS AERUGINOSA	3-20								
PCADA BACFI	PROBABILE CADMIUM-TRANSPORTING ATPASE	BACILLUS FIRMIUS	30-57	100-131	165-192	276-306	533-567				
PCADA STAAU	PROBABILE CADMIUM-TRANSPORTING ATPASE	STAPHYLOCOCCUS AUREUS	282-309	536-570							
PCADC ECOLI	TRANSCRIPTIONAL ACTIVATOR CADG	ESCHERICHIA COLI	54-85	412-443							
PCAF4 YERPE	F1 CAPSULE ANCHORING PROTEIN PRECURSOR	YERSINIA PESTIS	203-240	416-437	530-557	619-646					
PCAPB BACAN	CAPP PROTEIN	BACILLUS ANTHRACIS	108-138								
PCAPP ANANI	PHOSPHOENOLPYRUVATE CARBOXYLASE	ANACYSTIS NIDULANS	36-70								
PCAPP ANASP	PHOSPHOENOLPYRUVATE CARBOXYLASE	ANABENA SP	248-293								
PCAPP CORGL	PHOSPHOENOLPYRUVATE CARBOXYLASE	CORYNEBACTERIUM GLUTAMICUM	98-125	157-184	687-728						
PCAPP ECOLI	PHOSPHOENOLPYRUVATE CARBOXYLASE	ESCHERICHIA COLI	15-42								
PCARA BACSU	CARBAMOYL-PHOSPHATE SYNTHASE	BACILLUS SUBTILIS	35-62								
PCARB BACSU	CARBAMOYL-PHOSPHATE SYNTHASE	BACILLUS SUBTILIS	274-319								
PCARB ECOLI	CARBAMOYL-PHOSPHATE SYNTHASE (LARGE CHAI)	ESCHERICHIA COLI	790-831								
PCAT2 STAAU	CHLORAMPHENICOL ACETYLTRANSFERASE	STAPHYLOCOCCUS AUREUS	434-481								
PCAT3 STAAU	CHLORAMPHENICOL ACETYLTRANSFERASE	STAPHYLOCOCCUS AUREUS	7-34	87-114							
PCAT4 AGICA	CATECHOL 1,2-DIOXYGENASE	ACINETOBACTER CALCOACETICUS	7-34	87-114							
PCATA BACST	PEROXIDASE / CATALASE	BACILLUS STEAROTHERMOPHILUS	31-65								
PCATA ECOLI	CATALASE HPI	ESCHERICHIA COLI	440-470								
PCATA MICLU	CATALASE	MICROCOCCUS LUTEUS	570-606								
PCATE ECOLI	CATALASE HPI	ESCHERICHIA COLI	433-480								
PCATE ECOLI	CATALASE HPI	SALMONELLA TYPHIMURUM	515-542	580-607							
PCAT CANCO	CHLORAMPHENICOL ACETYLTRANSFERASE	CAMPYLOBACTER COLI	175-202								
PCAT CLOBO	CHLORAMPHENICOL ACETYLTRANSFERASE	CLOSTRIDIUM BUTYRICUM	84-111								
PCAT ECOLI	CHLORAMPHENICOL ACETYLTRANSFERASE	ESCHERICHIA COLI	88-115								
PCAT ECOLI	CHLORAMPHENICOL ACETYLTRANSFERASE	PROTEUS MIRABILIS	92-119								
PCAT FROME	CHLORAMPHENICOL ACETYLTRANSFERASE	STAPHYLOCOCCUS INTERMEDIUS	7-34	87-114							
PCAT STAG	CHLORAMPHENICOL ACETYLTRANSFERASE	STREPTOCOCCUS AGALACTICAE	7-34	87-114							
PCAT STAG	CHLORAMPHENICOL ACETYLTRANSFERASE	COXIELLA BURNETII	309-336								
PCBHE COXBU	CBHE PROTEIN	THERMOACTINOMYCES VULGARIS	48-75								
PCBFT THEVU	CARBOXYPEPTIDASE T PRECURSOR	ESCHERICHIA COLI	376-403								
PCCA ECOLI	TRNA NUCLEOTIDYLTRANSFERASE	SYNECHOCOCUS SP	29-36								
PCCH4 STN97	COI CONC MECH PROTEIN CCN4	SYNECHOCOCUS SP	212-236	331-372	445-486						
PCDAS THEET	CYCLOMALTODEXTRINASE	THERMOANEROBACTER ETIANOLICUS	205-232								
PCD01 BACMA	CYCLOMALTODEXTE GLUCANOTRANS PRECURSOR	BACILLUS NACERANS	439-466	616-643							
PCD02 BACMA	CYCLOMALTODEXTE GLUCANOTRANS PRECURSOR	BACILLUS NACERANS	210-231	436-466	615-642						
PCD03 BACCI	CYCLOMALTODEXTE GLUCANOTRANS PRECURSOR	BACILLUS CIRCULANS	217-244	442-472	594-631						
PCD04 BACCI	CYCLOMALTODEXTE GLUCANOTRANS PRECURSOR	BACILLUS CIRCULANS	217-244	442-472	594-631						
PCD05 BACOH	CYCLOMALTODEXTE GLUCANOTRANS PRECURSOR	BACILLUS LICIENIFORMIS	217-244	442-472	594-631						
PCD06 BACOH	CYCLOMALTODEXTE GLUCANOTRANS PRECURSOR	BACILLUS OHBENSIS	430-471								
PCD07 BAC50	CYCLOMALTODEXTE GLUCANOTRANS PRECURSOR	BACILLUS SP	210-237	433-462	615-642						
PCD08 BAC51	CYCLOMALTODEXTE GLUCANOTRANS PRECURSOR	BACILLUS SP	409-471								
PCD09 BAC51	CYCLOMALTODEXTE GLUCANOTRANS PRECURSOR	BACILLUS SP	210-237	433-462	614-641						
PCD10 BAC51	CYCLOMALTODEXTE GLUCANOTRANS PRECURSOR	BACILLUS SP	210-237	433-465	615-642						
PCD11 BAC51	CYCLOMALTODEXTE GLUCANOTRANS PRECURSOR	BACILLUS SP	217-244	442-472	594-631						
PCD12 BAC51	CYCLOMALTODEXTE GLUCANOTRANS PRECURSOR	BACILLUS STEAROTHERMOPHILUS	536-646								
PCD13 KLEPN	CYCLOMALTODEXTE GLUCANOTRANS PRECURSOR	KLEBSIELLA PNEUMONIAE	212-239								
PCD14 ECOLI	COLICIN E1 PROTEIN	ESCHERICHIA COLI	44-71	283-326							
PCD15 ECOLI	COLICIN E1* PROTEIN	SHIGELLA SONNEI	44-71	284-325	413-440						
PCD16 ECOLI	COLICIN E2	ESCHERICHIA COLI	334-368								
PCD17 ECOLI	COLICIN E3	ESCHERICHIA COLI	334-368								
PCD18 ECOLI	COLICIN E6	ESCHERICHIA COLI	334-368								
PCD19 ECOLI	COLICIN B	ESCHERICHIA COLI	283-341								

PCGENE	1011214	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PCAD ECOLI	COLICIN D	ESCHERICHIA COLI	244-311								
PCAM ECOLI	COLICIN M	ESCHERICHIA COLI	178-227								
PCAN ECOLI	COLICIN N	ESCHERICHIA COLI	119-146								
PCAA CITR	COLICIN A	CITROBACTER FREUNDII	224-258								
PCFD STRCL	ISOPENICILLIN N EPIMERASE	STREPTOMYCES CLAVULIGERUS	170-197								
PCFA ECOLI	COLICIN IA PROTEIN	ESCHERICHIA COLI	68-93	255-282	378-412	415-432					
PCIB ECOLI	COLICIN IB PROTEIN	ESCHERICHIA COLI	68-93	255-282	378-412	415-432					
PCEA ACEXY	UTP URIDYLYLTRANSFERASE	ACETOBACTER XYLINUM	59-89								
PCLA ECOLI	PROTEIN CELA	ESCHERICHIA COLI	76-103								
PCFAA ECOLI	CFAT FIMBRIAL SUBUNIT A PRECURSOR	ESCHERICHIA COLI	27-38								
PCFAC ECOLI	CFAT FIMBRIAL SUBUNIT C PRECURSOR	ESCHERICHIA COLI	138-187	388-456	561-595						
PCFAD ECOLI	CFAT FIMBRIAL SUBUNIT D	ESCHERICHIA COLI	133-160								
PCFAE ECOLI	CFAT FIMBRIAL SUBUNIT E	ESCHERICHIA COLI	180-207	244-271							
PCH10 ACTPS	10 KD CHAPERONIN	ACTYRTHOSIPHON PISUM SYMBIOTIC BACTERIU	57-95								
PCH10 BACSU	10 KD CHAPERONIN	BACILLUS SUBTILIS	66-93								
PCH10 CHLTR	10 KD CHAPERONIN	CHLAMYDIA TRACHOMATIS	64-91								
PCH10 ECOLI	10 KD CHAPERONIN	ESCHERICHIA COLI	57-84								
PCH10 HAEDU	10 KD CHAPERONIN	HAEMOPHILUS DUCREYI	68-93								
PCH10 LEGMI	10 KD CHAPERONIN	LEGIONELLA MICDADEI	57-84								
PCH10 RICTS	10 KD CHAPERONIN	RICKETTSIA TSUTSUGAMUSHI	65-92								
PCH10 THEP3	10 KD CHAPERONIN	THERMOPHILIC BACTERIUM PS-3	66-93								
PCH40 ACTPS	60 KD CHAPERONIN	ACTYRTHOSIPHON PISUM SYMBIOTIC BACTERIU	341-382								
PCH60 AORTU	60 KD CHAPERONIN	AGROBACTERIUM TUMEFACIENS	117-163	339-370	435-466						
PCH60 AMOPS	60 KD CHAPERONIN	AMOEBA PROTEUS SYMBIOTIC BACTERIUM	299-333								
PCH60 BACSU	60 KD CHAPERONIN	BACILLUS SUBTILIS	298-332	337-364							
PCH60 BORB	60 KD CHAPERONIN	BORRELIA BURGDORFERI	125-163	299-368							
PCH60 BRUAB	60 KD CHAPERONIN	BRUCELLA ABORTUS	117-144	339-366							
PCH60 CHLPN	60 KD CHAPERONIN	CHLAMYDIA PNEUMONIAE	4-31								
PCH60 CHLTR	60 KD CHAPERONIN	CHLAMYDIA TRACHOMATIS	4-31								
PCH60 CHRV1	60 KD CHAPERONIN	CHROMATIUM VINOSUM	300-327								
PCH40 CLOAB	60 KD CHAPERONIN	CLOSTRIDIUM ACETOBUTYLICUM	218-332	337-364	435-482						
PCH60 CLOPE	60 KD CHAPERONIN	CLOSTRIDIUM PERFRINGENS	337-368	417-444							
PCH60 COXBU	60 KD CHAPERONIN	COXIELLA BURNETII	300-327	346-382							
PCH60 HAEDU	60 KD CHAPERONIN	HAEMOPHILUS DUCREYI	339-366	417-444							
PCH60 LEGMI	60 KD CHAPERONIN	LEGIONELLA MICDADEI	299-333								
PCH40 LEGPN	60 KD CHAPERONIN	LEGIONELLA PNEUMOPHILA	298-332	452-479							
PCH60 MYCLE	60 KD CHAPERONIN	MYCOBACTERIUM LEPTAE	125-152	236-363	337-364						
PCH60 MYCTU	60 KD CHAPERONIN	MYCOBACTERIUM TUBERCULOSIS & BOVIS	125-152	236-363	337-364						
PCH60 PSEAE	60 KD CHAPERONIN	PSEUDOMONAS AERUGINOSA	339-366								
PCH60 RHILV	60 KD CHAPERONIN	RHIZOBIUM LEGUMINOSARUM	117-163	322-370	423-466						
PCH40 RICTS	60 KD CHAPERONIN	RICKETTSIA TSUTSUGAMUSHI	103-130	293-336	360-394						
PCH60 STNPF	60 KD CHAPERONIN	SYNECHOCOCCUS SP	308-333	337-380							
PCH60 STNPF	60 KD CHAPERONIN	SYNECHOCOCCUS SP	338-363	455-489							
PCH60 THEP3	60 KD CHAPERONIN	THERMOPHILIC BACTERIUM PS-3	337-364								
PCH43 STRAL	60 KD CHAPERONIN 2	STREPTOMYCES ALBUS G	116-148	337-364							
PCHB VBHA	N,N-DIACETYLCHITINBIASE PRECURSOR	VIBRIO HARVEYI	21-48	772-799							
PCHBA BACSU	CHEMOTAXIS PROTEIN CHEA	BACILLUS SUBTILIS	373-400	590-617							
PCHBA ECOLI	CHEMOTAXIS PROTEIN CHEA	ESCHERICHIA COLI	256-386								
PCHBA SALTY	CHEMOTAXIS PROTEIN CHEA	SALMONELLA TYPHIMURIUM	162-197								
PCHBA BACSU	CHEMOTAXIS PROTEIN METHYLTRANSFERASE	BACILLUS SUBTILIS	124-151								
PCHBW ECOLI	PURINE-BINDING CHEMOTAXIS PROTEIN	ESCHERICHIA COLI	88-115								
PCHBW SALTY	PURINE-BINDING CHEMOTAXIS PROTEIN	SALMONELLA TYPHIMURIUM	88-115								
PCHBY ECOLI	CHEMOTAXIS PROTEIN CHEY	ESCHERICHIA COLI	22-49								
PCHBY SALTY	CHEMOTAXIS PROTEIN CHEY	SALMONELLA TYPHIMURIUM	22-49								
PCHII BACCI	CHITINASE A1 PRECURSOR	BACILLUS CIRCULANS	491-518	566-593							
PCHIA ALT50	CHITINASE A PRECURSOR	ALTERNONAS SP	345-372								
PCHIA SERMA	CHITINASE A PRECURSOR	SERRATIA MARCESCENS	146-373								

PCGENE	10117144	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ULK1NAMK	PROTEIN	ORGANISMI	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PC10D BACCI	CHITINASE D PRECURSOR	BACILLUS CIRCULANS	102-161	189-216							
PC10T SACER	CHITINASE	SACCHAROPOLYSPORA ERYTHRAEA	92-119								
PC10T STRPL	CHITINASE G3 PRECURSOR	STREPTONYCES PULCATUS	250-284								
PC10M BACSU	CHONISMATE MUTASE	BACILLUS SUBTILIS	3-17								
PC10D BREST	CHOLESTEROL OXIDASE PRECURSOR	BREVIBACTERIUM STEROLICUM	263-290								
PC10A VIBCH	CHOLESTEROL ENTEROTOXIN A CHAIN PRECURSOR	VIBRIO CHOLERAE	79-106								
PC10V AGRTU	BETA-1,7-GLUCAN EXPORT PROTEIN	AGROBACTERIUM TUMEFACIENS	4-31	181-208							
PC10V AGRTU	RECEPTOR PROTEIN CHVE PRECURSOR	AGROBACTERIUM TUMEFACIENS	100-127								
PC10I CITFR	CITROLYSIN PROTEIN I	CITROBACTER FREUNDII	413-462								
PC10A ECOLI	COLICIN I RECEPTOR PRECURSOR	ESCHERICHIA COLI	146-173								
PC10A BACSU	PUTATIVE DNA RECOMBINASE	BACILLUS SUBTILIS	378-405								
PC10Y ACAN	CITRATE SYNTHASE	ACINETOBACTER ANITRATUM	143-170								
PC10Y BACCO	CITRATE SYNTHASE	BACILLUS COAGULANS	24-51								
PC10A SALTY	CITRATE-PROTON SYMPORT	SALMONELLA TYPHIMURIUM	154-181								
PC10N KLEPN	CITRATE-SODIUM SYMPORT	KLEBSIELLA PNEUMONIAE	194-221								
PC10N SALDU	CITRATE-SODIUM SYMPORT	SALMONELLA DUBLIN	194-221								
PC10N SALPU	CITRATE-SODIUM SYMPORT	SALMONELLA PULLORUM	194-221								
PC10A PSEPU	CHLOROCATECHOL 1,2-DIOXYGENASE	PSEUDOMONAS PUTIDA	13-36								
PC10D ECOLI	CHAIN LENGTH DETERMINANT PROTEIN	ESCHERICHIA COLI	131-167								
PC10D ECOLI	CHAIN LENGTH DETERMINANT PROTEIN	ESCHERICHIA COLI	178-212	250-277							
PC10D SALTY	CHAIN LENGTH DETERMINANT PROTEIN	SALMONELLA TYPHIMURIUM	96-127	151-212							
PC10S CLOHI	ALPHA-CLOSTRUPAIN PRECURSOR	CLOSTRIDIUM HISTOLYTICUM	30-58	497-524							
PC10A ECOLI	ATP-BINDING SUBUNIT CLPA	ESCHERICHIA COLI	653-693								
PC10A RHOB	CLPA HOMOLOG PROTEIN	RHODOSPIRIDIUM BLASTICA	419-466								
PC10B BACNO	CLPB HOMOLOG PROTEIN	BACTEROIDES NODOSUS	116-137	442-476	558-595						
PC10B ECOLI	CLPB PROTEIN	ESCHERICHIA COLI	444-489	563-590							
PC10X AZOV1	CLPX HOMOLOG PROTEIN	AZOTOBACTER VINELANDII	213-242	312-339							
PC10X ECOLI	ATP-BINDING SUBUNIT CLPX	ESCHERICHIA COLI	353-383								
PC10B ECOLI	2,3-CYCLO-NUC 2-PHOSPHODIESTERASE PRECURS	ESCHERICHIA COLI	50-77								
PC10A ECOLI	CYTOSINE DEAMINASE	ESCHERICHIA COLI	102-129								
PC10M BACSU	A COMPETENCE PROTEIN I	BACILLUS SUBTILIS	108-135	186-213							
PC10M BACSU	COMPETENCE REGULATORY PROTEIN	BACILLUS SUBTILIS	154-239								
PC10P STAAU	COP-4 PROTEIN	STAPHYLOCOCCUS AUREUS	2-53								
PC10P FRESM	COPPER RESISTANCE PROTEIN B PRECURSOR	PSEUDOMONAS SYRINGAE	140-167								
PC10A ECOLI	MAGNESIUM/COBALT TRANSPORT PROTEIN CORA	ESCHERICHIA COLI	134-161								
PC10A SALTY	MAGNESIUM/COBALT TRANSPORT PROTEIN CORA	SALMONELLA TYPHIMURIUM	134-161								
PC10E BACSU	SPORE COAT PROTEIN E	BACILLUS SUBTILIS	42-92								
PC10X BRAJA	CYTCHROME C OXIDASE POLYPEPTIDE I	BRADYRHIZOBIUM JAPONICUM	380-407								
PC10X PARDE	CYTCHROME C OXIDASE POLYPEPTIDE I	PARACOCCLUS DENTRIFICANS	383-410								
PC10X RHOSH	CYTCHROME C OXIDASE POLYPEPTIDE I	RHODOBACTER SPHAEROIDES	396-423								
PC10X BACFI	OXIDASE ASSEMBLY FACTOR	BACILLUS FIRMIUS	36-63								
PC10X BACSU	OXIDASE ASSEMBLY FACTOR	BACILLUS SUBTILIS	49-76								
PC10B REIGO	CRYPTIC PLASMID PROTEIN B	NEISSERIA GONORRHOEA	72-99	163-209							
PC10B ECOLI	MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE	ESCHERICHIA COLI	309-336								
PC10B SALTY	MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE	SALMONELLA TYPHIMURIUM	311-338								
PC10A ECOLI	SENSOR PROTEIN CPXA	ESCHERICHIA COLI	254-281								
PC10X STRSQ	CYTCHROME P450 10C1	STREPTOMYCES SP	157-184								
PC10X SACER	6-DEOXYERYTHRONOLIDE B (DEB) HYDROXYLASE	SACCHAROPOLYSPORA ERYTHRAEA	231-260								
PC10X BACSU	CYTCHROME P450 109	BACILLUS SUBTILIS	240-283								
PC10X ANASP	PROBABLE CYTOCHROME P450	ANABENA SP	98-125								
PC10T BACTI	37 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	153-187								
PC10T BACTM	37 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	153-187								
PC10I BACSH	1.9 KD INSECTICIDAL TOXIN	BACILLUS SPHAEICUS	276-308								
PC10J BACSH	1.9 KD INSECTICIDAL TOXIN	BACILLUS SPHAEICUS	276-308								
PC10J BACSH	41.9 KD INSECTICIDAL TOXIN	BACILLUS SPHAEICUS	276-308								
PC10B BACTD	70 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	207-234	252-279	439-463						
PC10T BACTO	73 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	57-84	173-159	437-464						

PCGENK	1071284	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILENAME	PROTEIN	ORGANISM	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PCRD_BACTI	70 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	99-226	244-271	421-433						
PCRT1_BACTI	70 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	91-133	191-218	552-615						
PCRT2_BACTI	71 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	74-111	381-414							
PCRT3_BACTI	70 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	91-133	191-218	552-593						
PCRT7_BACTI	77 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	308-335	502-529							
PCRED_ECOLI	SENSOR PROTEIN CREC	ESCHERICHIA COLI	102-130								
PCRED_ECOLI	INNER MEMBRANE PROTEIN CREC	ESCHERICHIA COLI	94-121								
PCRP_ECOLI	CATABOLITE GENE ACTIVATOR	ESCHERICHIA COLI &	26-53	127-134							
PCRP_SALTY	CATABOLITE GENE ACTIVATOR	SHIGELLA FLEXNERI	26-53	127-134							
PCRT1_ERVHE	PHYTOENE DEHYDROGENASE	SALMONELLA TYPHIMURUM	26-53	127-134							
PCRT1_RHOCA	PHYTOENE DEHYDROGENASE	KLEBSIELLA AEROGENES	231-238								
PCRT1_RHOCA	CRY7 PROTEIN	ERWINIA HERBICOLA	389-416								
PCRY5_BACTI	132 KD CRYSTAL PROTEIN	RHODOBACTER CAPSULATUS	133-160	314-361	431-438						
PCRY5_BACTI	130 KD CRYSTAL PROTEIN	RHODOBACTER CAPSULATUS	721-755	875-902							
PCRY5_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	710-771	865-892	1031-1080						
PCRY5_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	710-771	865-892							
PCRY5_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	218-252	701-728	775-802						
PCRY5_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	737-771	865-892	1031-1080						
PCRY5_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	736-770	890-917							
PCRY5_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	710-771	865-892	1031-1080						
PCRYT_BACTI	134 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	745-779	899-926							
PCRYT_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	217-231	354-384	701-728	775-802					
PCRYT_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	737-771	865-892							
PCRYU_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	736-770	890-917							
PCRYU_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	317-231	700-722	774-801						
PCRYU_BACTI	131 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	718-772	866-891	1034-1081						
PCRYV_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	737-771	865-892	1031-1080						
PCRYV_BACTI	133 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	110-131	745-772	819-846						
PCRYW_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	736-770	890-917							
PCRYW_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	745-779								
PCRYW_BACTI	130 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	608-639	862-896	892-919						
PCRYX_BACTI	139 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	92-119	227-254	605-632	783-817	937-964				
PC311_ECOLI	CS3 PILI SYNTHESIS 63 KD PROTEIN	ESCHERICHIA COLI	42-69	226-253	290-317	344-378					
PC311_ECOLI	CS3 PILI SYNTHESIS 48 KD PROTEIN	ESCHERICHIA COLI	90-117	154-181	208-242						
PC314_ECOLI	CS3 PILI SYNTHESIS 33 KD PROTEIN	ESCHERICHIA COLI	20-47	74-108							
PC314_ECOLI	CELL SURFACE GLYCOPROTEIN PRECURSOR	HALOBACTERIUM HALOBURUM	256-283	384-611							
PC314_ECOLI	CELL SURFACE GLYCOPROTEIN PRECURSOR	HALOBACTERIUM VOLCANII	143-170	237-271							
PC314_ECOLI	CELL SURFACE GLYCOPROTEIN PRECURSOR	METHANOTHERMUS FERVIDUS	59-107								
PC314_ECOLI	CELL SURFACE GLYCOPROTEIN PRECURSOR	METHANOTHERMUS SOCIABILIS	59-107								
PC314_ECOLI	CELL SURFACE GLYCOPROTEIN PRECURSOR	ESCHERICHIA COLI	25-56								
PC314_ECOLI	COA-TRANSFERASE SUBUNIT A	CLOSTRIDIUM ACETOBUTYLICUM	118-143								
PC314_ECOLI	COA-TRANSFERASE SUBUNIT B	CLOSTRIDIUM ACETOBUTYLICUM	174-208								
PC314_ECOLI	INNER MEMBRANE PROTEIN CTRB	NEISSERIA MENINGITIDIS	152-193								
PC314_ECOLI	CYTOTOXIN PRECURSOR	PSEUDOMONAS AERUGINOSA	78-115	124-151	160-194	217-231					
PC314_ECOLI	COLICIN V SECRETION PROTEIN CVAA	ESCHERICHIA COLI	104-118	161-219							
PC314_ECOLI	COLICIN V SECRETION PROTEIN CVAB	ESCHERICHIA COLI	151-178								
PC314_ECOLI	MIDDLE CELL WALL PROTEIN PRECURSOR	BACILLUS BREVIS	197-224	411-438	1010-1044						
PC314_ECOLI	OUTER CELL WALL PROTEIN PRECURSOR	BACILLUS BREVIS	178-216	360-387	947-988						
PC314_ECOLI	ADENYLATE CYCLASE PRECURSOR	BORDETELLA PERTUSSIS	48-75	612-659	962-996						
PC314_ECOLI	ADENYLATE CYCLASE	YERSINIA INTERMEDIA	343-387	591-620							
PC314_ECOLI	CYAD PROTEIN	BORDETELLA PERTUSSIS	541-568								
PC314_ECOLI	CYAD PROTEIN	BORDETELLA PERTUSSIS	178-212								
PC314_ECOLI	CYAD PROTEIN	BORDETELLA PERTUSSIS	313-340								
PC314_ECOLI	CYTOCHROME B	RHODOBACTER CAPSULATUS	38-63								
PC314_ECOLI	TRANSPORT PROTEIN CYDD	ESCHERICHIA COLI	3-30	382-409							
PC314_ECOLI	APOCYTOCHROME F PRECURSOR	NOSTOC SP	209-243								

PCGENE	10711784	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PCYMO ACISF	CYCLOHEXANONE MONOOXYGENASE	ACINETOBACTER SP	419-471								
PCYNT SYNPT	CARBONIC ANHYDRASE	SYNECHOCOCCUS SP	170-200								
PCYNX ECOLI	CYNX PROTEIN	ESCHERICHIA COLI	51-80								
PCYOB ECOLI	CYTODROME O-UBIQUINOL OXIDASE SUBUNIT I	ESCHERICHIA COLI	31-58								
PCYTH SYNPT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE	SYNECHOCOCCUS SP	107-141								
PCYSA ECOLI	SULFATE PERMEASE A PROTEIN	ESCHERICHIA COLI	164-191								
PCYSB ECOLI	CYS REGULATOR TRANSCRIPTIONAL ACTIVATOR	ESCHERICHIA COLI	3-30								
PCYSB SALTY	CYS REGULATOR TRANSCRIPTIONAL ACTIVATOR	SALMONELLA TYPHIMURUM	3-30								
PCYSE ECOLI	SERINE ACETYLTRANSFERASE	ESCHERICHIA COLI	164-191								
PCYSE ECOLI	SERINE ACETYLTRANSFERASE	SALMONELLA TYPHIMURUM	164-191								
PCYSO ECOLI	SIROHEM SYNTHASE	ESCHERICHIA COLI	405-432								
PCYSO SALTY	SIROHEM SYNTHASE	SALMONELLA TYPHIMURUM	405-432								
PCYSN ECOLI	SULFATE ADENYLATE TRANSFERASE SUBUNIT I	ESCHERICHIA COLI	64-91								
PCYSW ECOLI	SULFATE PERMEASE W PROTEIN	ESCHERICHIA COLI	201-228								
PCYSW SYNPT	SULFATE PERMEASE W PROTEIN	SYNECHOCOCCUS SP	211-238								
PCZCB ALCEU	CATION EFFLUX SYSTEM PROTEIN CZCB	ALCALIGENES EUTROPIUS	241-268	283-320	364-391						
PCZCD ALCEU	CATION EFFLUX SYSTEM PROTEIN CZCD	ALCALIGENES EUTROPIUS	139-169								
PDACB BACSU	PENICILLIN-BINDING PROTEIN 1* PRECURSOR	BACILLUS SUBTILIS	80-107								
PDADA ECOLI	D-AMINO ACID DEHYDROGENASE	ESCHERICHIA COLI	127-154								
PDAGA ALTHA	NA(+)-LINKED D-ALANINE GLYCINE PERMEASE	ALTERONONAS HALOPLANKTIS	372-373								
PDAMX ECOLI	DAMX PROTEIN	ESCHERICHIA COLI	68-93	349-380							
PDAPA ECOLI	DIIHYDRODIPICOLINATE SYNTHASE	ESCHERICHIA COLI	27-54	157-184							
PDATI BACSU	DNA-PROTEIN-CYSSTEINE METHYLTRANSFERASE	BACILLUS SUBTILIS	13-47								
PDDBH ECOLI	DNA-BINDING PROTEIN HU-ALPHA	ESCHERICHIA COLI	12-39								
PDDBH CLOFA	DNA-BINDING PROTEIN HU	CLOSTRIDIUM PASTEURIANUM	12-39								
PDCCM ECOLI	DECARBOXYLASE PROENZYME	ESCHERICHIA COLI	146-173								
PDCCA CORGL	DIAMINOPIMELATE DECARBOXYLASE	CORYNEBACTERIUM GLUTINICUM	134-161								
PDCCA PSEAE	DIAMINOPIMELATE DECARBOXYLASE	PSEUDOMONAS AERUGINOSA	53-84								
PDCEB ECOLI	GLUTAMATE DECARBOXYLASE BETA	ESCHERICHIA COLI	4-31								
PDCHS ENTAE	HISTIDINE DECARBOXYLASE	ENTEROBACTER AEROGENES	111-138								
PDCHS KLEPL	HISTIDINE DECARBOXYLASE	KLEBSIELLA PLANTICOLA	111-138								
PDCHS MORMO	HISTIDINE DECARBOXYLASE	MORGANELLA MORGANII	111-138								
PDCCD BACSU	DIPETIDE TRANSPORT PROTEIN DCIAD	BACILLUS SUBTILIS	188-222								
PDCLY HAFAL	LYSINE DECARBOXYLASE	HAFNIA ALVEI	305-332								
PDCCA KLEPN	OXALOACETATE DECARBOXYLASE ALPHA CHAIN	KLEBSIELLA PNEUMONIAE	261-288	342-369							
PDCCA SALTY	OXALOACETATE DECARBOXYLASE ALPHA CHAIN	SALMONELLA TYPHIMURUM	261-288	342-369							
PDCCB SALTY	OXALOACETATE DECARBOXYLASE BETA CHAIN	SALMONELLA TYPHIMURUM	261-288	342-369							
PDCCB RHELE	TRANSPORT SENSOR PROTEIN DCTB	RHIZOBIUM LEGUMINOSARUM	377-411								
PDCTB RHIME	TRANSPORT SENSOR PROTEIN DCTB	RHIZOBIUM NELLOTTI	511-538								
PDEAD ECOLI	ATP-DEPENDENT RNA HELICASE DEAD	ESCHERICHIA COLI	268-293	518-545							
PDEAD KLEPN	ATP-DEPENDENT RNA HELICASE DEAD	KLEBSIELLA PNEUMONIAE	267-294	519-546							
PDEDA ECOLI	DEDA PROTEIN	ESCHERICHIA COLI	106-133								
PDEGS BACSU	SENSOR PROTEIN DEGS	BACILLUS SUBTILIS	31-70	75-139	292-327						
PDEHI MORSP	HALOACETATE DEHALOGENASE H-2	MORAXELLA SP	114-141								
PDEOC ECOLI	DEOXYRIBOSE-PHOSPHATE ALDOLASE	ESCHERICHIA COLI	134-161								
PDEHAL PSEOL	ALDHYDE DEHYDROGENASE	PSEUDOMONAS OLEOVORANS	6-33								
PDHAS BACSU	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE	BACILLUS SUBTILIS	150-184								
PDHAS CORGL	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE	CORYNEBACTERIUM GLUTINICUM	43-70	312-339							
PDHAS VIBCH	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE	ESCHERICHIA COLI	229-256								
PDHAS VIBCH	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE	VIBRIO CHOLERAE	109-136								
PDHAS BACSH	ALANINE DEHYDROGENASE	BACILLUS SPHAERICUS	149-176								
PDHAS BACST	ALANINE DEHYDROGENASE	BACILLUS STEAROTHERIOPHILUS	94-121								
PHEH3 CLODI	NAD-SPECIFIC GLUTAMATE DEHYDROGENASE	CLOSTRIDIUM DIFFICILE	116-143								
PHEH3 PEPAS	D-SPECIFIC GLUTAMATE DEHYDROGENASE	PEPTOSTREPTOCOCCUS ASACCHAROLYTICUS	247-274	345-380							
PHEH3 SULSO	GLUTAMATE DEHYDROGENASE	SULFOLOBUS SOLEFARICUS	2-36								
PHEH3 CORGL	NADP-SPECIFIC GLUTAMATE DEHYDROGENASE	CORYNEBACTERIUM GLUTINICUM	184-215	229-256							
PHEHA ACICA	GLUCOSE DEHYDROGENASE-A	ACINETOBACTER CALCOACETICUS	10-59	190-217							

PCGENE	1071711.4	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
BLKMANE	PROTEIN	ORGANISMI	27-57								
PDHGB	BACME	BACILLUS MEGATERIUM									
PDHGC	GLUCOSE DEHYDROGENASE	ESCHERICHIA COLI	416-463								
PDHKL	STAVN	STREPTOMYCES VIOLACEORUBER	168-195								
PDHLE	BACST	BACILLUS STEAROTHERMOPHILUS	192-219								
PDHLO	AGRT4	D-LYSOPINE DEHYDROGENASE	317-344								
PDHML	METEX	METHANOL DEHYDROGENASE SUBUNIT I PREC	131-187	190-224							
PDHMI	MEOR	METHANOL DEHYDROGENASE SUBUNIT I PREC	153-187	190-224							
PDHMT	PANDE	METHANOL DEHYDROGENASE SUBUNIT I PREC	195-222								
PDHNA	BACSP	PARACOCUS DENITRIFICANS	284-314								
PDHNA	ECOLI	BACILLUS SP	180-214								
PDHOM	BACSU	ESCHERICHIA COLI	73-107	406-433							
PDHOM	CORGL	BACILLUS SUBTILIS	105-132								
PDHPI	BACSH	CORYNEBACTERIUM GLUTAMICUM	212-239								
PDHSA	ECOLI	BACILLUS SPHAERICUS	482-512								
PDHSS	ANACY	ANABAENA CYLINDRICA	86-113	130-168							
PDHSS	SYNPI	SYNECHOCOCCUS SP	131-160								
PDHMT	MEIME	METHYLOTROPHUS METHYLOPHILUS	439-466								
PDHNG	ECOLI	ESCHERICHIA COLI	584-611								
PDHVB	BACSU	BACILLUS SUBTILIS	54-82	114-141							
PDHDI	PSEPU	PSEUDOMONAS PUTIDA	93-120								
PDLDH	AZOV1	AZOTOBACTER VINELANDII	18-45	224-276							
PDLDH	BACST	BACILLUS STEAROTHERMOPHILUS	82-124								
PDLDH	BACSU	BACILLUS SUBTILIS	82-109								
PDLDH	ECOLI	ESCHERICHIA COLI	108-135								
PDLDH	PSEEL	PSEUDOMONAS FLUORESCENS	124-151	223-275							
PDMNP	PSEPU	PSEUDOMONAS PUTIDA	63-90								
PDMN1	BACSU	BACILLUS SUBTILIS	497-524	548-581							
PDMN2	BACSU	BACILLUS SUBTILIS	456-483								
PDMN3	BACSU	BACILLUS SUBTILIS	316-380								
PDMN4	BORBU	BORRELIA BURGDORFERI	182-216	248-275	341-387	436-463					
PDMN5	BUCAP	BUCHNERA APHIDICOLA	73-100	111-138	353-380						
PDMN6	ECOLI	ESCHERICHIA COLI	366-400								
PDMN7	MICLU	MICROCOCCUS LUTEUS	383-413								
PDMN8	MYCCA	MYCOPLASMA CAPRICOLUM	8-36	75-112	274-310	330-389					
PDMN9	PROMI	PROTEUS MIRABILIS	365-399								
PDMN10	PSEPU	PSEUDOMONAS PUTIDA	398-439								
PDMN11	SPICI	SPIROPLASMA CITRI	45-72	76-110	145-180						
PDMN12	CHLTR	CHLAMYDIA TRACHOMATIS	312-353								
PDMN13	ECOLI	ESCHERICHIA COLI	82-109								
PDMN14	SALTY	SALMONELLA TYPHIMURUM	146-190								
PDMN15	ECOLI	ESCHERICHIA COLI	497-524	548-581							
PDMN16	BACME	BACILLUS MEGATERIUM	512-594								
PDMN17	BORBU	BORRELIA BURGDORFERI	248-275	512-546							
PDMN18	BRUOV	BRUCELLA OVIS	561-588								
PDMN19	CAUCR	CAULOBACTER CRESCENTUS	496-526								
PDMN20	CLOAB	CLOSTRIDIUM ACETOBUTYLICUM	502-529								
PDMN21	CLOPE	CLOSTRIDIUM PERRINGENS	45-72	533-572							
PDMN22	MEHNA	METHANOSARCINA NAZEI	523-550								
PDMN23	MYCTU	MYCOBACTERIUM TUBERCULOSIS	502-529								
PDMN24	STRCO	STREPTOMYCES COELICOLOR	114-141								
PDMN25	ECOLI	ESCHERICHIA COLI	658-712								
PDMN26	ZYMAMO	ZYMOGONAS MOBILIS	24-51								
PDMN27	STRPE	STREPTOMYCES PEUCETIUS	104-172								
PDMN28	SULSO	SULFOLOBUS SOLFATRICUS	58-83	417-444	1382-1416						
PDMN29	BACSU	BACILLUS SUBTILIS	72-104								
PDMN30	ECOLI	ESCHERICHIA COLI	230-257								
PDMN31	SACER	SACCHAROPOLYSORA ENYTHRAEA									



PCGENE	1011714	Proteolytic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PROTEIN												
PEPTU_MICLU	ELONGATION FACTOR TU	MICROCOCCUS LUTEUS	221-248									
PEPTU_MYCHO	ELONGATION FACTOR TU	MYCOPLASMA HOMINIS	222-249									
PEPTU_MYCLB	ELONGATION FACTOR TU	MYCOBACTERIUM LIPRAE	220-247									
PEPTU_MYCTU	ELONGATION FACTOR TU	MYCOBACTERIUM TUBERCULOSIS	220-247									
PEPTU_SHEPU	ELONGATION FACTOR TU	STREPTOCOCCUS ORALIS	222-259									
PEPTU_STORU	ELONGATION FACTOR TU	STREPTOCOCCUS ORALIS	222-259									
PELAS_PSEAE	PSEUDOLYSIN PRECURSOR	PSEUDOMONAS AERUGINOSA	141-168									
PELTI_ECOLI	T-LABILE ENTEROTOXIN A CHAIN PRECURSOR	ESCHERICHIA COLI	78-103									
PELTI_ECOLI	T-LABILE ENTEROTOXIN A CHAIN PRECURSOR	ESCHERICHIA COLI	79-106									
PELTI_ECOLI	T-LABILE ENTEROTOXIN B CHAIN PRECURSOR	CLOSTRIDIUM PERFRINGENS	228-269									
PELTI_ECOLI	T-LABILE ENTEROTOXIN B CHAIN PRECURSOR	ESCHERICHIA COLI	154-188									
PENVA_SALTY	ENVM PROTEIN	SALMONELLA TYPHIMURIUM	34-61									
PEPUB_STAEP	117 KD MEMBRANE ASSOCIATED PROTEIN	STAPHYLOCOCCUS EPIDERMIDIS	51-80	125-229	290-325	387-421	857-889					
PEPIC_STAEP	EPIDERMIS BIOSYNTHESIS PROTEIN EPIC	STAPHYLOCOCCUS EPIDERMIDIS	411-447									
PEPIP_STAEP	SERINE PROTEASE EPIC PRECURSOR	STAPHYLOCOCCUS EPIDERMIDIS	2-58	202-321								
PEPIY_STAEP	HYPOTHEICAL 16.7 KD PROTEIN IN EPIA 3 REGION	STAPHYLOCOCCUS EPIDERMIDIS	70-101									
PEPIZ_STAEP	HYPOTHEICAL 16.7 KD PROTEIN IN EPIA 3 REGION	STAPHYLOCOCCUS EPIDERMIDIS	42-100									
PEKA_ECOLI	GTP-BINDING ERA PROTEIN	ESCHERICHIA COLI	18-43									
PERAS_SACER	SENSORY TRANSDUCTION PROTEIN ERVC1	SACCHAROPOLYSPORA ERYTHRAEA	209-241									
PEREA_ECOLI	EARYTHROMYCIN ESTERASE TYPE I	ESCHERICHIA COLI	37-64	143-170								
PERAT_SACER	EARYTHROMYCIN ESTERASE TYPE I	SACCHAROPOLYSPORA ERYTHRAEA	9-36	967-994	1117-1144							
PESTA_STRSC	ESTERASE PRECURSOR	STREPTOMYCES SCABIES	128-155									
PESTE_PSEFL	ARYLESTERASE	PSEUDOMONAS FLUORESCENS	162-189									
PETCI_STAAT	ENTEROTOXIN TYPE C-1 PRECURSOR	STAPHYLOCOCCUS AUREUS	76-117	155-206								
PETCI_STAAT	ENTEROTOXIN TYPE C-2 PRECURSOR	STAPHYLOCOCCUS AUREUS	76-117	155-206								
PETCI_STAAT	ENTEROTOXIN TYPE C-3 PRECURSOR	STAPHYLOCOCCUS AUREUS	76-117	155-206								
PETKA_STAAT	ENTEROTOXIN TYPE A PRECURSOR	STAPHYLOCOCCUS AUREUS	26-69	165-192								
PETXB_CLOPE	EPSILON-TOXIN TYPE B PRECURSOR	CLOSTRIDIUM PERFRINGENS	209-236									
PETXB_STAAT	ENTEROTOXIN TYPE B PRECURSOR	STAPHYLOCOCCUS AUREUS	84-101	173-207								
PETXD_STAAT	ENTEROTOXIN TYPE D PRECURSOR	STAPHYLOCOCCUS AUREUS	153-200									
PETXE_STAAT	ENTEROTOXIN TYPE E PRECURSOR	STAPHYLOCOCCUS AUREUS	26-69	88-115								
PEUTC_SALTY	ETHANOLAMINE AMMONIA-LYASE LIGHT CHAIN	SALMONELLA TYPHIMURIUM	116-150									
PEVGA_ECOLI	PUTATIVE TRANSCRIPTION REG EVGA	ESCHERICHIA COLI	62-89									
PEVGS_ECOLI	PUTATIVE SENSOR PROTEIN EVGS	ESCHERICHIA COLI	45-79	249-276	431-458	526-553	829-856					
PEXOB_ECOLI	EXODEOXYRIBONUCLEASE V	ESCHERICHIA COLI	226-253									
PEXOB_ECOLI	EXODEOXYRIBONUCLEASE V	ESCHERICHIA COLI	80-107									
PEXOA_RHIME	BIOPOLYMER TRANSPORT EXOB PROTEIN	RHIZOBIUM MELLIOTI	180-207									
PEXOB_RHIME	EXODEOXYRIBONUCLEASE	STREPTOCOCCUS PNEUMONIAE	216-234									
PEXOF_RHIME	EXOP PROTEIN	RHIZOBIUM MELLIOTI	216-270	327-361								
PEXOH_RHIME	SUCCINOGLYCAN BIOSYNTHESIS PROTEIN EXOH	RHIZOBIUM MELLIOTI	252-279									
PEXOP_RHIME	SUCCINOGLYCAN BIOSYNTHESIS PROTEIN EXOP	RHIZOBIUM MELLIOTI	211-242	272-299	350-391							
PFADB_ECOLI	FATTY ACID TRANSPORT PROTEIN PRECURSOR	ESCHERICHIA COLI	36-63	177-204								
PFADL_ECOLI	FATTY ACID TRANSPORT PROTEIN PRECURSOR	ESCHERICHIA COLI	220-247									
PFADF_ECOLI	OUTER MEMBRANE PROTEIN FADF PRECURSOR	ESCHERICHIA COLI	223-257	421-453	507-541							
PFADF_ECOLI	K18 MBOR FMBRUAL SUBUNIT PRECURSOR	ESCHERICHIA COLI	18-48									
PFANE_ECOLI	FAND PROTEIN PRECURSOR	ESCHERICHIA COLI	160-194	386-421	596-623	710-757						
PFANG_ECOLI	FANG PROTEIN PRECURSOR	ESCHERICHIA COLI	104-131									
PFANH_ECOLI	FANH PROTEIN PRECURSOR	ESCHERICHIA COLI	83-141									
PFAPB_PSEFR	FATTY OXIDATION COMPLEX ALPHA SUBUNIT	PSEUDOMONAS FRAGI	8-42	295-322								
PFDFH_WOLSU	FORMATE DEHYDROGENASE	WOLINELLA SUCCINOGENES	64-98									
PFDFH_ECOLI	FORMATE DEHYDROGENASE	ESCHERICHIA COLI	613-640									
PFDFH_PSEK	FORMATE DEHYDROGENASE	PSEUDOMONAS SP	49-76	366-393								
PFDFH_ECOLI	FORMATE DEHYDROGENASE	ESCHERICHIA COLI	284-315	323-350	696-710							
PFECG_ECOLI	TRANSPORT PROTEIN PECA PRECURSOR	ESCHERICHIA COLI	531-561									
PFECG_ECOLI	TRANSPORT PROTEIN I, CYTOSOLIC	ESCHERICHIA COLI	210-237									
PFECI_ECOLI	PECI PROTEIN	ESCHERICHIA COLI	131-158									



PCGENE	1071714	Prokaryotic Sequences	AUEA1	AUEA2	AUEA3	AUEA4	AUEA5	AUEA6	AUEA7	AUEA8	AUEA9
KILE.NANP	PROTEIN	URICANIN	22-56								
PFEMD STAAU	POSSIBLE PROTEIN FEMD	STAPHYLOCOCCUS AUREUS									
PFENK STNPI	FERRIC DOXIN-NADP REDUCTASE	SYNECHOCOCCUS SP	4-31								
PFEPF ECOLI	FERRIC ENTEROACTIN TRANSPORT PROTEIN FEPF	ESCHERICHIA COLI	176-203								
PFEPF ECOLI	FERRIC ENTEROACTIN TRANSPORT PROTEIN FEPF	ESCHERICHIA COLI	182-214	281-308							
PFEPF ECOLI	FERRIC ENTEROACTIN TRANSPORT PROTEIN FEPF	ESCHERICHIA COLI	128-155								
PFERR ANASP	FERREDOXIN, HETEROCYST	ANABAEANA SP	2-29								
PFERR ANASP	FERREDOXIN-LIKE PROTEIN IN NIF REGION	ANABAEANA SP	67-94								
PFHAB BORPE	FILAMENTOUS HEMAGGLUTININ	BORDETELLA PERTUSSIS	1128-1158	1359-1386	2063-2114	2841-2868	1051-1085	3167-3194			
PFHAC BORPE	HAEMOLYSIN-LIKE PROTEIN FHAC PRECURSOR	BORDETELLA PERTUSSIS	342-369								
PFHUA ECOLI	FORMATE HYDROGENLYASE TRANSACTIVATOR	ESCHERICHIA COLI	36-63	350-384	401-428						
PFHUA ECOLI	FERRIC CHROMO-IRON RECEPTOR PRECURSOR	ESCHERICHIA COLI	458-485								
PFHUB ECOLI	PROTEIN FHB PRECURSOR	ESCHERICHIA COLI	222-254								
PFHUE ECOLI	OUTER-MEMBRANE RECEPTOR	ESCHERICHIA COLI	587-614								
PFIB SPICI	FIBRIL PROTEIN	SPIROPLASMA CITRI	161-195	326-367							
PFIC ECOLI	CELL FILAMENTATION PROTEIN FIC	ESCHERICHIA COLI	151-178								
PFIC SALTY	CELL FILAMENTATION PROTEIN FIC	SALMONELLA TYPHIMURIUM	151-178								
PFIMC BORPE	OUTER MEMBRANE PROTEIN FIMC PRECURSOR	BORDETELLA PERTUSSIS	208-235	540-567	618-645						
PFIMC ECOLI	CHAPERONE PROTEIN FIMC PRECURSOR	ESCHERICHIA COLI	51-78								
PFIND ECOLI	FIND PROTEIN PRECURSOR	ESCHERICHIA COLI	222-253	458-485	534-561	563-590					
PFIME ECOLI	TYPE 1 FIMBRIAE REGULATORY PROTEIN FIME	ESCHERICHIA COLI	163-192								
PFIMY SALTY	FIMBRIAE Y PROTEIN	SALMONELLA TYPHIMURIUM	49-76								
PFIMZ ECOLI	FIMBRIAE Z PROTEIN	ESCHERICHIA COLI	42-69	162-192	196-230						
PFIMZ SALTY	FIMBRIAE Z PROTEIN	SALMONELLA TYPHIMURIUM	175-209								
PFINQ ECOLI	FINQ PROTEIN	ESCHERICHIA COLI	143-172								
PFIRA RICKI	FIRA PROTEIN	RICKETTSIA RICKETTSII	162-189								
PFIXC AZOCA	FIXC PROTEIN	AZORHIZOBIUM CAULINODANS	139-156								
PFIXC AZOCA	SENSOR PROTEIN FIXL	AZORHIZOBIUM CAULINODANS	247-274								
PFIXC BRUJA	SENSOR PROTEIN FIXL	BRADYRHIZOBIUM JAPONICUM	27-54	253-280							
PLA1 BORBU	FLAGELLAR FILAMENT 41 KD CORE PROTEIN	BORDELLA BURGDORFERI	8-35	271-298							
PLA1 HALHA	FLAGELLIN A1 PRECURSOR	HALOBACTERIUM HALOBURIUM	63-92	157-184							
PLA1 METVO	FLAGELLIN B1 PRECURSOR	METHANOCOCCUS VOLTAE	38-73	133-160							
PLA2 METVO	FLAGELLIN B1 PRECURSOR	METHANOCOCCUS VOLTAE	28-66								
PLA3 HALHA	FLAGELLIN B1 PRECURSOR	HALOBACTERIUM HALOBURIUM	36-63								
PLA3 METVO	FLAGELLIN B1 PRECURSOR	METHANOCOCCUS VOLTAE	35-76								
PLA4 HALHA	FLAGELLIN B1 PRECURSOR	HALOBACTERIUM HALOBURIUM	36-90	152-184							
PLA4 METVO	FLAGELLIN B1 PRECURSOR	METHANOCOCCUS VOLTAE	36-63	154-181							
PLA6 BACSU	FLA LOCUS 219 KD PROTEIN	BACILLUS SUBTILIS	73-149	155-186							
PLA6 CAMIE	FLAGELLIN A	CAMPYLOBACTER COLI	15-42	144-191	497-535						
PLA6 CAMIE	FLAGELLIN A	CAMPYLOBACTER JEJUNI	220-266	310-337	500-538						
PLA6 METVO	FLAGELLIN A PRECURSOR	METHANOCOCCUS VOLTAE	28-62								
PLA6 PREAE	FLAGELLIN A	PSEUDOMONAS AERUGINOSA	3-41	51-88	97-124						
PLA6 RHIME	FLAGELLIN	RHIZOBIUM MELIOTI	181-219	228-265	360-391						
PLA6 SPIAU	FLAGELLAR FILAMENT PROTEIN PRECURSOR	SPIROCHAETA AURANTIA	162-189								
PLA6 TREPA	FLAGELLAR FILAMENT PROTEIN PRECURSOR	TREPONEMA HYODYSENTERIAE	55-89	219-285							
PLA6 CAMCO	FLAGELLIN B	TREPONEMA PALLIDUM	243-270								
PLA6 CAMIE	FLAGELLIN B	CAMPYLOBACTER COLI	144-191	497-535							
PLA6 RHIME	FLAGELLIN B	CAMPYLOBACTER JEJUNI	220-266	310-337	500-538						
PLA6 CLOMP	FLAYDOXIN	RHIZOBIUM MELIOTI	86-113	177-219	228-255	360-391					
PLA6 CAUCR	REGULATORY PROTEIN FLAY	CLOSTRIDIUM MP	18-52								
PLA6 BACSU	FLAGELLIN	CAULOBACTER CRESCENTUS	291-318	551-578							
PLA6 BACSU	FLAGELLAR BASAL-BODY ROD PROTEIN FLGG	BACILLUS SUBTILIS	102-129	228-255							
PLA6 SALTY	FLAGELLAR HOOK-ASSOCIATED PROTEIN 1	BACILLUS SUBTILIS	62-89								
PLA6 ECOLI	FLAGELLAR HOOK-ASSOCIATED PROTEIN 1	SALMONELLA TYPHIMURIUM	12-50	333-360	456-480						
PLA6 ECOLI	FLAGELLAR HOOK-ASSOCIATED PROTEIN 3	ESCHERICHIA COLI	61-105	229-266							
PLA6 ECOLI	FLAGELLAR HOOK-ASSOCIATED PROTEIN 3	SALMONELLA TYPHIMURIUM	61-105	229-266							
PLA6 ECOLI	FLAGELLAR TRANSCRIPTIONAL ACTIVATOR FLHD	ESCHERICHIA COLI	6-33								
PLA6 PREAE	FLAGELLAR OPERON RNA POL SIGMA FACTOR	PSEUDOMONAS AERUGINOSA	198-232								

PCGENE	1071784	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ELKNAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PELIC ECOLI	FLAGELLIN	ESCHERICHIA COLI	1-41	186-213	295-379	431-466					
PELIC SALCH	FLAGELLIN	SALMONELLA CHOLERAESUIS	5-41	54-125	136-198						
PELIC SALMU	FLAGELLIN	SALMONELLA MUECHEN	5-41	54-88	136-177						
PELIC SALPA	FLAGELLIN	SALMONELLA PARATYPHA	5-41	54-135	136-184						
PELIC SALRU	FLAGELLIN	SALMONELLA RUBISLAW	5-41	54-125	136-196						
PELIC SALTY	FLAGELLIN	SALMONELLA TYPHIMURUM	5-41	54-125	136-200						
PELIC SERMA	FLAGELLIN	SERATIA MARCESCENS	5-41	54-125	136-200						
PELIC ECOLI	FLAGELLAR HOOK-ASSOCIATED PROTEIN 2	ESCHERICHIA COLI	32-66	106-133	160-187	216-298	386-445				
PELIC SALTY	FLAGELLAR HOOK-ASSOCIATED PROTEIN 2	SALMONELLA TYPHIMURUM	32-66	106-133	255-299	407-438					
PELIC BACSU	FLAG HOOK-BASAL BODY PROTEIN FLIE	BACILLUS SUBTILIS	8-35								
PELIC CAUCR	FLAGELLAR M-RING PROTEIN	BACILLUS SUBTILIS	327-361	391-418							
PELIC CAUCR	FLAGELLAR M-RING PROTEIN	CAULOBACTER CRESCENTUS	24-51	297-324	361-388						
PELIC SALTY	FLAGELLAR M-RING PROTEIN	SALMONELLA TYPHIMURUM	484-529								
PELIC BACSU	FLAGELLAR SWITCH PROTEIN FLG	BACILLUS SUBTILIS	35-62								
PELIC ECOLI	FLAGELLAR SWITCH PROTEIN FLG	ESCHERICHIA COLI	44-71								
PELIC BACSU	PROBABLE FLIIH PROTEIN	BACILLUS SUBTILIS	19-46	105-132							
PELIC BACSU	FLAGELLAR FLIIH PROTEIN	BACILLUS SUBTILIS	7-37								
PELIC SALTY	FLAGELLAR FLIIH PROTEIN	SALMONELLA TYPHIMURUM	75-118								
PELIC BACSU	PROBABLE FLIK PROTEIN	BACILLUS SUBTILIS	97-104	117-144							
PELIC BACSU	FLII PROTEIN	BACILLUS SUBTILIS	30-71	78-105	109-136						
PELIC ECOLI	FLII PROTEIN	ESCHERICHIA COLI	103-132								
PELIC SALTY	FLII PROTEIN	SALMONELLA TYPHIMURUM	103-133								
PELIC BACSU	FLIM PROTEIN	BACILLUS SUBTILIS	148-175								
PELIC ECOLI	FLIM PROTEIN	ESCHERICHIA COLI	251-278								
PELIC CAUCR	FLAGELLAR MOTOR SWITCH PROTEIN	CAULOBACTER CRESCENTUS	56-83								
PELIC ECOLI	FLAGELLAR PROTEIN FLIS	ESCHERICHIA COLI	59-86								
PELIC SALTY	FLAGELLAR PROTEIN FLIT	SALMONELLA TYPHIMURUM	9-46	67-106							
PELIC ECOLI	TYPE-1 FIMBRIAL PROTEIN A CHAIN PRECURSOR	PSEUDOMONAS AERUGINOSA	30-67	80-114							
PELIC ECOLI	TYPE-1 FIMBRIAL PROTEIN C CHAIN PRECURSOR	ESCHERICHIA COLI	5-32								
PELIC ACTVI	FIMBRIAL SUBUNIT TYPE 1 PRECURSOR	ESCHERICHIA COLI	11-38								
PELIC ECOLI	FIMBRIAL SUBUNIT TYPE 1 PRECURSOR	ACTINOMYCES VISCOSUS	248-282	352-379	417-444						
PELIC ECOLI	FIMBRIAL PROTEIN PRECURSOR	ESCHERICHIA COLI	114-141								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	110-137								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	107-134								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	110-137								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	123-150								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	107-141								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	95-122								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	111-145								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS	96-123								
PELIC BACNO	FIMBRIAL PROTEIN PRECURSOR	PSEUDOMONAS AERUGINOSA	70-97								
PELIC BACNO	POSSIBLE FIMBRIAL ASSEMBLY PROTEIN FIMD	BACTEROIDES NODOSUS	106-144	355-382							
PELIC BACNO	POSSIBLE FIMBRIAL ASSEMBLY PROTEIN FIMD	BACTEROIDES NODOSUS	106-144	355-382							
PELIC ECOLI	F17 FIMBRIAL PROTEIN PRECURSOR	ESCHERICHIA COLI	97-124								
PELIC NEIGR	FIMBRIAL PROTEIN PRECURSOR	NEISSERIA MENINGITIDIS	70-97								
PELIC NEIGR	FIMBRIAL PROTEIN PRECURSOR	NEISSERIA GONORRHOEA	66-97								
PELIC MORNO	FIMBRIAL PROTEIN PRECURSOR	MORAXELLA NONLUQUEFACIENS	108-146								
PELIC PSEAE	FIMBRIAL PROTEIN PRECURSOR	PSEUDOMONAS AERUGINOSA	30-67	80-114							
PELIC PSEAE	FIMBRIAL PROTEIN PRECURSOR	PSEUDOMONAS AERUGINOSA	70-97								
PELIC ECOLI	CS1 FIMBRIAL SUBUNIT A PRECURSOR	ESCHERICHIA COLI	60-87	112-139							
PELIC ECOLI	MAJOR FIMBRIAL SUBUNIT A PRECURSOR	ESCHERICHIA COLI	102-129								
PELIC ECOLI	FIBRONECTIN-BINDING PROTEIN PRECURSOR	HAEMOPHILUS INFLUENZAE	41-83								
PELIC ECOLI	FOLYGLUTAMATE SYNTHASE	ESCHERICHIA COLI	129-156								
PELIC LACCA	FOLYGLUTAMATE SYNTHASE	LACTOBACILLUS CASEI	129-156								
PELIC BACHT	FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE	BACILLUS FIRMS	153-180								

PGCENE	1071704.4	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FURNAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PFDA_ECOLI	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT	ESCHERICHIA COLI	395-472								
PFDA_WOLSU	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT	WOLINELLA SUCCINOGENES	8-15	487-514							
PFZE_MYXXA	GLIDING MOTILITY REGULATORY PROTEIN	MYXOCOCCUS XANTHILUS	15-42	478-505							
PFTHS_CLOTH	FORMATE--TETRAHYDROFOLATE LIGASE	CLOSTRIDIUM THERMOACETUM	163-190								
PFTR_METH	FORMYLTRANSFERASE	METHANOBACTERIUM THERMAUTOTROPHICUM	9-43								
PFTSA_BACSU	CELL DIVISION PROTEIN FTSA	BACILLUS SUBTILIS	76-110								
PFTSA_ECOLI	CELL DIVISION PROTEIN FTSA	ESCHERICHIA COLI	301-318	375-418							
PFTSL_ECOLI	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	4-31								
PFTSN_ECOLI	CELL DIVISION PROTEIN FTSN	ESCHERICHIA COLI	63-90								
PFTSX_ECOLI	CELL DIVISION PROTEIN FTSX	ESCHERICHIA COLI	151-188								
PFTSY_ECOLI	CELL DIVISION PROTEIN FTSY	ESCHERICHIA COLI	278-305								
PFUCR_ECOLI	L-FUCOSE OPERON ACTIVATOR	ESCHERICHIA COLI	210-260								
PFUNA_BACST	FUMARATE HYDROLYTASE CLASS I AEROBIC	ESCHERICHIA COLI	7-45								
PFUMH_BACSU	FUMARATE HYDRATASE	BACILLUS SUBTILIS	290-317								
PFUR_YERPE	FURRIC UPTAKE REGULATION PROTEIN	YERSINIA PESTIS	414-445								
PGIPT_ECOLI	GLYC 3-PHOS DEHYDROGENASE A	ESCHERICHIA COLI	994-1010								
PGIPT_ANAVA	GLYC 3-PHOS DEHYDROGENASE 2	ANABAENA VARIABILIS	302-329								
PGIPT_ANAVA	GLYC 3-PHOS DEHYDROGENASE 3	ANABAENA VARIABILIS	87-114								
PGIPT_ECOLI	GLYC 3-PHOS DEHYDROGENASE C	ESCHERICHIA COLI	162-189								
PGIP_BACME	GLYC 3-PHOS DEHYDROGENASE	BACILLUS MEGATERIUM	216-324								
PGIP_BACSU	GLYC 3-PHOS DEHYDROGENASE	BACILLUS SUBTILIS	49-76	237-271							
PGIP_PYRWO	GLYC 3-PHOS DEHYDROGENASE	PYROCOCOCUS WOESSEI	239-286								
PGIP_THEMA	GLYC 3-PHOS DEHYDROGENASE	THERMOTOGA MARITIMA	290-328								
PGIPB_BACST	GLUCOSE-6-PHOSPHATE ISOMERASE B	BACILLUS STEAROTHERMOPHILUS	103-143	241-268							
PGIPD_ECOLI	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	301-378								
PGIPD_ZYMOO	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE	ZYMONOMAS MOBILIS	165-192								
PGACA_PSEFL	CYANIDE CONTROL PROTEIN	PSEUDOMONAS FLUORESCENS	178-205								
PGALT_SALTY	GALACTURINASE	SALMONELLA TYPHIMURUM	86-113								
PGALT_HAEIN	GAL-1-PHOS URIDYL YLTRANSFERASE	HAEMOPHILUS INFLUENZAE	124-158	239-269							
PGALT_LACHE	GAL-1-PHOS URIDYL YLTRANSFERASE	LACTOBACILLUS HELVETICUS	304-338								
PGALT_SALTY	GALACTOSE OPERON REPRESSOR	SALMONELLA TYPHIMURUM	53-91								
PGALR_HAEIN	GALACTOSE OPERON REPRESSOR	HAEMOPHILUS INFLUENZAE	182-209								
PGAL_PSEFL	DE-D-GALACTOSE 1-DEHYDROGENASE	PSEUDOMONAS FLUORESCENS	251-278								
PGCHE_ECOLI	GTP CYCLOHYDROLASE II	ESCHERICHIA COLI	78-105								
PGCH2_PHOLE	GTP CYCLOHYDROLASE II	PHOTOBACTERIUM LEIOGNATHI	197-227	246-273							
PGCSP_ECOLI	GLYCINE CLEAVAGE SYSTEM H PROTEIN	ESCHERICHIA COLI	10-37								
PGCVA_ECOLI	GLYCINE CLEAVAGE SYSTEM TRANSACTIVATOR	ESCHERICHIA COLI	216-246								
PGENK_ECOLI	PROTEIN K	ESCHERICHIA COLI	60-94								
PGER1_BACSU	SPORE GERMINATION PROTEIN I	BACILLUS SUBTILIS	24-51								
PGER3_BACSU	SPORE GERMINATION PROTEIN III PRECURSOR	BACILLUS SUBTILIS	49-83	182-216	350-384						
PGERE_BACSU	GERMINATION PROTEIN GENE	BACILLUS SUBTILIS	291-323								
PGGIZ_STAHA	ANTIBACTERIAL PROTEIN 2	STAPHYLOCOCCUS HAEMOLYTICUS	13-40								
PGGIZ_STAHA	ANTIBACTERIAL PROTEIN 3	STAPHYLOCOCCUS HAEMOLYTICUS	6-33								
PGIDA_BACSU	GLUCOSE INHIBITED DIVISION PROTEIN A	BACILLUS SUBTILIS	396-423								
PGIDA_ECOLI	GLUCOSE INHIBITED DIVISION PROTEIN A	ESCHERICHIA COLI	533-568								
PGIDA_PSEPU	GLUCOSE INHIBITED DIVISION PROTEIN A	PSEUDOMONAS PUTIDA	539-566								
PGIDB_BACSU	GLUCOSE INHIBITED DIVISION PROTEIN B	BACILLUS SUBTILIS	34-61								
PGIDB_PSEPU	GLUCOSE INHIBITED DIVISION PROTEIN B	PSEUDOMONAS PUTIDA	25-52								
PGLCP_STYNT	GLUCOSE TRANSPORT PROTEIN	SYNECHOCYSTIS SP	288-322								
PGLDA_BACST	GLYCEROL DEHYDROGENASE	BACILLUS STEAROTHERMOPHILUS	20-79								
PGLGA_ECOLI	GLYCOCEN SYNTHASE	ESCHERICHIA COLI	256-283								
PGLGC_ECOLI	GLUCOSE-1-PHOSPHATE ADENYL YLTRANSFERASE	ESCHERICHIA COLI	114-141								
PGLGC_SALTY	GLUCOSE-1-PHOSPHATE ADENYL YLTRANSFERASE	SALMONELLA TYPHIMURUM	114-141								
PGLMS_ECOLI	GLUC-6-FRUC-6-PHOSPHOTRANSFERASE	ESCHERICHIA COLI	209-243								
PGLNI_METTL	GLNB-LIKE PROTEIN 1	METHANOCOCCUS THERMOLITHOTROPHICUS	58-85								

PCGENE	10711784	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILENARIE	PROTEIN	ORGANISMA	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PGLNA ANASP	GLUTAMINE SYNTHETASE	ANADENIA SP	8-42								
PGLNA BACSU	GLUTAMINE SYNTHETASE	BACILLUS SUBTILIS	4-31								
PGLNA CLOAB	GLUTAMINE SYNTHETASE	CLOSTRIDIUM ACETOBUTYLICUM	413-440								
PGLNA ECOLI	GLUTAMINE SYNTHETASE	ESCHERICHIA COLI	144-171								
PGLNA METVO	GLUTAMINE SYNTHETASE	METHANOCOCCUS VOLTAE	203-230								
PGLNA PROVI	GLUTAMINE SYNTHETASE	PROTEUS VULGARIS	142-169								
PGLNA PYREU	GLUTAMINE SYNTHETASE	PYROCOCCUS FURIOSUS	391-421								
PGLNA SALTY	GLUTAMINE SYNTHETASE	SALMONELLA TYPHIMURUM	144-171								
PGLNA STRCO	GLUTAMINE SYNTHETASE	STREPTOMYCES COELICOLOR	186-211								
PGLNI AZOIR	NITROGEN REGULATORY PROTEIN P-II	AZOSPIRILLUM BRASILENSE	15-49								
PGLNB RHQCA	NITROGEN REGULATORY PROTEIN P-II	RHODOBACTER CAPSULATUS	15-49								
PGLND SYNRP	NITROGEN REGULATORY PROTEIN P-II	SYNECHOCOCCUS SP	52-79								
PGLND ECOLI	UDP URIDYL TRANSFERASE	ESCHERICHIA COLI	120-147	151-178							
PGLND SALTY	UDP URIDYL TRANSFERASE	SALMONELLA TYPHIMURUM	151-178								
PGLNE ECOLI	ADENYL TRANSFERASE	ESCHERICHIA COLI	103-130	431-460							
PGLNI ECOLI	GLUTAMINE-BINDING PROTEIN PRECURSOR	ESCHERICHIA COLI	126-153								
PGLNQ BACST	GLUTAMINE PERMEASE OPERON PROTEIN GLNQ	BACILLUS STEAROTHERMOPHILUS	7-34								
PGLPD BACSU	AEROBIC GLYC-3-PHOS DEHYDROGENASE	BACILLUS SUBTILIS	194-230								
PGLPD ECOLI	AEROBIC GLYC-3-PHOS DEHYDROGENASE	ESCHERICHIA COLI	410-437								
PGLPF BACSU	GLYCEROL UPTAKE FACILITATOR PROTEIN	BACILLUS SUBTILIS	233-274								
PGLPK BACSU	GLYCEROL KINASE	BACILLUS SUBTILIS	44-93								
PGLPK ECOLI	GLYCEROL KINASE	ESCHERICHIA COLI	56-90								
PGLPR ECOLI	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR	ESCHERICHIA COLI	5-32								
PGLPX ECOLI	GLXP PROTEIN	ESCHERICHIA COLI	297-324								
PGLPX SHIFL	GLXP PROTEIN	SHIGELLA FLEXNERI	297-324								
PGLXX ECOLI	GLUTAREDOXIN	ESCHERICHIA COLI	24-51								
PGLTB ECOLI	GLUTAMATE SYNTHASE	ESCHERICHIA COLI	482-509								
PGLTP ECOLI	PROTON GLUTAMATE SYMPORT PROTEIN	ESCHERICHIA COLI	316-346								
PGLVB ECOLI	PHOSPHOTRANSFERASE ENZYME TYPE IIB	ESCHERICHIA COLI	110-137								
PGLVA BRAJA	SERINE HYDROXYMETHYL TRANSFERASE	BRADYRHIZOBIUM JAPONICUM	30-60								
PGLVA CAMJE	SERINE HYDROXYMETHYL TRANSFERASE	CAMPYLOBACTER JEJUNI	376-401								
PGLVA HYPAE	SERINE HYDROXYMETHYL TRANSFERASE	HYPHONICROBIUM METHYLOVORUM	28-53								
POMOT BACSU	COMO OPERON PROTEIN 7	BACILLUS SUBTILIS	37-67								
POMOT BACSU	GLUCONOKINASE	BACILLUS SUBTILIS	88-122								
POMOT BACSU	GLUCONOKINASE	BACILLUS SUBTILIS	238-271								
PGPID CHLTR	VIRULENCE PROTEIN PGPI-10	CHLAMYDIA TRACHOMATIS	312-353								
PGPID CHLTR	VIRULENCE PROTEIN PGPI-20	CHLAMYDIA TRACHOMATIS	97-131								
PGPID CHLTR	VIRULENCE PROTEIN PGPI-30	CHLAMYDIA TRACHOMATIS	25-52								
PGPID CHLTR	VIRULENCE PROTEIN PGPI-40	CHLAMYDIA TRACHOMATIS	61-106	193-230							
PGPID CHLTR	VIRULENCE PROTEIN PGPI-50	CHLAMYDIA TRACHOMATIS	12-60								
PGPID CHLTR	VIRULENCE PROTEIN PGPI-60	CHLAMYDIA TRACHOMATIS	94-121								
PGREA BICPR	TRANSCRIPTION ELONGATION FACTOR GRE A	RICKETTSIA PROWAZEKII	15-49								
PGPPE BACSU	GRPE-LIKE PROTEIN	BACILLUS SUBTILIS	27-71								
PGPPE BACSU	GRPE-LIKE PROTEIN	BORRELIA BURGDORFERI	2-79								
PGPPE CLOAB	GRPE-LIKE PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	12-83								
PGPPE BACBR	GRAMICIDIN 3 SYNTHETASE	BACILLUS BREVIS	545-572								
PGPPE BACBR	GRAMICIDIN 3 SYNTHETASE II	BACILLUS BREVIS	48-75	94-121							
PGSHR ECOLI	GLUTAMATE-CYSTEINE LIASE	ESCHERICHIA COLI	239-266	274-301							
PGSHR ECOLI	GLUTATHIONE REDUCTASE	ESCHERICHIA COLI	100-134	270-311							
PGSHR PSEAE	GLUTATHIONE REDUCTASE	PSEUDOMONAS AERUGINOSA	80-114								
PGSIA BACSU	STARVATION-INDUCIBLE PROTEIN A	BACILLUS SUBTILIS	74-101	265-296							
PGSPD ERWCA	PROTEIN D PRECURSOR	ERWINIA CAROTOVORA	238-285	316-343							
PGSPD ERWCH	PROTEIN D PRECURSOR	ERWINIA CHRYSANTHEMI	239-266	307-338							
PGSPD KLEPN	PROTEIN D PRECURSOR	KLEBSIELLA PNEUMONIAE	339-386								
PGSPE ERWCA	PROTEIN E	ERWINIA CAROTOVORA	329-367								
PGSPE ERWCH	PROTEIN E	ERWINIA CHRYSANTHEMI	329-367								
PGSPE KLEPN	PROTEIN E	KLEBSIELLA PNEUMONIAE	323-361								
PGSPE PSEAE	PROTEIN E	PSEUDOMONAS AERUGINOSA	331-369								



ECGENE	10717184	Polyarthritis Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
CHLORAMPHENICOL	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PGUTD ECOLI	SORBITOL-4-PHOSPHATE 2-DEHYDROGENASE	ESCHERICHIA COLI	138-163								
PGV1 HALIA	GAS VESICLE PROTEIN, PLASMID	HALOBACTERIUM HALOBIIUM	36-63								
PGV2 HALIA	GAS VESICLE PROTEIN, CHROMOSOMAL	HALOBACTERIUM HALOBIIUM	36-63								
PGV3 APHEL	GAS VESICLE PROTEIN	APHANIZONEN FLOS-AQUIAE	4-31	39-66							
PGV4 FREDI	GAS VESICLE PROTEIN	FREMYELLA DIPLOPHON	4-31	39-66							
PGV5 HALME	GAS VESICLE PROTEIN	HALOBACTERIUM MEDITERRANEI	37-64								
PGV6 MICBC	GAS VESICLE PROTEIN	MICROCYSTIS SP.	39-66								
PGV7 PSEAN	GAS VESICLE PROTEIN	PSEUDONANADAENA SP.	4-31	39-66							
PGV8 APHEL	GAS VESICLE PROTEIN C	APHANIZONEN FLOS-AQUIAE	8-49								
PGV9 HALIA	GAS VESICLE PROTEIN C	HALOBACTERIUM HALOBIIUM	150-249								
PGV10 HALME	GAS VESICLE PROTEIN C	HALOBACTERIUM MEDITERRANEI	139-169								
PGV11 HALIA	GVPD PROTEIN, PLASMID	HALOBACTERIUM HALOBIIUM	110-147								
PGV12 HALME	GVPD PROTEIN	HALOBACTERIUM MEDITERRANEI	110-147								
PGV13 HALIA	GVPF PROTEIN, PLASMID	HALOBACTERIUM HALOBIIUM	13-47	135-169							
PGV14 HALME	GVPF PROTEIN	HALOBACTERIUM MEDITERRANEI	13-47								
PGV15 HALIA	GVPF PROTEIN	HALOBACTERIUM HALOBIIUM	8-49								
PGV16 HALIA	GVPG PROTEIN, PLASMID	HALOBACTERIUM HALOBIIUM	38-65								
PGV17 HALIA	GVPD PROTEIN	HALOBACTERIUM MEDITERRANEI	38-72								
PGV18 HALIA	GVPH PROTEIN	HALOBACTERIUM HALOBIIUM	10-40								
PGV19 HALME	GVPF PROTEIN	HALOBACTERIUM MEDITERRANEI	5-32								
PGV20 HALIA	GVPK PROTEIN	HALOBACTERIUM HALOBIIUM	45-76								
PGV21 HALME	GVPK PROTEIN	HALOBACTERIUM MEDITERRANEI	12-39	42-74							
PGV22 HALIA	GVPK PROTEIN	HALOBACTERIUM HALOBIIUM	11-38	50-77							
PGV23 HALIA	GVPK PROTEIN	HALOBACTERIUM MEDITERRANEI	44-78								
PGV24 HALIA	GVPN PROTEIN	HALOBACTERIUM HALOBIIUM	113-140								
PGV25 HALME	GVPN PROTEIN	HALOBACTERIUM MEDITERRANEI	15-56								
PGV26 HALIA	GVPD PROTEIN	HALOBACTERIUM MEDITERRANEI	49-96	105-132							
PGV27 HALIA	DNA GYRASE SUBUNIT A	BACILLUS SUBTILIS	180-407	429-499							
PGV28 HALIA	DNA GYRASE SUBUNIT A	CAMPYLOBACTER JEJUNI	267-310	381-408	452-479	665-695					
PGV29 HALIA	DNA GYRASE SUBUNIT A	ESCHERICHIA COLI	266-393	449-497							
PGV30 HALIA	DNA GYRASE SUBUNIT A	KLEBSIELLA PNEUMONIAE	266-393	448-496	518-545						
PGV31 HALIA	DNA GYRASE SUBUNIT A	MYCOPLASMA PNEUMONIAE	4-31								
PGV32 HALIA	DNA GYRASE SUBUNIT A	STAPHYLOCOCCUS AUREUS	129-156	346-373	430-479	647-674	812-839				
PGV33 HALIA	DNA GYRASE SUBUNIT B	BACILLUS SUBTILIS	198-239								
PGV34 HALIA	DNA GYRASE SUBUNIT B	BORRELIA BURGDORFERI	154-181								
PGV35 HALIA	DNA GYRASE SUBUNIT B	ESCHERICHIA COLI	616-643								
PGV36 HALIA	DNA GYRASE SUBUNIT B	HALOPHAX SP.	230-237								
PGV37 HALIA	DNA GYRASE SUBUNIT B	MYCOPLASMA PNEUMONIAE	249-283								
PGV38 HALIA	DNA GYRASE SUBUNIT B	NEISSERIA GONORRHOEA	524-558	618-645							
PGV39 HALIA	DNA GYRASE SUBUNIT B	PSEUDOMONAS PUTIDA	122-149	684-711							
PGV40 HALIA	DNA GYRASE SUBUNIT B	SPIROPLASMA CITRI	40-74	189-238	283-310	341-368	540-579				
PGV41 HALIA	DNA GYRASE SUBUNIT B	STAPHYLOCOCCUS AUREUS	252-279	291-318							
PGV42 HALIA	DNA GYRASE SUBUNIT B	ESCHERICHIA COLI	71-98								
PGV43 HALIA	HELICASE IV	ESCHERICHIA COLI	100-134	529-556							
PGV44 HALIA	LIPROTEIN E PRECURSOR	HAEMOPHILUS INFLUENZAE	58-85								
PGV45 HALIA	GLUTAMYL-TRNA REDUCTASE	CHLORIDIUM VIBRIOFORMES	222-259								
PGV46 HALIA	GLUTAMYL-TRNA REDUCTASE	ESCHERICHIA COLI	289-316								
PGV47 HALIA	3-AMINOLEVULINIC ACID SYNTHASE	RHODOBACTER SPHAEROIDES	71-100								
PGV48 HALIA	GLUTAMYL-TRNA REDUCTASE	SALMONELLA TYPHIMURUM	289-316	344-371							
PGV49 HALIA	GLUTAMYL-TRNA REDUCTASE	SYNCHOCYSTIS SP.	163-190	330-377							
PGV50 HALIA	DELTA-AMINOLEVULINIC ACID DEHYDRATASE	METHANOTHERMUS SOCIABILIS	131-158								
PGV51 HALIA	PUTATIVE UROPHORPHINOGEN-III SYNTHASE	BACILLUS SUBTILIS	10-37								
PGV52 HALIA	UROPHORPHINOGEN-III SYNTHASE	ESCHERICHIA COLI	211-238								
PGV53 HALIA	HEMAM PROTEIN	ESCHERICHIA COLI	143-174								
PGV54 HALIA	HEMAM RECEPTOR PRECURSOR	YERSINIA ENTEROCOLITICA	234-261								
PGV55 HALIA	PUTATIVE METHYL-TRANSFERASE	ESCHERICHIA COLI	69-138	185-219							
PGV56 HALIA	HEMAM PROTEIN	BACILLUS SUBTILIS	217-262								







PCGENE	107117144	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ELKJANJE	PROTEIN	ORGANISM	285-312								
PIPA7 SHIFL	60 KD ANTIGEN	SHIGELLA FLEXNERI									
PIPA8 SHIFL	70 KD ANTIGEN	SHIGELLA FLEXNERI	95-136	417-475	491-557	596-630					
PIPA9 SHIFL	63 KD MEMBRANE ANTIGEN	SHIGELLA FLEXNERI	28-55	71-169	480-507	522-556					
PIPA10 SHIFL	63 KD MEMBRANE ANTIGEN	SHIGELLA FLEXNERI	28-55	71-169	480-507	522-556					
PIPA11 SHIFL	42 KD MEMBRANE ANTIGEN PRECURSOR	SHIGELLA FLEXNERI	21-57	113-161	273-300	324-378					
PIPA12 SHIFL	42 KD MEMBRANE ANTIGEN PRECURSOR	SHIGELLA FLEXNERI	21-57	113-161	273-300	324-378					
PIPA13 SHIFL	37 KD MEMBRANE ANTIGEN IPAD	SHIGELLA DYSENTERIAE	26-57	113-161	273-300	324-378					
PIPA14 SHIFL	36 KD MEMBRANE ANTIGEN	SHIGELLA DYSENTERIAE	47-86	291-318							
PIPA15 SHIFL	IPGB PROTEIN	SHIGELLA FLEXNERI	175-202	259-286	291-318						
PIPA16 SHIFL	IPGB PROTEIN	SHIGELLA FLEXNERI	175-202								
PIPA17 SHIFL	ISOPENTENYL TRANSFERASE	PSEUDOMONAS SYRINGAE	53-87	143-172							
PIPA18 SHIFL	INORGANIC PYROPHOSPHATASE	ESCHERICHIA COLI	138-172								
PIPA19 SHIFL	VIRULENCE PROTEIN PRECURSOR	VIBRIO CHOLERAE	212-239	336-377							
PIPA20 SHIFL	VIRULENCE REGULATORY PROTEIN IRGB	VIBRIO CHOLERAE	62-97								
PIPA21 SHIFL	IRON-REGULATED PROTEIN A	SYNCHOCOCCLUS SP	162-194								
PIPA22 SHIFL	INSERTION ELEMENT ISO-1SD PROTEIN INSB	SHIGELLA DYSENTERIAE	86-113								
PIPA23 SHIFL	INSERTION ELEMENT ISO-1SD PROTEIN INSB	SHIGELLA DYSENTERIAE	86-113								
PIPA24 SHIFL	INSERTION ELEMENT (S1) PROTEIN INSB	ESCHERICHIA COLI	122-149								
PIPA25 SHIFL	INSERTION ELEMENT (S1) PROTEIN INSB	SHIGELLA FLEXNERI	86-113								
PIPA26 SHIFL	INSERTION ELEMENT (S1) PROTEIN INSB	SHIGELLA SONNEI	86-113								
PIPA27 SHIFL	MAJOR INTRACELLULAR SERINE PROTEASE	BACILLUS SUBTILIS	113-142	197-224	233-280						
PIPA28 SHIFL	INTRACELLULAR SERINE PROTEASE	BACILLUS SUBTILIS	109-141								
PIPA29 SHIFL	ISTA PROTEIN	ESCHERICHIA COLI	182-210								
PIPA30 SHIFL	ISTA PROTEIN	SHIGELLA SONNEI	182-210								
PIPA31 SHIFL	FERRIC AEROBACTIN RECEPTOR PRECURSOR	ESCHERICHIA COLI	186-213	525-552	559-593						
PIPA32 SHIFL	JAG PROTEIN	BACILLUS SUBTILIS	68-93								
PIPA33 SHIFL	6-PHOSPHOFRUCTOKINASE ISOZYME 2	ESCHERICHIA COLI	143-170								
PIPA34 SHIFL	ADENYLATE KINASE	BACILLUS SUBTILIS	188-215								
PIPA35 SHIFL	ADENYLATE KINASE	LACTOCOCCUS LACTIS	186-213								
PIPA36 SHIFL	KANAMYCIN NUCLEOTIDYLTRANSFERASE	BACILLUS SP	89-96								
PIPA37 SHIFL	KANAMYCIN NUCLEOTIDYLTRANSFERASE	STAPHYLOCOCCUS AUREUS	69-96								
PIPA38 SHIFL	2-KETO-3-DEOXYGLUCONATE PERMEASE	ESCHERICHIA COLI	70-97								
PIPA39 SHIFL	2-KETO-3-DEOXYGLUCONATE PERMEASE	ERWINIA CHRYSANTHEMI	126-153								
PIPA40 SHIFL	3-DEOXY-D-MANNONOCTULONIC-ACID TRANS	ESCHERICHIA COLI	369-396								
PIPA41 SHIFL	ALPHA-KETOGLUTARATE PERMEASE	ESCHERICHIA COLI	7-34								
PIPA42 SHIFL	GUANYLATE KINASE	ESCHERICHIA COLI	162-189								
PIPA43 SHIFL	HOMOSERINE KINASE	BACILLUS SUBTILIS	49-76								
PIPA44 SHIFL	HOMOSERINE KINASE	FREMYELLA DIPLOPHON	52-79								
PIPA45 SHIFL	ADENOSINE CYCLIDE 5'-PHOSPHOTRANSFERASE	BACILLUS CIRCULANS	12-39								
PIPA46 SHIFL	KORD TRANSCRIPTIONAL REPRESSOR PROTEIN	ESCHERICHIA COLI	228-255								
PIPA47 SHIFL	PYRUVATE KINASE	SPIROPLASMA CITRI	112-148								
PIPA48 SHIFL	PYRUVATE KINASE	BACILLUS STEAROTHERMOPHILUS	311-374								
PIPA49 SHIFL	ISOMERASE LACA SUBUNIT	STAPHYLOCOCCUS AUREUS	9-64								
PIPA50 SHIFL	ISOMERASE LACA SUBUNIT	STREPTOCOCCUS MUTANS	26-60								
PIPA51 SHIFL	TAGATOSE-6-PHOSPHATE KINASE	STREPTOCOCCUS MUTANS	36-83	283-310							
PIPA52 SHIFL	6-PHOSPHO-BETA-GALACTOSIDASE	LACTOBACILLUS CASEI	290-317								
PIPA53 SHIFL	LACTOSE OPERON REPRESSOR	ESCHERICHIA COLI	9-36								
PIPA54 SHIFL	LACTOSE OPERON REPRESSOR	KLEBSIELLA PNEUMONIAE	195-229								
PIPA55 SHIFL	PHOSPHOTRANSFERASE REPRESSOR	STAPHYLOCOCCUS AUREUS	2-29								
PIPA56 SHIFL	PHOSPHOTRANSFERASE REPRESSOR	STREPTOCOCCUS MUTANS	2-32								
PIPA57 SHIFL	LACTOSE PERMEASE	LACTOBACILLUS DELBRUECKII	196-230								
PIPA58 SHIFL	FLAGELLAR HOOK-ASSOCIATED PROTEIN 2	VIBRIO PARAHAEEMOLYTICUS	62-89	388-415							
PIPA59 SHIFL	MALTOTROPIN PRECURSOR	KLEBSIELLA PNEUMONIAE	337-364								
PIPA60 SHIFL	ENDO-1,4-BETA-GLUCANASE PRECURSOR	CLOSTRIDIUM THERMOCILLUM	132-159								
PIPA61 SHIFL	OHHL-SYNTHESIS PROTEIN LASI	PSEUDOMONAS AERUGINOSA	171-198								
PIPA62 SHIFL	PROBABLE LEUCOCIN A IMMUNITY PROTEIN	LEUCONOSTOC GELIDUM	41-71								
PIPA63 SHIFL	LACTOCOCCIN A SECRETION PROTEIN LGNC	LACTOCOCCUS LACTIS	162-189	207-234	318-433						



PCGENE	1071784	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PLUXA_KRYAL	ALKANAL MONOOXYGENASE ALPHA CHAIN	KRYPTOPHANAKON ALFREDI	190-217	257-291							
PLUXB_PHOPO	ALKANAL MONOOXYGENASE BETA CHAIN	PHOTOBACTERIUM PHOSPHOREUM	188-217	373-400							
PLUXB_VIBHA	ALKANAL MONOOXYGENASE BETA CHAIN	VIBRIO HARVEYI	373-400								
PLUXC_PHOLE	ACYL-COA REDUCTASE	PHOTOBACTERIUM LEIOGNATHII	44-81								
PLUXC_PHOPO	ACYL-COA REDUCTASE	PHOTOBACTERIUM PHOSPHOREUM	54-91								
PLUXC_VIBFI	ACYL-COA REDUCTASE	VIBRIO FISCHERI	16-65								
PLUXD_XENLU	ACYL-COA REDUCTASE	XENORHABDUS LUMINESCENS	39-69								
PLUXD_PHOLE	ACYL-COA REDUCTASE	PHOTOBACTERIUM LEIOGNATHII	89-119	218-245							
PLUXE_VIBHA	LUCIFERIN-COMPONENT LIGASE	VIBRIO HARVEYI	30-57								
PLUXF_PHOLE	NON-FLUORESCENT FLAVOPROTEIN	PHOTOBACTERIUM LEIOGNATHII	145-172								
PLUXF_PHOPO	NON-FLUORESCENT FLAVOPROTEIN	PHOTOBACTERIUM PHOSPHOREUM	37-85	99-126							
PLUXG_VIBFI	PROBABLE FLAVIN REDUCTASE	VIBRIO FISCHERI	137-168								
PLUXH_VIBHA	LUXH PROTEIN	VIBRIO HARVEYI	96-123								
PLUXI_VIBFI	OHML SYNTHESIS PROTEIN LUXI	VIBRIO FISCHERI	30-58								
PLUXJ_VIBFI	OHML SYNTHESIS PROTEIN LUXI	VIBRIO FISCHERI	30-57								
PLUXK_VIBHA	LUMAZINE PROTEIN	PHOTOBACTERIUM PHOSPHOREUM	51-85	162-189							
PLUXL_VIBHA	LUXR REGULATORY PROTEIN	VIBRIO HARVEYI	61-88								
PLXB1_PHOLE	ALKANAL MONOOXYGENASE BETA CHAIN	PHOTOBACTERIUM LEIOGNATHII	368-395								
PLXB2_PHOLE	ALKANAL MONOOXYGENASE BETA CHAIN	PHOTOBACTERIUM LEIOGNATHII	278-355								
PLYB_BACSU	BENZYLNE	BACILLUS SUBTILIS	87-114								
PLYC_CLOAB	AUTOLYTIC LYSOZYME	CLOSTRIDIUM ACETOETIUTYLICUM	91-118								
PLYSP_ECOLI	LYSINE-SPECIFIC PEPTIDASE	ESCHERICHIA COLI	142-176								
PLYTB_ECOLI	AMIDASE ENHANCER PRECURSOR	BACILLUS SUBTILIS	55-82	150-177	467-513	555-585					
PLYTR_BACSU	AMIDASE PRECURSOR	ESCHERICHIA COLI	210-237								
PLYTR_BACSU	MEMBRANE-BOUND PROTEIN LYTR	BACILLUS SUBTILIS	179-213	225-252							
PN12_STRPY	M PROTEIN, SEROTYPE 12 PRECURSOR	BACILLUS SUBTILIS	11-64	259-303							
PN12_STRPY	M PROTEIN, SEROTYPE 12 PRECURSOR	STREPTOCOCCUS PYOGENES	46-92	114-156	191-300	305-342	383-417	436-494			
PN12_STRPY	M PROTEIN, SEROTYPE 24 PRECURSOR	STREPTOCOCCUS PYOGENES	12-46	89-128	175-202	245-272	280-313	399-457			
PN19_STRPY	M PROTEIN, SEROTYPE 19 PRECURSOR	STREPTOCOCCUS PYOGENES	12-174	269-327							
PN19_STRPY	M PROTEIN, SEROTYPE 3 PRECURSOR	STREPTOCOCCUS PYOGENES	5-39	56-263	306-313	332-410					
PN19_STRPY	M PROTEIN, SEROTYPE 6 PRECURSOR	STREPTOCOCCUS PYOGENES	12-39	70-282	290-324	343-401					
PN19_STRPY	MALTOSE-BINDING PROTEIN PRECURSOR	ESCHERICHIA COLI	20-47								
PN19_STRPY	MALTOSE-BINDING PROTEIN PRECURSOR	ENTEROBACTER AEROGENES	20-47								
PN19_STRPY	MALTOSE-BINDING PROTEIN PRECURSOR	ENTEROBACTER AEROGENES	3-30								
PN19_STRPY	MALTOSE-BINDING PROTEIN PRECURSOR	ESCHERICHIA COLI	852-919								
PN19_STRPY	MALX REGULATORY PROTEIN	STREPTOCOCCUS PNEUMONIAE	40-67	180-207							
PN19_STRPY	MALX REGULATORY PROTEIN	BACILLUS SP	410-441								
PN19_STRPY	1,4-BETA-MANNOSIDASE A AND B PREC	CALDOCCELLUM SACCHAROTYLICUM	389-423	592-626	1222-1256	1296-1323					
PN19_STRPY	1,4-BETA-MANNOSIDASE A AND B PREC	BACILLUS STEAROTHERIOTRINITILUS	246-273								
PN19_STRPY	ANTIBIOTIC RESISTANCE PROTEIN MARX	ESCHERICHIA COLI	95-122								
PN19_STRPY	ANTIBIOTIC RESISTANCE PROTEIN MARX	ESCHERICHIA COLI	18-65	100-134							
PN19_STRPY	QUINOLONE-RESISTANCE HYDROLYASE	WOLINELLA SUCCINOGENES	440-471								
PN19_STRPY	QUINOLONE-RESISTANCE HYDROLYASE	ESCHERICHIA COLI	47-74	122-163							
PN19_STRPY	MCBD PROTEIN	ESCHERICHIA COLI	172-206	226-253	306-345						
PN19_STRPY	METHYL-ACCEPTING CHEMOTAXIS PROTEIN I	ESCHERICHIA COLI	272-299								
PN19_STRPY	METHYL-ACCEPTING CHEMOTAXIS PROTEIN II	ESCHERICHIA COLI	258-306								
PN19_STRPY	METHYL-ACCEPTING CHEMOTAXIS PROTEIN II	SALMONELLA TYPHIMURIUM	258-306								
PN19_STRPY	METHYL-ACCEPTING CHEMOTAXIS PROTEIN III	ESCHERICHIA COLI	288-315								
PN19_STRPY	METHYL-ACCEPTING CHEMOTAXIS PROTEIN IV	ESCHERICHIA COLI	111-145	164-191	277-304						
PN19_STRPY	CHEMORECEPTOR MCPA	CAULOBACTER CRESCENTUS	260-287	369-403	516-540						
PN19_STRPY	CHEMOTAXIS CITRATE TRANSDUCER	SALMONELLA TYPHIMURIUM	314-348								
PN19_STRPY	CHEMOTAXIS ASPARTATE TRANSDUCER	ENTEROBACTER AEROGENES	275-302								
PN19_STRPY	CHEMOTAXIS SERINE TRANSDUCER	ENTEROBACTER AEROGENES	41-68	158-208	317-351	488-522					
PN19_STRPY	SPECIFIC RESTRICTION ENZYMAE A	ESCHERICHIA COLI	37-71								
PN19_STRPY	METHYL-COENZYME M REDUCTASE	METHANOSARCINA BARKERII	375-405								
PN19_STRPY	METHYL-COENZYME M REDUCTASE	METHANOCOCCUS VANNIELII	335-362								
PN19_STRPY	METHYL-COENZYME M REDUCTASE	METHANOCOCCUS VOLTAE	336-363								





PCGENE	10117414	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.1	AREA.2
FILENAME	PROTEIN	ORGANISM	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.1	AREA.2
PNUTB_PROFR	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT	PROFIBIBACTERIUM FREIDENREICHI	546-576							
PNUTB_SALTY	IG-SPECIFIC ADENINE GLYCOSYLASE	SALMONELLA TYPHIMURIUM	273-300							
PNUTB_STRCM	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT	STREPTOMYCES CINNAMOMONENSIS	481-508							
PNUTL_ECOLI	DNA MISMATCH REPAIR PROTEIN MUTL	ESCHERICHIA COLI	80-114							
PNUTL_SALTY	DNA MISMATCH REPAIR PROTEIN MUTL	SALMONELLA TYPHIMURIUM	80-114							
PNUTL_VIBCH	PROTEIN MUTL	VIBRIO CHOLERAE	134-169							
PNUTS_ECOLI	DNA MISMATCH REPAIR PROTEIN MUTS	ESCHERICHIA COLI	119-153							
PNUTT_STRAM	MUTT-LIKE PROTEIN	STREPTOMYCES AMBOFACIENS	60-87							
PNVAA_PSEMV	COENZYME A REDUCTASE	PSEUDOMONAS NIEVALONII	341-368							
PNAX_STRPY	MARLELATED PROTEIN PRECURSOR	STREPTOCOCCUS PYOGENES	5-29	148-182	190-217	240-301				
PNAYCO_STRCI	MYCOLYSIN PRECURSOR	STREPTOMYCES CACAOI	300-332							
PNMYC_YEREN	MYTC PROTEIN PRECURSOR	YERSINIA ENTEROCOLITICA	210-237							
PNADC_SALTY	NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE	SALMONELLA TYPHIMURIUM	123-134	235-289						
PNADR_SALTY	TRANSCRIPTIONAL REGULATOR NADR	SALMONELLA TYPHIMURIUM	233-260							
PNAGD_ECOLI	NAGD PROTEIN	ESCHERICHIA COLI	35-102							
PNAGH_CLOPE	HYALURONOGLUCOSAMINIDASE	CLOSTRIDIUM PERRINGENS	48-75	990-1017						
PNAGR_ECOLI	NAGR PROTEIN	ESCHERICHIA COLI	119-153							
PNANH_CLOSE	SIALIDASE PRECURSOR	CLOSTRIDIUM SEPTICUM	11-42	289-310	922-988					
PNANH_CLOSO	SIALIDASE PRECURSOR	CLOSTRIDIUM SORDELLI	377-404							
PNANH_SALTY	SIALIDASE	SALMONELLA TYPHIMURIUM	290-317							
PNAPA_ENTHR	NAI*(PH*) ANTIPORTER	ENTEROCOCCUS HIRAE	386-420							
PNARG_ECOLI	RESPIRATORY NITRATE REDUCTASE ALPHA CHAIN	ESCHERICHIA COLI	76-103							
PNARP_ECOLI	REGULATOR PROTEIN NARP	ESCHERICHIA COLI	153-189							
PNARX_ECOLI	REGULATOR PROTEIN NARX	ESCHERICHIA COLI	220-247							
PNVAX_RHIME	NITRATE/NITRITE SENSOR PROTEIN NARX	ESCHERICHIA COLI	212-239							
PNVDA_STRCY	BETA(1->3)GLUCAN EXPORT PROTEIN	RHIZOBIUM MELILOTI	348-375	338-385	431-458	503-538				
PNVDA_STRCY	NEOMYCIN RESISTANCE PROTEIN	STREPTOMYCES CYANOGENUS	148-332							
PNVDA_STRCY	ACYLNEURAMINATE CYTIDYLTRANSFERASE	ESCHERICHIA COLI	218-252							
PNVDA_STRCY	ADSORPTION PROTEIN A PRECURSOR	ESCHERICHIA COLI	490-517							
PNVDA_STRCY	ADSORPTION PROTEIN B	ESCHERICHIA COLI	2-43	186-220	511-538					
PNVDA_STRCY	ADSORPTION PROTEIN C	ESCHERICHIA COLI	315-342							
PNVDA_STRCY	ADSORPTION PROTEIN D	ENTEROBACTER CLOACAE	9-36							
PNVDA_STRCY	ADSORPTION PROTEIN E	ESCHERICHIA COLI	206-233							
PNVDA_STRCY	ADSORPTION PROTEIN F	ESCHERICHIA COLI	271-305							
PNVDA_STRCY	ADSORPTION PROTEIN G	PSEUDOMONAS CHLORORAPHIS	71-101							
PNVDA_STRCY	ADSORPTION PROTEIN H	RHIZOBIUM LEGUMINOSARUM	61-93							
PNVDA_STRCY	ADSORPTION PROTEIN I	RHIZOBIUM MELILOTI	7-44							
PNVDA_STRCY	ADSORPTION PROTEIN J	ADSORPTION PROTEIN J	352-279							
PNVDA_STRCY	ADSORPTION PROTEIN K	ADSORPTION PROTEIN K	9-31	162-203	327-334					
PNVDA_STRCY	ADSORPTION PROTEIN L	ADSORPTION PROTEIN L	100-127							
PNVDA_STRCY	ADSORPTION PROTEIN M	ADSORPTION PROTEIN M	260-287							
PNVDA_STRCY	ADSORPTION PROTEIN N	ADSORPTION PROTEIN N	342-369							
PNVDA_STRCY	ADSORPTION PROTEIN O	ADSORPTION PROTEIN O	154-181							
PNVDA_STRCY	ADSORPTION PROTEIN P	ADSORPTION PROTEIN P	374-401							
PNVDA_STRCY	ADSORPTION PROTEIN Q	ADSORPTION PROTEIN Q	377-404							
PNVDA_STRCY	ADSORPTION PROTEIN R	ADSORPTION PROTEIN R	387-414							
PNVDA_STRCY	ADSORPTION PROTEIN S	ADSORPTION PROTEIN S	383-410							
PNVDA_STRCY	ADSORPTION PROTEIN T	ADSORPTION PROTEIN T	359-386							
PNVDA_STRCY	ADSORPTION PROTEIN U	ADSORPTION PROTEIN U	356-383							
PNVDA_STRCY	ADSORPTION PROTEIN V	ADSORPTION PROTEIN V	267-294							
PNVDA_STRCY	ADSORPTION PROTEIN W	ADSORPTION PROTEIN W	430-457							
PNVDA_STRCY	ADSORPTION PROTEIN X	ADSORPTION PROTEIN X	483-510							
PNVDA_STRCY	ADSORPTION PROTEIN Y	ADSORPTION PROTEIN Y	418-503							
PNVDA_STRCY	ADSORPTION PROTEIN Z	ADSORPTION PROTEIN Z	227-254							
PNVDA_STRCY	ADSORPTION PROTEIN A	ADSORPTION PROTEIN A	479-506							
PNVDA_STRCY	ADSORPTION PROTEIN B	ADSORPTION PROTEIN B	265-292							

PCGENE	10217844	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PNFN BRAJA	BIOSYNTHESIS PROTEIN NFN	BRADYRHIZOBIUM JAPONICUM	219-266							
PNFS ANASP	NIFS PROTEIN	ANABAENA SP	112-139							
PNFS LACDE	NIFS PROTEIN HOMOLOG	LACTOBACILLUS DELBRUECKII	59-86							
PNFT AZOVI	NIFT PROTEIN	AZOTODACTER VINELANDII	6-31							
PNFU ANASL	NFU PROTEIN	ANABAENA SP	7-49							
PNFU ANASP	NFU PROTEIN	ANABAENA SP	148-178							
PNFU KLEPN	NFU PROTEIN	KLEBSIELLA PNEUMONIAE	66-93							
PNKA ECOLI	NICKEL TRANSPORT PROTEIN NIKK	ESCHERICHIA COLI	122-149	282-309	456-483					
PNKE ECOLI	NICKEL TRANSPORT PROTEIN NIKK	ESCHERICHIA COLI	172-204							
PNKB ECOLI	NITRITE REDUCTASE	ESCHERICHIA COLI	54-81	345-372						
PNRC ECOLI	NIRC PROTEIN	ESCHERICHIA COLI	212-239							
PNRS PSEST	PSEUDOMONAS CYTOCHROME OXIDASE PRECURSOR	PSEUDOMONAS STUTZERI	303-333							
PNIS LACLA	117 KD MEMBRANE ASSOCIATED PROTEIN	LACTOCOCCUS LACTIS	202-229	287-312	663-697	886-920				
PNIS LACLA	NISIN BIOSYNTHESIS PROTEIN NISC	LACTOCOCCUS LACTIS	52-92	140-188						
PNIS LACLA	NISIN BIOSYNTHESIS PROTEIN NISC	LACTOCOCCUS LACTIS	223-257	278-305	426-470					
PNIV CLOPA	HOMOCITRATE SYNTHASE, ALPHA SUBUNIT	CLOSTRIDIUM PASTEURIANUM	100-127	224-268						
PNIV CLOPA	HOMOCITRATE SYNTHASE, OMEGA SUBUNIT	CLOSTRIDIUM PASTEURIANUM	63-94	103-132	213-240	283-310				
PNPC ECOLI	POBIN PROTEIN NMPC PRECURSOR	ESCHERICHIA COLI	22-49	69-96	335-362					
PNDC BRASP	MODULATION PROTEIN C	BRADYRHIZOBIUM SP	3-30							
PNDC RHILQ	MODULATION PROTEIN C	RHIZOBIUM LOTI	286-313							
PNDC RHILQ	MODULATION PROTEIN C	RHIZOBIUM LEGUMINOSARUM	14-48							
PNDF RHILV	MODULATION PROTEIN F	RHIZOBIUM LEGUMINOSARUM	31-58							
PNDF RHILV	MODULATION PROTEIN F	RHIZOBIUM MELILOTI	39-66							
PNDD RHIMS	MODULATION PROTEIN G	RHIZOBIUM MELILOTI	8-35							
PNDD RHIMS	MODULATION PROTEIN G	RHIZOBIUM MELILOTI	8-35							
PNDD RHILV	MODULATION PROTEIN L	RHIZOBIUM LEGUMINOSARUM	26-53							
PNDD AZOBR	MODULATION PROTEIN Q	AZOSPIRILLUM BRASILENSE	60-87							
PNDDT RHILT	MODULATION PROTEIN T	RHIZOBIUM LEGUMINOSARUM	104-134	355-382	420-454					
PNDDT RHILT	MODULATION PROTEIN T	RHIZOBIUM LEGUMINOSARUM	364-391	416-443						
PNDDU RHIFR	MODULATION PROTEIN U	RHIZOBIUM FREDII	506-536							
PNDDV BRAJA	MODULATION PROTEIN V	BRADYRHIZOBIUM JAPONICUM	378-419	739-766						
PNDDX RHILV	MODULATION PROTEIN X	RHIZOBIUM LEGUMINOSARUM	232-259							
PNDL RHIFR	MODULATION PROTEIN NDL	RHIZOBIUM FREDII	131-160							
PNDL RHIME	MODULATION PROTEIN NDL	RHIZOBIUM MELILOTI	88-115							
PNOSR PSEST	REGULATORY PROTEIN NOSR	PSEUDOMONAS STUTZERI	319-346							
PNOSR PSEST	REGULATORY PROTEIN NOSR	PSEUDOMONAS STUTZERI	127-154							
PNOSZ ANEAE	NITROUS-OXIDE REDUCTASE PRECURSOR	PSEUDOMONAS AERUGINOSA	267-294							
PNOSZ ANEAE	NITROUS-OXIDE REDUCTASE PRECURSOR	PSEUDOMONAS STUTZERI	557-591							
PNPRAE BACAM	BACILLOLYSIN PRECURSOR	BACILLUS ANTHROPUS	113-147	217-244						
PNPRAE BACAM	BACILLOLYSIN PRECURSOR	BACILLUS ANTHROPUS	57-91	187-218						
PNPRAE BACAM	BACILLOLYSIN PRECURSOR	BACILLUS SUBTILIS	116-146	307-334						
PNPDY PARDE	NADH-UBIQUINONE OXIDOREDUCTASE 21 KD CHAIN	PARACOCOCUS DENITRIFICANS	4-45							
PNPDY PARDE	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD CHAIN	PARACOCOCUS DENITRIFICANS	125-152							
PNPDY PARDE	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD CHAIN	PARACOCOCUS DENITRIFICANS	91-125							
PNPFA ECOLI	CYTOCHROME C551 PRECURSOR	ESCHERICHIA COLI	319-346							
PNPFA ECOLI	CYTOCHROME C551 PRECURSOR	ESCHERICHIA COLI	72-111							
PNPFO ECOLI	ALIPHATIC NITRILASE	ESCHERICHIA COLI	109-136							
PNRIL RHORH	ALIPHATIC NITRILASE	RHODOCOCCUS RHODOCITRUS	52-79	135-162						
PNR LACLA	NISIN-RESISTANCE PROTEIN	ANABAENA SP	65-92							
PNR LACLA	NISIN-RESISTANCE PROTEIN	ANABAENA SP	44-91							
PNRCA ANASP	RNA-BINDING PROTEIN VFI	SYNECHOCOCCUS SP								
PNRCA SYN77	GLOBAL NITROGEN REGULATOR	SYNECHOCOCCUS SP	67-94							
PNRCA SYN77	GLOBAL NITROGEN REGULATOR	SYNECHOCOCCUS SP	194-223							
PNRTR VIBAL	NITROGEN REGULATION PROTEIN NTRB	VIBRIO ALGINOLYTICUS	385-412							
PNTRC PRUVU	NITROGEN REGULATION PROTEIN NR	PROTEUS VULGARIS	451-478							
PNTRC RHIME	NITROGEN ASSIMILATION REGULATORY PROTEIN	RHIZOBIUM MELILOTI	80-107							
PNJUC SYN73	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN	SYNECHOCOCCUS SP	27-54							
PNJUC SYN73	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN	SYNECHOCOCCUS SP	614-641							

PCGENE	10717844	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ELKNAME	PROTEIN	ORGANISMS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PNURC SYN1	PROB NADH-UBIQUINONE OXIDOREDUCTASE SUBU	SYNECHOCYSTIS SP	161-190								
PNURC SYN2	PROB NADH-UBIQUINONE OXIDOREDUCTASE SUBU	SYNECHOCYSTIS SP	169-199								
PNULX SYN1	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN	SYNECHOCYSTIS SP	46-80								
PNUGG ECOLI	NADH DEHYDROGENASE I CHAIN G	ESCHERICHIA COLI	368-402								
PNUGL ECOLI	NADH DEHYDROGENASE I CHAIN L	ESCHERICHIA COLI	30-57	496-523							
PNUGN ECOLI	NADH DEHYDROGENASE I CHAIN N	ESCHERICHIA COLI	392-419								
PNUPC ECOLI	NUCLEOTIDE PHOSPHATASE	ESCHERICHIA COLI	13-43	134-164	156-183						
PNUSA ECOLI	NUCLEASE	ESCHERICHIA COLI	21-62								
PNUSG ECOLI	NUCLEASE	ESCHERICHIA COLI	17-65	70-97							
PNUSG ECOLI	TRANSCRIPTION ANTI-TERMINATION PROTEIN NUS	ESCHERICHIA COLI	141-168								
PNUSG THEMIA	TRANSCRIPTION ANTI-TERMINATION PROTEIN NUS	THEMOTOGA MARITIMA	201-230								
PNYLB FLASP	6-AMINOHEXANOATE-DIMER HYDROLASE	FLAVOBACTERIUM SP	221-230								
PNYLC FLASP	6-AMINOHEXANOATE-DIMER HYDROLASE	FLAVOBACTERIUM SP	221-230								
POTMG BACCE	OLIGO-1,6-GLUCOSIDASE	BACILLUS CEREUS	101-128								
POCCT AGRT6	OC TOPIIN- BINDING PROTEIN T PRECURSOR	AGROBACTERIUM TUMEFACIENS	172-202								
POD01 AZOVI	2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT	AZOTOBACTER VINELANDII	829-856								
POD01 BACSU	2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT	BACILLUS SUBTILIS	487-524	809-850							
POD01 ECOLI	2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT	BACILLUS SUBTILIS	16-33								
POD02 BACSU	DIHYDROLIPOAMIDE SUC-TRANSF COMP	BACILLUS SUBTILIS	30-60								
POD0B PSEPU	2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT	PSEUDOMONAS PUTIDA	223-234								
POD01 ECOLI	PYRUVATE DEHYDROGENASE E1 COMPONENT	ESCHERICHIA COLI	624-651								
POD02 AZOVI	DIHYDROLIPOAMIDE ACETAMANS COMP	AZOTOBACTER VINELANDII	518-545								
POD02 ECOLI	DIHYDROLIPOAMIDE ACETAMANS COMP	ESCHERICHIA COLI	14-41	117-144							
POD0A BACST	PYRUVATE DEHYDROGENASE E1 COMPONENT	BACILLUS STEAROTHERMOPHILUS	299-333								
POD0B BACST	PYRUVATE DEHYDROGENASE E1 COMPONENT	BACILLUS SUBTILIS	305-332								
POD0B BACST	PYRUVATE DEHYDROGENASE E1 COMPONENT	BACILLUS STEAROTHERMOPHILUS	23-50								
POD0B BACSU	PYRUVATE DEHYDROGENASE E1 COMPONENT	BACILLUS SUBTILIS	16-50								
POMIE CHLTR	13 KD CYSTEINE-RICH PROTEIN, SEROVAR E	CILANTHIA TRACIONATIS	38-65								
POM1A1 NEIGO	OUTER MEMBRANE PROTEIN P1 A PRECURSOR	NEISSERIA GONORRHOEAE	61-90								
POM1A1 NEIME	OUTER MEMBRANE PROTEIN P1 A PRECURSOR	NEISSERIA MENINGITIDIS	359-386								
POM1A2 NEIME	OUTER MEMBRANE PROTEIN P1 A PRECURSOR	NEISSERIA MENINGITIDIS	353-380								
POM1B1 NEIGO	OUTER MEMBRANE PROTEIN P1 B PRECURSOR	NEISSERIA GONORRHOEAE	61-90								
POM1B1 NEIME	OUTER MEMBRANE PROTEIN P1 B PRECURSOR	NEISSERIA MENINGITIDIS	61-90								
POM1B2 NEIGO	OUTER MEMBRANE PROTEIN P1 B PRECURSOR	NEISSERIA GONORRHOEAE	61-90								
POM1B2 NEIME	OUTER MEMBRANE PROTEIN P1 B PRECURSOR	NEISSERIA MENINGITIDIS	61-90								
POM1B3 NEIME	OUTER MEMBRANE PROTEIN P1 B PRECURSOR	NEISSERIA MENINGITIDIS	61-90								
POM1B4 NEIME	OUTER MEMBRANE PROTEIN P1 B PRECURSOR	NEISSERIA MENINGITIDIS	61-90								
POM1B5 NEIME	OUTER MEMBRANE PROTEIN P1 B PRECURSOR	NEISSERIA MENINGITIDIS	24-51	61-90							
POM1B NEISA	OUTER MEMBRANE PROTEIN P1 B PRECURSOR	NEISSERIA LACTAMICA	116-143								
POM1B NEISA	OUTER MEMBRANE PROTEIN P1 B PRECURSOR	NEISSERIA SICCA	24-51	61-90							
POM1A ACTPL	OUTER MEMBRANE LIPOPROTEIN PRECURSOR	ACTINOBACILLUS PLEUROPNEUMONIAE	144-151								
POM1P1 HAEIN	OUTER MEMBRANE PROTEIN P1 PRECURSOR	HAEMOPHILUS INFLUENZAE	154-184	303-330	341-368						
POM1P2 HAEIN	OUTER MEMBRANE PROTEIN P2 PRECURSOR	HAEMOPHILUS INFLUENZAE	16-71	220-234	326-353						
POM1P3 NEIGO	OUTER MEMBRANE PROTEIN P3 PRECURSOR	NEISSERIA GONORRHOEAE	14-41								
POM1P7 STAAU	70 KD OUTER MEMBRANE PROTEIN PRECURSOR	STAPHYLOCOCCUS AUREUS	51-80	88-115							
POMPA THEMIA	OUTER MEMBRANE PROTEIN ALPHA PRECURSOR	THEMOTOGA MARITIMA	100-128	131-178	183-249	255-292	301-328	331-383			
POMPC ECOLI	OUTER MEMBRANE PROTEIN C PRECURSOR	ESCHERICHIA COLI	89-123	64-94							
POMPC NEIGO	OUTER MEMBRANE PROTEIN C PRECURSOR	NEISSERIA GONORRHOEAE	89-123								
POMPC SALT1	OUTER MEMBRANE PROTEIN C PRECURSOR	SALMONELLA TYPHII	166-193								
POMPF ECOLI	OUTER MEMBRANE PROTEIN F PRECURSOR	ESCHERICHIA COLI	21-55	231-258							
POMPH PTH19	OMPH PROTEIN	PHOTOBACTERIUM SP	292-319								
POMPT ECOLI	PROTEASE VII PRECURSOR	ESCHERICHIA COLI	37-64								
POMPA3 NEIGO	OPACITY PROTEIN OPA63	NEISSERIA GONORRHOEAE	71-111								
POMPA6 NEIGO	OPACITY PROTEIN OPA67	NEISSERIA GONORRHOEAE	72-109								
POMPA8 NEIGO	OPACITY PROTEIN OPA83	NEISSERIA GONORRHOEAE	71-123	140-167							
POMPA9 NEIGO	OPACITY PROTEIN OPA93	NEISSERIA GONORRHOEAE	80-107	140-167							
POMPA1 NEIGO	OPACITY PROTEIN OPA14	NEISSERIA GONORRHOEAE	80-107								
POMPA2 NEIGO	OPACITY PROTEIN OPA58	NEISSERIA GONORRHOEAE	71-103								





PGCENE	10717844	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILENAME	PROTEIN	ORGANISM	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PPBP4_BACSU	PENICILLIN-BINDING PROTEIN 4*	BACILLUS SUBTILIS	374-401								
PPBP4_ECOLI	PENICILLIN-BINDING PROTEIN 4 PRECURSOR	ESCHERICHIA COLI	316-363								
PPBP4_ECOLI	PENICILLIN-BINDING PROTEIN 1A	ESCHERICHIA COLI	145-172								
PPBP4_ECOLI	PENICILLIN-BINDING PROTEIN 1B	ESCHERICHIA COLI	62-96	262-290							
PPBPX_STRPN	PENICILLIN-BINDING PROTEIN 2X	STREPTOCOCCUS PNEUMONIAE	39-116	706-733							
PPBPX_STAAL	PENICILLIN-BINDING PROTEIN	STAPHYLOCOCCUS AUREUS	78-108	176-203	502-529						
PPCAB_PSEFU	CYCLOISOMERASE	PSEUDOMONAS PUTIDA	115-142	226-253							
PPEL3_ERWCA	PECTATE LYASE III PRECURSOR	ERWINIA CAROTOVORA	110-137								
PPEL4_ERWCA	PECTATE LYASE A PRECURSOR	ERWINIA CAROTOVORA	110-137								
PPELB_ERWCA	PECTATE LYASE B PRECURSOR	ERWINIA CAROTOVORA	110-137								
PPELC_ERWCA	PECTATE LYASE C PRECURSOR	ERWINIA CAROTOVORA	110-137								
PPELF_ERWCH	PECTATE LYASE F PRECURSOR	ERWINIA CHRYSANTHEMI	40-67	209-243							
PPELP_ERWCA	PERIPLASMIC PECTATE LYASE PRECURSOR	ERWINIA CAROTOVORA	455-482								
PPELP_YERP5	PERIPLASMIC PECTATE LYASE PRECURSOR	YERSINIA PSEUDOTUBERCULOSIS	459-489								
PPELX_ERWCA	PUTATIVE PECTATE LYASE X PRECURSOR	ERWINIA CAROTOVORA	188-218								
PPELX_ERWCH	EXOPOLYGALACTURONATE LYASE PRECURSOR	ERWINIA CHRYSANTHEMI	466-493								
PPEPD_ECOLI	AMINOACYL-HISTIDINE DIPEPTIDASE	ESCHERICHIA COLI	264-314								
PPEPQ_ECOLI	X-PRO DIPEPTIDASE	ESCHERICHIA COLI	351-278								
PPERT_BORBR	PERTACTIN PRECURSOR	BORDETTELLA BRONCHISEPTICA	617-644								
PPERT_BORPA	PERTACTIN PRECURSOR	BORDETTELLA PARAPERTUSSIS	628-655								
PPERT_BORBE	PERTACTIN PRECURSOR	BORDETTELLA PERTUSSIS	616-643								
PPCK_CONGL	PHOSPHOGLYCERATE KINASE	CORYNEBACTERIUM GLUTINICUM	83-117								
PPCK_ECOLI	PHOSPHOGLYCERATE KINASE	ESCHERICHIA COLI	186-216								
PPCK_METBR	PHOSPHOGLYCERATE KINASE	METHANOBACTERIUM BRYANTII	36-63								
PPCK_THETH	PHOSPHOGLYCERATE KINASE	THERMUS AQUATICUS	222-249								
PPGL1_ERWCA	ENDO-POLYGALACTURONASE PRECURSOR	ERWINIA CAROTOVORA	332-271								
PPGTE_SALTY	OUTER MEMBRANE PROTEASE E PRECURSOR	SALMONELLA TYPHIMURUM	66-93								
PPHA1_FREDI	C-PHYCOCYANIN-1 ALPHA CHAIN	FREMYELLA DIPLOSPHORI	21-48								
PPHA2_FREDI	C-PHYCOCYANIN-2 ALPHA CHAIN	FREMYELLA DIPLOSPHORI	21-48								
PPHA3_FREDI	POLY(3-HYDROXYALKANOATE) POLYMERASE I	PSEUDOMONAS OLEOVORANS	264-291								
PPHAB_ANACV	ALLOPHYCOCYANIN BETA CHAIN	ANABAENA CYLINDRICA	7-48								
PPHAB_ANAVA	ALLOPHYCOCYANIN BETA CHAIN	ANABAENA VARIABILIS	14-48								
PPHAB_FREDI	ALLOPHYCOCYANIN BETA CHAIN	FREMYELLA DIPLOSPHORI	8-49								
PPHAB_MASLA	ALLOPHYCOCYANIN BETA CHAIN	MASTIGOCALDUS LAMINOSUS	14-41								
PPHAB_SYN96	ALLOPHYCOCYANIN BETA CHAIN	SYNECHOCOCCUS SP	14-41								
PPHAC_SYN96	ALLOPHYCOCYANIN ALPHA-B CHAIN	SYNECHOCOCCUS SP	33-60								
PPHAG_FREDI	ALLOPHYCOCYANIN GAMMA CHAIN	FREMYELLA DIPLOSPHORI	32-59								
PPHB3_FREDI	C-PHYCOCYANIN-3 BETA CHAIN	FREMYELLA DIPLOSPHORI	29-56								
PPHBD_ALCEU	ACETOACETYL-COA REDUCTASE	ALCALIGENES EUTROPIUS	35-85								
PPHCA_SYNVI	C-PHYCOCYANIN ALPHA CHAIN	SYNECHOCYSTIS SP	21-55								
PPHCB_SYN96	C-PHYCOCYANIN BETA CHAIN	SYNECHOCOCCUS SP	38-55								
PPHCB_SYN97	C-PHYCOCYANIN BETA CHAIN	SYNECHOCOCCUS SP	28-55								
PPHCB_SYN71	C-PHYCOCYANIN BETA CHAIN	SYNECHOCYSTIS SP	21-55								
PPHEA_ECOLI	CHORISMATE MUTASE	ESCHERICHIA COLI	10-37								
PPHEA_ERWBE	CHORISMATE MUTASE	ERWINIA HERBICOLA	10-37	159-186	252-286						
PPHEA_PESP	PHENOL 2-MONOOXYGENASE	PSEUDOMONAS SP	171-201	282-314	437-464						
PPHEB_MASLA	PHYCOERYTHROCYANIN BETA CHAIN	MASTIGOCALDUS LAMINOSUS	21-62								
PPHEB_PESP	CATECHOL 1,2-DIOXYGENASE	PSEUDOMONAS SP	24-51								
PPHEO_SYN97	LINKER POLYPEPTIDE	SYNECHOCOCCUS SP	158-185								
PPHEP_ECOLI	PHENYLALANINE-SPECIFIC PERMEASE	ESCHERICHIA COLI	384-311								
PPHF1_CLOPA	PERIPLASMIC [FE] HYDROGENASE I	CLOSTRIDIUM PASTEURIANUM	414-471								
PPHL1_BACCE	SPHINGOMYELINASE C PRECURSOR	BACILLUS CEREUS	2-36								
PPHL2_BACCE	SPHINGOMYELINASE C PRECURSOR	BACILLUS CEREUS	2-36								
PPHL3_BACCE	SPHINGOMYELINASE C PRECURSOR	BACILLUS CEREUS	2-36								
PPHLC_BACCE	PHOSPHOLIPASE C PRECURSOR	BACILLUS CEREUS	32-59								
PPHLC_CLOBI	PHOSPHOLIPASE C PRECURSOR	CLOSTRIDIUM BIFERMENTANS	30-77	179-206							
PPHLC_CLOPE	PHOSPHOLIPASE C PRECURSOR	CLOSTRIDIUM PERRINGENS	210-237	335-365							
			169-198								

ECSENE	1071714	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10
FILE NAME	PROTEIN	ORGANISM	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10
PHLC LISMO	PHOSPHOLIPASE C PRECURSOR	LISTERIA MONOCYTOGENES	147-174									
PHLC PSEAE	HEMOLYTIC PHOSPHOLIPASE C PRECURSOR	PSEUDOMONAS AERUGINOSA	685-712									
PHLC STAAU	PHOSPHOLIPASE C PRECURSOR	STAPHYLOCOCCUS AUREUS	6-33									
PHLD BACCE	PHOSPHOLIPASE C PRECURSOR	BACILLUS CEREUS	179-206									
PHLD LEPIN	SPHINGOMYELINASE C PRECURSOR	LEPTOSPIRA INTERROGANS	10-57	394-428								
PHND ECOLI	PHND PROTEIN	ESCHERICHIA COLI	296-326									
PHNK ECOLI	PHNK PROTEIN	ESCHERICHIA COLI	178-205									
PHNM ECOLI	PHNM PROTEIN	ESCHERICHIA COLI	5-35									
PHOB CITR	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	CITROBACTER FREUNDII	13-40	42-105								
PHOE ECOLI	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	ESCHERICHIA COLI	13-40	64-105	188-195	226-233						
PHOE KLEOX	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	KLEBSIELLA OXYTOCA	13-40	64-91								
PHOE KLEPN	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	KLEBSIELLA PNEUMONIAE	13-40	64-105								
PHOE SALTU	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	SALMONELLA TYPHIMURUM	61-104	320-347								
PHOD BACSU	ALK PHOS SYNTHESIS TRANS REG PROTEIN	BACILLUS SUBTILIS	185-219									
PHOO ECOLI	SENSOR PROTEIN PHOO	ESCHERICHIA COLI	244-278									
PHOO SALTU	VIRULENCE SENSOR PROTEIN PHOO	SALMONELLA TYPHIMURUM	226-260									
PHOR BACSU	ALK PHOS SYNTHESIS SENSOR PROTEIN PHOR	BACILLUS SUBTILIS	89-145	387-425								
PHRA ECOLI	PHOTOREPAIR PROTEIN PHRA	ESCHERICHIA COLI	61-90	207-241								
PHRA SYNPP	R-PHYCOCYANIN II ALPHA CHAIN	SYNECHOCOCCUS SP	20-47									
PHRA SYNPP2	R-PHYCOCYANIN II ALPHA CHAIN	SYNECHOCOCCUS SP	20-47									
PHSO ECOLI	GLYCOCEN PHOSPHORYLASE	ESCHERICHIA COLI	157-184	488-515								
PHSM ECOLI	MALTODEXTRIN PHOSPHORYLASE	ESCHERICHIA COLI	71-108									
PILA NEGO	PROB SIGNAL RECOGNITION PARTICLE PROTEIN	NEISSERIA GONORRHOEAE	17-68									
PILB PSEAE	FIMBRIAL ASSEMBLY PROTEIN PILB	PSEUDOMONAS AERUGINOSA	16-60									
PILC PSEAE	PILC PROTEIN	PSEUDOMONAS AERUGINOSA	143-170									
PILD NEGO	LEADER PEPTIDASE	NEISSERIA GONORRHOEAE	110-137									
PILQ PSEAE	FIMBRIAL ASSEMBLY PROTEIN PILQ PRECURSOR	PSEUDOMONAS AERUGINOSA	71-115	639-666								
PILS PSEAE	SENSOR PROTEIN PILS	PSEUDOMONAS AERUGINOSA	9-46									
PILR ECOLI	PI PROTEIN	ESCHERICHIA COLI	156-188									
PILV MORBO	PILIN GENE INVERTING PROTEIN	MORAXELLA BOVIS	42-69	152-182								
PILV MORLA	PILIN GENE INVERTING PROTEIN	MORAXELLA LACUNATA	152-182									
PLC BACCE	PHOSPHODIESTERASE PRECURSOR	BACILLUS CEREUS	217-245									
PLC BACTU	PHOSPHODIESTERASE PRECURSOR	BACILLUS THURINGIENSIS	216-245									
PLC LISMO	PHOSPHODIESTERASE PRECURSOR	LISTERIA MONOCYTOGENES	238-265									
PLSC ECOLI	ACYLTRANSFERASE	ESCHERICHIA COLI	106-133									
PLSX ECOLI	PLSX PROTEIN	ESCHERICHIA COLI	241-270									
PPLYD ERWCA	PECTIN LYASE	ERWINIA CAROTOVORA	27-92									
PNBA ECOLI	PNBA PROTEIN	ESCHERICHIA COLI	9-50									
PNBE ERWCH	PECTINESTERASE PRECURSOR	ERWINIA CHRYSANTHEMI	60-87									
PNBY ECOLI	PHOSPHOGLYCERATE MUTASE	ESCHERICHIA COLI	82-116									
PNBY ZYMM	PHOSPHOGLYCERATE MUTASE	ZYMONOMAS MOBILIS	13-40	80-110								
PNP ECOLI	POLYRIBONUC NUCLEOTIDYL TRANSF	ESCHERICHIA COLI	260-294									
PNP ECOLI	POLYRIBONUC NUCLEOTIDYL TRANSF	SALMONELLA TYPHIMURUM	176-205									
PNP ECOLI	PNP PROTEIN	SALMONELLA TYPHIMURUM	51-78									
POD BACSY	PYRUVATE ORTHOPHOSPHATE DIKINASE	BACTEROIDES SYMBIOSUS	111-138									
POF PSESY	OUTER MEMBRANE PORIN F PRECURSOR	PSEUDOMONAS SYRINGAE	390-424									
POF PSEAE	PORIN O PRECURSOR	PSEUDOMONAS AERUGINOSA	139-181	260-287	360-396							
POF PSEAE	PORIN P PRECURSOR	PSEUDOMONAS AERUGINOSA	139-181	260-287	360-396							
PROD ECOLI	BINDING PROTEIN PRECURSOR	ESCHERICHIA COLI	320-347									
PROTE ECOLI	PUTRISCIN-ORNITHINE ANTIUNITA	ESCHERICHIA COLI	91-118									
POXB ECOLI	PYRUVATE DEHYDROGENASE	ESCHERICHIA COLI	8-38									
PPB BACSU	ALKALINE PHOSPHATASE III PRECURSOR	BACILLUS SUBTILIS	109-150	433-460								
PPB BACSU	ALKALINE PHOSPHATASE IV PRECURSOR	BACILLUS SUBTILIS	85-123	336-363								
PPB ECOLI	ALKALINE PHOSPHATASE PRECURSOR	ESCHERICHIA COLI	235-262									
PPB ESCFE	ALKALINE PHOSPHATASE PRECURSOR	ESCHERICHIA COLI	235-262									
PPCE FLAME	PROLYL ENDOPEPTIDASE PRECURSOR	FLAVOBACTERIUM MENINGOSEPTICUM	158-199									
PPCE FLAME	PROLYL ENDOPEPTIDASE PRECURSOR	FLAVOBACTERIUM MENINGOSEPTICUM	158-199									
PPCK ECOLI	PHOSPHOENOLPYRUVATE CARBOXYKINASE	ESCHERICHIA COLI	45-72									

PCGENE	10117144	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
ELLENANR	PROTEIN	ORGANISM	73-107								
PPDA CLOPE	PROTEIN A PRECURSOR	CLOSTRIDIUM PERFRINGENS	49-76								
PPQA ECOLI	PHOSPHENOLPYRUVATE SYNTHASE	ESCHERICHIA COLI	40-74								
PPQ2 ACICA	COENZYME POO SYNTHESIS PROTEIN II	ACINETOBACTER CALCOACETICUS	371-398								
PPRA ANAVA	CALCIUM DEPENDENT PROTEINASE PRECURSOR	ANABAENA VARIABILIS	88-115								
PPRC THEAC	PROTEASOME, ALPHA SUBUNIT	THIENOPHOSPHATA ACIDOPHILUM	158-192								
PPRE ECOLI	TAIL-SPECIFIC PROTEINASE PRECURSOR	ESCHERICHIA COLI	27-78	266-393							
PPREJ STAAU	PLASMID RECOMBINATION ENZYME	STAPHYLOCOCCUS AUREUS	152-179	264-147							
PPREI STAAU	PLASMID RECOMBINATION ENZYME	STAPHYLOCOCCUS AUREUS	48-75	181-208	310-361						
PPREA LACPL	PLASMID RECOMBINATION ENZYME	LACTOBACILLUS PLANTARUM	37-71	291-318							
PPRE BACLI	REGULATORY PROTEIN	BACILLUS LICHENIFORMIS	2-40								
PPRE BACSF	PLASMID RECOMBINATION ENZYME	BACILLUS SP	181-224	288-345							
PPRE STRAG	PLASMID RECOMBINATION ENZYME	STREPTOCOCCUS AGALACTIAE	385-319	332-339	420-454						
PPRFA LISMO	LISTERIOLYSIN REGULATORY PROTEIN	LISTERIA MONOCYTOGENES	76-110	173-204							
PPRIA ECOLI	PRIMOSOMAL PROTEIN N	ESCHERICHIA COLI	218-245								
PPRIM BACSU	DNA PRIMASE	BACILLUS SUBTILIS	383-433								
PPRIM BUCAP	DNA PRIMASE	BUCHNERA APHIDICOLA	13-43	282-319							
PPRIM CLOAB	DNA PRIMASE	CLOSTRIDIUM ACETOBUTYLICUM	87-114								
PPRIM LACLA	DNA PRIMASE	LACTOCOCCUS LACTIS	269-296								
PPRIM RUCPR	DNA PRIMASE	RICKETTSIA PROWAZEKII	10-37	245-286	477-504	526-593					
PPRIS DESDE	PRISMALINE PROTEIN	DESULFOVIBRIO DESULFURICANS	30-57								
PPRLB AGHLY	BETA-LYTIC METALLOENDOPEPTIDASE	ACHROMOBACTER LYTIUS	317-344								
PPRLB LYSEN	BETA-LYTIC METALLOENDOPEPTIDASE	LYSOBACTER ENZYMOGENES	121-148								
PPROJ LISMO	ZINC METALLOPROTEINASE PRECURSOR	LISTERIA MONOCYTOGENES	111-145	275-316							
PPROJ LISMO	ZINC METALLOPROTEINASE PRECURSOR	LISTERIA MONOCYTOGENES	111-145								
PPROA SERMA	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE	SERRATIA MARCESCENS	309-336								
PPROA STAAU	PROTEIN A PRECURSOR	STAPHYLOCOCCUS AUREUS	2-29								
PPROB SERMA	GLUTAMATE KINASE	SERRATIA MARCESCENS	7-34								
PPROB STRAG	PROTEIN B	STREPTOCOCCUS AGALACTIAE	58-85								
PPROC PSEAE	PYRROLINE-5-CARBOXYLATE REDUCTASE	PSEUDOMONAS AERUGINOSA	148-175								
PPROH BACSU	PYRROLINE-5-CARBOXYLATE REDUCTASE HOMOL	BACILLUS SUBTILIS	200-227								
PPROP ECOLI	PROLINBETAINE TRANSPORTER	ESCHERICHIA COLI	460-487								
PPROV ECOLI	PERIPHERAL MEMBRANE PROTEIN PROV	ESCHERICHIA COLI	24-34								
PPROV SALT	PERIPHERAL MEMBRANE PROTEIN PROV	SALMONELLA TYPHIMURUM	24-34								
PPRB ECOLI	PRBB PROTEIN	ESCHERICHIA COLI	170-197								
PPRC ECOLI	ANTICODON NUCLEASE	ESCHERICHIA COLI	282-309								
PPRD ECOLI	PRRD PROTEIN	ESCHERICHIA COLI	278-305								
PPRSA DACSU	PROTEIN EXPORT PROTEIN PRSA PRECURSOR	BACILLUS SUBTILIS	52-87	95-157							
PPRTA STRGR	SECRETED PROTEASE C PRECURSOR	STREPTOMYCES GRISEUS	56-110								
PPRTC ERWCH	COLLAGENASE PRECURSOR	ERWINIA CHRYSANTHEMI	103-130								
PPRTD ERWCH	PROTEASES SECRETION PROTEIN PRTD	PORPHYROMONAS GINGIVALIS	285-312								
PPRTE DACNO	EXTRACELLULAR SERINE PROTEINASE PRECURSOR	ERWINIA CHRYSANTHEMI	328-355								
PPRTL UNWCI	PROTEINASES SECRETION PROTEIN PRTE	DACTYLOIDES NODOSUS	106-133	219-265	346-384						
PPRTT ERWCH	PROTEASES SECRETION PROTEIN PRTE	ERWINIA CHRYSANTHEMI	108-135	158-192	231-290						
PPRTM LACLA	PROTEASE MATURATION PROTEIN PRECURSOR	ERWINIA CHRYSANTHEMI	280-310								
PPRTM LACPL	PROTEASE MATURATION PROTEIN PRECURSOR	LACTOCOCCUS LACTIS	76-103	112-139							
PPRTM LACPL	PROTEASE MATURATION PROTEIN PRECURSOR	LACTOBACILLUS PARACASEI	26-53	76-103	112-139						
PPRTS SERMA	EXTRACELLULAR SERINE PROTEINASE PRECURSOR	SERRATIA MARCESCENS	104-331	576-607	1007-1041						
PPRTX ERWCH	SECRETED PROTEASE C PRECURSOR	SERRATIA MARCESCENS	304-331	462-491	1007-1041						
PPSAA SYNEN	CHLOROPHYLL A APOPROTEIN A1	ERWINIA CHRYSANTHEMI	314-341								
PPSAA SYN2	CHLOROPHYLL A APOPROTEIN A1	SYNECHOCOCCUS ELONGATUS NAEGEL	120-147								
PPSAA SYN3	CHLOROPHYLL A APOPROTEIN A1	SYNECHOCOCCUS SP	109-136	326-356							
PPSAA SYN4	CHLOROPHYLL A APOPROTEIN A1	SYNECHOCOCCUS VULCANUS	120-147								
PPSAA SYN5	CHLOROPHYLL A APOPROTEIN A1	SYNECHOCOCCUS SP	44-71	120-147	318-368						
PPSAD YERPE	CIANIFERONE PROTEIN PSAD PRECURSOR	YERSINIA PESTIS	244-271								
PPSAD SYN6	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II	SYNECHOCOCCUS SP	11-38								
PPSAE YERPE	PSAE PROTEIN PRECURSOR	YERSINIA PESTIS	66-118								

PCGENE	10/11/1714	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE.MARIE	PROTEIN	ORGANISMI	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PPSBO ANANI	STABILIZING POLYPEPTIDE PRECURSOR	ANACYSTIS NIDULANS	99-126	209-241							
PPSPA ECOLI	PHAGE SHOCK PROTEIN A	ESCHERICHIA COLI	55-82								
PPSRA WOLSU	POLYSULFIDE REDUCTASE CHAIN A PRECURSOR	WOLINELLA SUCCINOHENES	114-141								
PPSTS ECOLI	PHOSPHATIDYL-INDING PROTEIN PRECURSOR	ESCHERICHIA COLI	105-24								
PPTL BACSU	PHOSPHOTRANSFERASE	BACILLUS SUBTILIS	26-60								
PPTL ECOLI	PHOSPHOTRANSFERASE	ESCHERICHIA COLI	115-162	399-426							
PPTL SALTY	PHOSPHOTRANSFERASE	SALMONELLA TYPHIMURIUM	212-239	399-426							
PPTL STACA	PHOSPHOTRANSFERASE	STAPHYLOCOCCUS CARNOSUS	14-61								
PPTL STRSL	PHOSPHOTRANSFERASE	STREPTOCOCCUS SALIVARIUS	14-61	198-232							
PPTLB BACSU	PHOSPHOTRANSFERASE ENZYME II	ERWINIA CHRYSAETHIUM	127-154								
PPTLG BACSU	PHOSPHOTRANSFERASE ENZYME II	BACILLUS SUBTILIS	670-697								
PPTL LACCA	PHOSPHOTRANSFERASE ENZYME II	LACTOBACILLUS CASEI	517-544								
PPTL LACLA	PHOSPHOTRANSFERASE ENZYME II	LACTOCOCCUS LACTIS	183-214	409-436							
PPTL STAAU	PHOSPHOTRANSFERASE ENZYME II	STAPHYLOCOCCUS AUREUS	421-448	530-557							
PPTL ECOLI	PHOSPHOTRANSFERASE ENZYME II	ESCHERICHIA COLI	445-489								
PPTLN STACA	PHOSPHOTRANSFERASE ENZYME II	STAPHYLOCOCCUS CARNOSUS	188-415								
PPTLN ECOLI	N-ACETYLGLUCOSAMINE-6-EPIMERASE	ESCHERICHIA COLI	370-400								
PPTLN STRAU	PHOSPHOTRANSFERASE ENZYME II	STREPTOCOCCUS MUTANS	600-627								
PPTLF SALTY	PHOSPHOTRANSFERASE ENZYME II	SALMONELLA TYPHIMURIUM	107-134								
PPTL LACCA	PHOSPHOTRANSFERASE FACTOR III	LACTOBACILLUS CASEI	40-67								
PPTL ECOLI	PHOSPHOCARBOXYPEPTIDASE	ESCHERICHIA COLI	31-65								
PPTHP KLEPN	PHOSPHOCARRIER PROTEIN HPR	SALMONELLA TYPHIMURIUM	31-65								
PPTHB ECOLI	PROTEINASE II	KLEBSIELLA PNEUMONIAE	31-65								
PPULA KLEAE	PULLULANASE	ESCHERICHIA COLI	94-121	217-251							
PPULO KLEPN	PULLULANASE	KLEBSIELLA AEROGES	894-928								
PPULO KLEPN	LEADER PEPTIDASE	KLEBSIELLA PNEUMONIAE	894-928								
PPULS KLEPN	PULS PRECURSOR	KLEBSIELLA PNEUMONIAE	178-205								
PPUR4 BACSU	UPTAKE PROTEIN PRECURSOR	PSEUDOMONAS PUTIDA	70-97								
PPUR1 BACSU	AMIDOPHOSPHORIBOSYLTRANSFERASE	BACILLUS SUBTILIS	112-162	210-237	439-463	716-763					
PPUR2 BACSU	PHOSPHORIBOSYLAMINE-GLYCINE LIGASE	BACILLUS SUBTILIS	394-421								
PPUR3 BACSU	FORMYLTRANSFERASE	BACILLUS SUBTILIS	349-376								
PPUR3 ECOLI	FORMYLTRANSFERASE	ESCHERICHIA COLI	149-176								
PPUR4 BACSU	SYNTHASE I	BACILLUS SUBTILIS	27-54								
PPUR4 BACSU	CYCLO-LIGASE	BACILLUS SUBTILIS	18-45								
PPUR6 ECOLI	AIR CARBOXYLASE	BACILLUS SUBTILIS	152-194								
PPUR7 BACSU	SAICAR SYNTHETASE	ESCHERICHIA COLI	131-158								
PPUR8 BACSU	ADENYLOSUCCLINATE LYASE	BACILLUS SUBTILIS	3-43								
PPUR8 ECOLI	ADENYLOSUCCLINATE LYASE	BACILLUS SUBTILIS	36-130	226-253							
PPUR9 BACSU	ADENYLOSUCCLINATE LYASE	ESCHERICHIA COLI	194-221	231-272							
PPUR9 ECOLI	ADENYLOSUCCLINATE LYASE	BACILLUS SUBTILIS	15-53	345-372							
PPUR9 SALTY	ADENYLOSUCCLINATE LYASE	BACILLUS SUBTILIS	239-268								
PPUR1 BACSU	ADENYLOSUCCLINATE LYASE	SALMONELLA TYPHIMURIUM	218-247								
PPUR1 ECOLI	ADENYLOSUCCLINATE LYASE	BACILLUS SUBTILIS	609-636								
PPYGI ANASP	LINKER POLYPEPTIDE CPCG1	ANABAEIA SP	88-115								
PPYGI MASLA	LINKER POLYPEPTIDE CPCG1	MASTIGLOCLADUS LAMINOSUS	89-116								
PPYGI ANASP	LINKER POLYPEPTIDE CPCG2	ANABAEIA SP	88-115								
PPYGI MASLA	LINKER POLYPEPTIDE CPCG2	MASTIGLOCLADUS LAMINOSUS	89-116								
PPYGI MASLA	LINKER POLYPEPTIDE CPCG3	MASTIGLOCLADUS LAMINOSUS	91-132								
PPYGI ANASP	LINKER POLYPEPTIDE CPCG4	ANABAEIA SP	90-131								
PPYR2 FREDI	32.1 KD LINKER POLYPEPTIDE	ANABAEIA SP	35-62								
PPYR2 FREDI	32.9 KD LINKER POLYPEPTIDE	FREMYELLA DIPLOSPHON	105-132								
PPYR4 FREDI	31.6 KD LINKER POLYPEPTIDE	FREMYELLA DIPLOSPHON	22-46								
PPYR4 FREDI	31.8 KD LINKER POLYPEPTIDE	FREMYELLA DIPLOSPHON	106-143								
PPYR6 FREDI	37.5 KD LINKER POLYPEPTIDE	FREMYELLA DIPLOSPHON	43-70	113-140							
PPYR6 BACSU	ASPARTATE CARBAMOYLTRANSFERASE	BACILLUS SUBTILIS	9-36								
PPYR6 SEMMA	ASPARTATE CARBAMOYLTRANSFERASE	SERRATIA MARCESCENS	70-97								
PPYRD ECOLI	DITHIOROTATE DEHYDROGENASE	ESCHERICHIA COLI	113-142								

PCGENE	10717114	Proteolytic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PPYD BACSU	DIHYDROOROTATE DEHYDROGENASE	SALMONELLA TYPHIMURUM	115-142	181-210							
PPYD BACSU	CTP SYNTHASE	BACILLUS SUBTILIS	275-302	322-349							
PPYD BACSU	PHENOLASE 9.7 KD LINKER POLYPEPTIDE	FREMYELLA DIPLOSPION	21-48								
PPYD BACSU	QUINONE OXIDOREDUCTASE	ESCHERICHIA COLI	180-215								
PPYD BACSU	QUEUOSINE BIOSYNTHESIS PROTEIN QUESA	ESCHERICHIA COLI	224-261								
PPYD BACSU	14.2 KD PROTEIN IN RUBREDOXIN OPERON	CLOSTRIDIUM PASTEURIANUM	231-50	157-232							
PPYD BACSU	RACC PROTEIN	ESCHERICHIA COLI	5-32								
PPYD BACSU	ASPARTATE RACEMASE	STREPTOCOCCUS THERMOPHILUS	152-189								
PPYD BACSU	PROBABLE AMINO ACID RACEMASE	BACILLUS SUBTILIS	132-162								
PPYD BACSU	ALPHA-GALACTOSIDASE	ESCHERICHIA COLI	86-116								
PPYD BACSU	RAFFINOSE INVERTASE	ESCHERICHIA COLI	348-375								
PPYD BACSU	RIBOSE TRANSPORT SYSTEM COMPONENT	ESCHERICHIA COLI	65-99	195-222							
PPYD BACSU	RIBOKINASE	ESCHERICHIA COLI	200-239								
PPYD BACSU	RIBITOL (RBT) OPERON REPRESSOR	ESCHERICHIA COLI	6-47								
PPYD BACSU	BIOSYNTHESIS ACTIVATION PROTEIN A	ESCHERICHIA COLI	170-197								
PPYD BACSU	BIOSYNTHESIS ACTIVATION PROTEIN A	ERWINIA AMYLOVORA	92-119	174-201							
PPYD BACSU	BIOSYNTHESIS ACTIVATION PROTEIN A	ERWINIA STEWARTII	174-201								
PPYD BACSU	BIOSYNTHESIS ACTIVATION PROTEIN A	ESCHERICHIA COLI	168-205								
PPYD BACSU	CAPSULE SYNTHESIS B COMPONENT	ESCHERICHIA COLI	14-41	159-186							
PPYD BACSU	RECA PROTEIN	LEGIONELLA PNEUMOPHILA	262-310								
PPYD BACSU	RECA PROTEIN	AGROBACTERIUM LAIDLAWII	281-310								
PPYD BACSU	RECA PROTEIN	AGROBACTERIUM TURFAGIENS	3-30	132-159	281-308						
PPYD BACSU	RECA PROTEIN	ANABANA VARABILIS	322-349								
PPYD BACSU	RECA PROTEIN	AQUIFEX PYROPHILUS	61-90	126-153							
PPYD BACSU	RECA PROTEIN	BACTERIOIDES FRAGILIS	108-135								
PPYD BACSU	RECA PROTEIN	BACILLUS SUBTILIS	262-294								
PPYD BACSU	RECA PROTEIN	BRUCELLA ABORTUS	3-30	132-159	240-307						
PPYD BACSU	RECA PROTEIN	BURKHOLDERIA CEPACIA	75-109								
PPYD BACSU	RECA PROTEIN	ERWINIA CAROTOVORA	284-311								
PPYD BACSU	RECA PROTEIN	LACTOBACILLUS DELBRUECKII	20-47								
PPYD BACSU	RECA PROTEIN	LACTOBACILLUS HELVETICUS	20-47								
PPYD BACSU	RECA PROTEIN	LACTOCOCCUS LACTIS	131-162	232-269	288-315						
PPYD BACSU	RECA PROTEIN	METHYLOHONAS CLARA	266-303								
PPYD BACSU	RECA PROTEIN	METHYLOBACILLUS FLAGELLATUM	276-303								
PPYD BACSU	RECA PROTEIN	MYCOPLASMA PULMONIS	10-57								
PPYD BACSU	RECA PROTEIN	MYCOBACTERIUM TUBERCULOSIS	249-276								
PPYD BACSU	RECA PROTEIN	NEISSERIA GONORRHOEA	261-310								
PPYD BACSU	RECA PROTEIN	PROTEUS MIRABILIS	283-310								
PPYD BACSU	RECA PROTEIN	PSEUDOMONAS AERUGINOSA	282-309								
PPYD BACSU	RECA PROTEIN	RHIZOBIUM LEGUMINOSARUM	3-30	131-158	210-307						
PPYD BACSU	RECA PROTEIN	RHIZOBIUM LEGUMINOSARUM	119-146	268-295							
PPYD BACSU	RECA PROTEIN	RHIZOBIUM MELIOTTI	119-146	268-295							
PPYD BACSU	RECA PROTEIN	RHODOBACTER SPHAEROIDES	119-146								
PPYD BACSU	RECA PROTEIN	STREPTOCOCCUS PNEUMONIAE	134-161	291-317							
PPYD BACSU	RECA PROTEIN	SYNECHOCOCCUS SP	124-151								
PPYD BACSU	RECA PROTEIN	VIBRIO CHOLERAE	290-317								
PPYD BACSU	RECA PROTEIN	BACILLUS SUBTILIS	4-31	178-205							
PPYD BACSU	RECA PROTEIN	ESCHERICHIA COLI	86-116	147-174							
PPYD BACSU	RECA PROTEIN	PROTEUS MIRABILIS	86-116								
PPYD BACSU	RECA PROTEIN	PSEUDOMONAS PUTIDA	84-111								
PPYD BACSU	RECA PROTEIN	SALMONELLA TYPHIMURUM	147-174								
PPYD BACSU	EXONUCLEASE RECJ	ESCHERICHIA COLI	52-79								
PPYD BACSU	RECOMBINATION PROTEIN	BACILLUS SUBTILIS	21-48	156-184	192-247	299-316	344-378				
PPYD BACSU	DNA HELICASE RECQ	ESCHERICHIA COLI	468-495								
PPYD BACSU	GTP PYROPHOSPHOKINASE	ESCHERICHIA COLI	680-707								
PPYD BACSU	REPLICATION AND MAINTENANCE PROTEIN	BACILLUS SUBTILIS	2-36	81-108							
PPYD BACSU	REPLICATION AND MAINTENANCE PROTEIN	STAPHYLOCOCCUS AUREUS	2-36	81-108							



FCGENE	10717244	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PR12 THMA	305 RIBOSOMAL PROTEIN L12	THEMOTOGA NARITINA	8-35	56-86							
PR14 BACST	305 RIBOSOMAL PROTEIN L14	BACILLUS STEAROTHERMOPHILUS	18-45								
PR14 MICLU	305 RIBOSOMAL PROTEIN L14	MICROCOCOCCUS LUTEUS	18-45								
PR14 MYCCA	305 RIBOSOMAL PROTEIN L14	MYCOPLASMA CAPRICOLUM	51-92								
PR15 BACLI	305 RIBOSOMAL PROTEIN L15	BACILLUS LUTHERI	21-48								
PR15 BACST	305 RIBOSOMAL PROTEIN L15	BACILLUS STEAROTHERMOPHILUS	95-114								
PR15 BACSU	305 RIBOSOMAL PROTEIN L15	BACILLUS SUBTILIS	95-122								
PR15 CHLTR	305 RIBOSOMAL PROTEIN L15	CITRIMONELLA TRICHOMONATIS	110-144								
PR15 ECOLI	305 RIBOSOMAL PROTEIN L15	ESCHERICHIA COLI	79-113								
PR15 LACLA	305 RIBOSOMAL PROTEIN L15	LACTOCOCCUS LACTIS	8-35								
PR15 METVA	305 RIBOSOMAL PROTEIN L15	METHANOCOCCUS VANNIELII	64-102								
PR15 MYCCA	305 RIBOSOMAL PROTEIN L15	MYCOPLASMA CAPRICOLUM	61-135								
PR18 BACST	305 RIBOSOMAL PROTEIN L18	BACILLUS STEAROTHERMOPHILUS	31-58								
PR18 CHLTR	305 RIBOSOMAL PROTEIN L18	CITRIMONELLA TRICHOMONATIS	32-86								
PR18 HALMA	305 RIBOSOMAL PROTEIN L18	HALOARCTIA MARISORTUJ	40-107								
PR18 MYCCA	305 RIBOSOMAL PROTEIN L18	MYCOPLASMA CAPRICOLUM	61-88								
PR19 ECOLI	305 RIBOSOMAL PROTEIN L19	ESCHERICHIA COLI	25-52								
PR19 HALMA	305 RIBOSOMAL PROTEIN L19	HALOARCTIA MARISORTUJ	101-128								
PR19 METVA	305 RIBOSOMAL PROTEIN L19	METHANOCOCCUS VANNIELII	45-72								
PR19 PROXY	305 RIBOSOMAL PROTEIN L19	PROTEUS VULGARIS	159-194								
PR17 SULSO	305 RIBOSOMAL PROTEIN L17	SULFOLOBUS SOLFATARICUS	5-32	184-211							
PR20 ECOLI	305 RIBOSOMAL PROTEIN L20	ESCHERICHIA COLI	14-41								
PR20 MYCCE	305 RIBOSOMAL PROTEIN L20	MYCOPLASMA FERNENTANS	14-41								
PR20 MYCCE	305 RIBOSOMAL PROTEIN L20	BACILLUS SUBTILIS	4-38								
PR21 BACSU	305 RIBOSOMAL PROTEIN L21	ESCHERICHIA COLI	28-55								
PR22 ECOLI	305 RIBOSOMAL PROTEIN L22	METHANOCOCCUS VANNIELII	30-57								
PR23 METVA	305 RIBOSOMAL PROTEIN L23	MYCOPLASMA CAPRICOLUM	32-59								
PR23 MYCCA	305 RIBOSOMAL PROTEIN L23	HALOARCTIA MARISORTUJ	48-75								
PR24 HALMA	305 RIBOSOMAL PROTEIN L24	METHANOCOCCUS VANNIELII	61-90								
PR24 METVA	305 RIBOSOMAL PROTEIN L24	MICROCOCOCCUS LUTEUS	36-63								
PR24 MICLU	305 RIBOSOMAL PROTEIN L24	CITRIMONELLA TRICHOMONATIS	39-66								
PR29 CHLTR	305 RIBOSOMAL PROTEIN L29	ESCHERICHIA COLI	36-63								
PR29 ECOLI	305 RIBOSOMAL PROTEIN L29	MYCOPLASMA CAPRICOLUM	39-83								
PR29 MYCCA	305 RIBOSOMAL PROTEIN L29	BACILLUS STEAROTHERMOPHILUS	141-168								
PR24 BACST	305 RIBOSOMAL PROTEIN L4	MYCOPLASMA CAPRICOLUM	144-198								
PR24 MYCCA	305 RIBOSOMAL PROTEIN L4	THEMUS AQUATICUS	38-65								
PR24 THETH	305 RIBOSOMAL PROTEIN L5	BACILLUS STEAROTHERMOPHILUS	79-106								
PR26 BACST	305 RIBOSOMAL PROTEIN L6	ESCHERICHIA COLI	19-46								
PR26 ECOLI	305 RIBOSOMAL PROTEIN L6	METHANOCOCCUS VANNIELII	129-159								
PR26 METVA	305 RIBOSOMAL PROTEIN L6	BACILLUS STEAROTHERMOPHILUS	47-77								
PR26 BACST	305 RIBOSOMAL PROTEIN L9	ESCHERICHIA COLI	122-149								
PR26 ECOLI	305 RIBOSOMAL PROTEIN L9	HALOARCTIA MARISORTUJ	138-182								
PR26 HALMA	305 RIBOSOMAL PROTEIN L9	HALOARCTIA MARISORTUJ	138-182								
PR26 HALMA	305 RIBOSOMAL PROTEIN L9	HALOARCTIA MARISORTUJ	64-91	153-184							
PR26 METVA	305 RIBOSOMAL PROTEIN L9	METHANOCOCCUS VANNIELII	194-221								
PR26 HALMA	305 RIBOSOMAL PROTEIN L9	HALOARCTIA MARISORTUJ	59-86								
PR26 HALMA	305 RIBOSOMAL PROTEIN L9	HALOARCTIA MARISORTUJ	2-29								
PR26 HALMA	305 RIBOSOMAL PROTEIN L9	HALOARCTIA MARISORTUJ	2-29								
PR26 METVA	305 RIBOSOMAL PROTEIN L9	METHANOCOCCUS VANNIELII	2-29								
PR26 METVA	305 RIBOSOMAL PROTEIN L9	MICROCOCOCCUS LUTEUS	55-82	90-117							
PR26 METVA	305 RIBOSOMAL PROTEIN L9	SALMONELLA TYPHIMURUM	226-260								
PR26 METVA	305 RIBOSOMAL PROTEIN L9	STAPHYLOCOCCUS AUREUS	3-30	102-132	266-300						
PR26 METVA	305 RIBOSOMAL PROTEIN L9	SALMONELLA TYPHIMURUM	19-53								
PR26 METVA	305 RIBOSOMAL PROTEIN L9	STAPHYLOCOCCUS AUREUS	3-30	102-133	261-295						
PR26 METVA	305 RIBOSOMAL PROTEIN L9	STAPHYLOCOCCUS AUREUS	3-30	146-216							
PR26 METVA	305 RIBOSOMAL PROTEIN L9	SULFOLOBUS SOLFATARICUS	32-62								
PR26 METVA	305 RIBOSOMAL PROTEIN L9	BACILLUS AMYLOLIQUEFACIENS	31-67	129-156							



PCGENE	10711784	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
ELLENANIE	PROTEIN	ORGANISMI	1037	117-144							
PRNC_ECOLI	RIBONUCLEASE III	ESCHERICHIA COLI	1037	117-144							
PRNE_ECOLI	RIBONUCLEASE E	ESCHERICHIA COLI	413-440	628-662							
PRNP7A_BUCSU	RIBONUCLEASE P PROTEIN COMPONENT	BUCHNERA APHIDICOLA	85-114								
PRNPH_BACSU	RIBONUCLEASE PH	BACILLUS SUBTILIS	159-186								
PRNS_ECOLI	REGULATORY PROTEIN RNS	ESCHERICHIA COLI	116-160								
PRN_BACCI	RIBONUCLEASE	BACILLUS CIRCULANS	82-109								
PRN_BACIN	RIBONUCLEASE PRECURSOR	BACILLUS INTERMEDIUS	38-72								
PRP2B_BACTK	RNA POLYMERASE SIGMA-28 FACTOR PRECURSOR	BACILLUS THURINGIENSIS	72-107								
PRP2J_GITFR	RNA POLYMERASE SIGMA-33 FACTOR	CITROBACTER FREUNDII	30-57								
PRP2L_BACTK	RNA POLYMERASE SIGMA-33 FACTOR PRECURSOR	BACILLUS THURINGIENSIS	8-35	61-90							
PRP3A_ALCEU	RNA POLYMERASE SIGMA-34 FACTOR	ALCALIGENES EUTROPHIUS	229-266								
PRP3A_AZOCU	RNA POLYMERASE SIGMA-34 FACTOR	AZORHIZOBIUM CAULINODANS	174-208								
PRP3A_BACSU	RNA POLYMERASE SIGMA-34 FACTOR	BACILLUS SUBTILIS	16-43	97-124	274-308	398-423					
PRP3A_BRAJA	RNA POLYMERASE SIGMA-34 FACTOR 1	BRADYRHIZOBIUM JAPONICUM	97-124								
PRP3A_KLEPN	RNA POLYMERASE SIGMA-34 FACTOR	KLEBSIELLA PNEUMONIAE	148-182								
PRP3A_RHOCA	RNA POLYMERASE SIGMA-34 FACTOR	RHODOBACTER CAPSULATUS	155-185								
PRP3A_BRAJA	RNA POLYMERASE SIGMA-34 FACTOR 2	BRADYRHIZOBIUM JAPONICUM	145-172								
PRP3M_ALCEU	PROBABLE SIGMA(34) MODULATION PROTEIN	ALCALIGENES EUTROPHIUS	21-51								
PRP3M_ECOLI	PROBABLE SIGMA(34) MODULATION PROTEIN	ESCHERICHIA COLI	21-67								
PRP3M_SALTY	PROBABLE SIGMA(34) MODULATION PROTEIN	SALMONELLA TYPHIMURUM	21-67								
PRP7B_BUCAP	RNA POLYMERASE SIGMA-70 FACTOR	BUCHNERA APHIDICOLA	69-96	109-136	172-217	228-255	303-337				
PRP7B_CHLTR	RNA POLYMERASE SIGMA-70 FACTOR	CHLAMYDIA TRACHOMATIS	5-32								
PRP7B_ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	ESCHERICHIA COLI	327-361								
PRP7B_PSEAE	RNA POLYMERASE SIGMA-70 FACTOR	PSEUDOMONAS AERUGINOSA	334-368								
PRP7D_RICPR	RNA POLYMERASE SIGMA-70 FACTOR	RICKETTSIA PROVAZEEKII	244-321	348-382							
PRP7D_MYXXA	RNA POLYMERASE SIGMA-80 FACTOR	MYXOCOCCUS XANTHUS	208-235	318-347	359-386						
PRP7C_SYNPP	BILIN BIOSYNTHESIS PROTEIN RBCF	SYNECHOCOCCUS SP	180-207								
PRP7A_BACSU	DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN	BACILLUS SUBTILIS	55-107								
PRP7A_ECOLI	DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN	ESCHERICHIA COLI &	57-105								
PRP7A_HALHA	DNA-DIRECTED RNA POLYMERASE SUBUNIT A	SALMONELLA TYPHIMURUM	863-904								
PRP7A_HALMO	DNA-DIRECTED RNA POLYMERASE SUBUNIT A	HALOBACTERIUM HALOBILIUM	239-270								
PRP7A_METH	DNA-DIRECTED RNA POLYMERASE SUBUNIT A	HALOCOCCUS MORRUIAE	218-245	486-513	642-669						
PRP7A_SULAC	DNA-DIRECTED RNA POLYMERASE SUBUNIT A	METHANOBACTERIUM THERMAUTOTROPICUM	222-256	500-537	691-720						
PRP7A_THECE	DNA-DIRECTED RNA POLYMERASE SUBUNIT A	SULFOLOBUS ACIDOCALDARIUS	228-262								
PRP7B_ECOLI	DNA-DIRECTED RNA POLYMERASE BETA CHAIN	THERMOCOCCUS CELER	599-626	1011-1038							
PRP7B_MYCLE	DNA-DIRECTED RNA POLYMERASE BETA CHAIN	ESCHERICHIA COLI	733-760	1084-1111							
PRP7B_SALTY	DNA-DIRECTED RNA POLYMERASE BETA CHAIN	MYCOBACTERIUM LEPRAE	599-626								
PRP7B_SULAC	DNA-DIRECTED RNA POLYMERASE BETA CHAIN	SALMONELLA TYPHIMURUM	160-187	958-985	1011-1038						
PRP7B_THEMA	DNA-DIRECTED RNA POLYMERASE BETA CHAIN	SULFOLOBUS ACIDOCALDARIUS	255-282	314-361	827-861						
PRP7C_ANASP	DNA-DIRECTED RNA POLYMERASE GAMMA CHAIN	THERMOTOGA MARITIMA	150-277								
PRP7C_ECOLI	DNA-DIRECTED RNA POLYMERASE BETA CHAIN	ANABAEANA SP	152-194								
PRP7C_HALHA	DNA-DIRECTED RNA POLYMERASE SUBUNIT C	ESCHERICHIA COLI	786-813	948-994	1231-1257						
PRP7C_HALMO	DNA-DIRECTED RNA POLYMERASE SUBUNIT C	HALOBACTERIUM HALOBILIUM	175-202								
PRP7C_HALHA	DNA-DIRECTED RNA POLYMERASE SUBUNIT C	HALOCOCCUS MORRUIAE	27-54	117-144	202-234						
PRP7C_MYCLE	DNA-DIRECTED RNA POLYMERASE BETA CHAIN	METHANOBACTERIUM THERMAUTOTROPICUM	58-85	272-302	372-394						
PRP7C_NOSCO	DNA-DIRECTED RNA POLYMERASE GAMMA CHAIN	MYCOBACTERIUM LEPRAE	273-300	860-887	911-938	1131-1158					
PRP7C_SULAC	DNA-DIRECTED RNA POLYMERASE SUBUNIT C	NOSTOC COMMUNE	36-63	150-192							
PRP7C_THECE	DNA-DIRECTED RNA POLYMERASE SUBUNIT A*	SULFOLOBUS ACIDOCALDARIUS	172-214	224-251							
PRP7D_NOSCO	DNA-DIRECTED RNA POLYMERASE DELTA CHAIN	THERMOCOCCUS CELER	21-58								
PRP7D_ECOLI	DNA-DIRECTED RNA POLYMERASE DELTA CHAIN	NOSTOC COMMUNE	72-116	402-449	539-566						
PRP7D_HALHA	DNA-DIRECTED RNA POLYMERASE SIGMA FACTOR KATF	ESCHERICHIA COLI	5-39								
PRP7D_HALMO	DNA-DIRECTED RNA POLYMERASE SUBUNIT B*	ESCHERICHIA COLI	281-308								
PRP7D_HALHA	DNA-DIRECTED RNA POLYMERASE SIGMA-A FACTOR	HALOBACTERIUM HALOBILIUM	91-118								
PRP7A_AGITU	RNA POLYMERASE SIGMA-A FACTOR	AGROBACTERIUM TUMEFACIENS	310-347	397-427							
PRP7A_ANASP	RNA POLYMERASE SIGMA-A FACTOR	ANABAEANA SP	71-105								
PRP7A_CLOAB	RNA POLYMERASE SIGMA-A FACTOR	CLOSTRIDIUM ACETOBUTYLICUM	2-29								
PRP7A_STRAU	RNA POLYMERASE SIGMA FACTOR RPOD*	STREPTOMYCES AUREOFACIENS	278-305								

GENE	1071214	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
ULKRAJIE	PROTEIN	ORGANISMI	4.31									
PRPSB ANAP	RNA POLYMERASE SIGMA-B FACTOR	ANABAEANA SP	4.31									
PRPSB BACSU	RNA POLYMERASE SIGMA-B FACTOR	BACILLUS SUBTILIS	5.35	169.196	190.210							
PRPSB MYAXA	RNA POLYMERASE SIGMA-B FACTOR	MYXOCOCCUS XANTHIUS	47.74									
PRPSD STAU	RNA POLYMERASE SIGMA-B FACTOR	STIGMATELLA AURANTIACA	96.123									
PRPSC ANASP	RNA POLYMERASE SIGMA-D FACTOR	ANABAEANA SP	58.83									
PRPSD BACSU	RNA POLYMERASE SIGMA-D FACTOR	BACILLUS SUBTILIS	192.249									
PRPSE BACSU	RNA POLYMERASE SIGMA-E FACTOR	BACILLUS SUBTILIS	61.90									
PRPSE CLOAR	RNA POLYMERASE SIGMA-E FACTOR	CLOSTRIDIUM ACETOBUTYLICUM	14.41	116.160								
PRPSF BACL1	RNA POLYMERASE SIGMA-F FACTOR	BACILLUS LICHENIFORMIS	4.31	191.248								
PRPSF BACME	RNA POLYMERASE SIGMA-F FACTOR	BACILLUS MEGATERIUM	191.223									
PRPSF BACSU	RNA POLYMERASE SIGMA-F FACTOR	BACILLUS SUBTILIS	4.31	191.248								
PRPSH BACL1	RNA POLYMERASE SIGMA-H FACTOR	BACILLUS LICHENIFORMIS	191.218									
PRPSH BACSU	RNA POLYMERASE SIGMA-H FACTOR	BACILLUS SUBTILIS	186.213									
PRPSK BACSU	RNA POLYMERASE SIGMA-K FACTOR	BACILLUS SUBTILIS	75.109	189.216								
PRPSW STAAU	RNA POLYMERASE SIGMA FACTOR PLAC	STAPHYLOCOCCUS AUREUS	19.46									
PRPSX BACTK	POSSIBLE RNA POLYMERASE SIGMA-G FACTOR	STREPTOMYCES COELICOLOR	232.273									
PRPSD ECOLI	POSSIBLE RNA POLYMERASE SIGMA-G FACTOR	BACILLUS THURINGIENSIS	33.40									
PRPSI BACSU	30S RIBOSOMAL PROTEIN S10	ESCHERICHIA COLI	3.70									
PRPSI BACSU	30S RIBOSOMAL PROTEIN S11	BACILLUS SUBTILIS	8.42									
PRPSI BACSU	30S RIBOSOMAL PROTEIN S13	BACILLUS SUBTILIS	44.85									
PRPSI BACSU	30S RIBOSOMAL PROTEIN S17	METHANOCOCCUS VANNIELII	34.73									
PRPSI ECOLI	30S RIBOSOMAL PROTEIN S1	ESCHERICHIA COLI	99.126	144.171								
PRPSI PROSP	30S RIBOSOMAL PROTEIN S1	PROVIDENCIA SP	99.46	265.292	149.376							
PRPSI RHIME	30S RIBOSOMAL PROTEIN S1	RHIZOBIUM MELLOTTI	91.125	172.217								
PRPSI BACST	30S RIBOSOMAL PROTEIN S31	BACILLUS STEAROTHERIOPHILUS	1.28									
PRPS2 SPICT	30S RIBOSOMAL PROTEIN S2	SPIROPLASMA CITRI	91.125									
PRPS3 ACHLA	30S RIBOSOMAL PROTEIN S3	ACHOLEPLASMA LAIDLAWII	83.110									
PRPS1 MYCCA	30S RIBOSOMAL PROTEIN S3	MYCOPLASMA CAPRICOLUM	71.106	134.163								
PRPS4 ECOLI	30S RIBOSOMAL PROTEIN S4	ESCHERICHIA COLI	50.77									
PRPS1 HALMA	30S RIBOSOMAL PROTEIN S5	HALOARGULA MARISORTUI	160.187									
PRPS3 MYCCA	30S RIBOSOMAL PROTEIN S5	MYCOPLASMA CAPRICOLUM	35.62	182.216								
PRPS6 THIEH	30S RIBOSOMAL PROTEIN S6	THERMUS AQUATICUS	16.43									
PRPS7 METVA	30S RIBOSOMAL PROTEIN S7	METHANOCOCCUS VANNIELII	69.96									
PRPS7 MYGLE	30S RIBOSOMAL PROTEIN S7	MYCOBACTERIUM LEPTAE	32.49									
PRPS1 MICLU	30S RIBOSOMAL PROTEIN S8	MICROCOCCUS LUTEUS	103.130									
PRPS8 MYCCA	30S RIBOSOMAL PROTEIN S8	MYCOPLASMA CAPRICOLUM	41.78									
PRPSGA ECOLI	FERRITIN LIKE PROTEIN	ESCHERICHIA COLI	80.107									
PRPSGA ECOLI	RNA-DIRECTED DNA POLYMERASE	ESCHERICHIA COLI	225.268									
PSACB BACAM	LEVANSUCRASE PRECURSOR	BACILLUS AMYLOLIQUEFACIENS	175.202	254.281								
PSACB BACSU	LEVANSUCRASE PRECURSOR	BACILLUS SUBTILIS	175.202	254.288								
PSACQ BACL1	SACQ REGULATORY FACTOR	BACILLUS LICHENIFORMIS	31.63	155.189	314.369							
PSAGP STRMU	STREPTOCOCCUS PRECURSOR	STREPTOCOCCUS MUTANS	2.46									
PSAGT BACSU	SACPA OPERON ANTITERMINATOR	BACILLUS SUBTILIS	102.139	189.216								
PSAGP STRPY	STREPTOCOCCAL ACID GLYCOPROTEIN	STREPTOCOCCUS PYOGENES	294.331	362.389								
PSAOX BACSN	SACOSINE OXIDASE	BACILLUS SP	350.377									
PSAS2 CLOBI	SPORE PROTEIN	CLOSTRIDIUM BIFERMENTANS	17.47									
PSASQ BACCE	SPORE PROTEIN GAMMA-TYPE	BACILLUS CEREUS	31.58									
PSASQ BACST	SPORE PROTEIN GAMMA-TYPE	BACILLUS STEAROTHERIOPHILUS	37.64									
PSBCC ECOLI	EXONUCLEASE SBCC	ESCHERICHIA COLI	218.260	337.364	535.385	672.656	778.812	821.865	915.942			
PSBCD ECOLI	EXONUCLEASE SBCC	ESCHERICHIA COLI	137.164	314.397								
PSBM ECOLI	SBM PROTEIN	ESCHERICHIA COLI	5.32	436.470	553.580							
PSBP BACSU	SBP PROTEIN	BACILLUS SUBTILIS	28.55									
PSCPA STRPY	CIA PEPTIDASE PRECURSOR	STREPTOCOCCUS PYOGENES	176.160	784.811	831.880							
PSCRB KLEPN	SUCROSE-6-PHOSPHATE HYDROLASE	KLEBSIELLA PNEUMONIAE	174.201									
PSCRD LACL1	SUCROSE-6-PHOSPHATE HYDROLASE	LACTOCOCCUS LACTIS	182.217	354.383	375.422							
PSCRD STRMU	SUCROSE-6-PHOSPHATE HYDROLASE	STREPTOCOCCUS MUTANS	335.362									
PSCRK SALTH	FRUCTOKINASE	SALMONELLA THOMPSON	97.124									



PGENE	10717144	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PSPAK_BACSU	SPINOR PROTEIN SPAK	BACILLUS SUBTILIS	90-107	224-231	790-724						
PSAP STRAU	CELL SURFACE ANTIGEN VII PRECURSOR	STREPTOCOCCUS MUTANS	122-276	281-463	538-565	576-610	1071-1098	1155-1182	1377-1430		
PSAP_BACSU	REGULATORY PROTEIN	BACILLUS SUBTILIS	4-31	172-199							
PSPAT_BACSU	SUBTILIN TRANSPORT PROTEIN SPAT	BACILLUS SUBTILIS	55-82	226-267							
PSPEC STRPY	EXOTOXIN TYPE C PRECURSOR	STREPTOCOCCUS PYOGENES	12-39								
PSPIR SPICI	SPIRALIN	SPIROPLASMA CITRI	82-109	153-182							
PSPIR SPIIME	SPIRALIN	SPIROPLASMA MELLIFERUM	195-222								
PSPT_ECOLI	GUAN-3,5-BIS(DIPIIOS)3-PYROPHOSPHOHYDROLA	ESCHERICHIA COLI	637-664								
PSPPA_ECOLI	PROTEASE IV	ESCHERICHIA COLI	278-305								
PSQHC_ZYMAO	SQUALENE-HOPENE CYCLASE	ZYMONOMONAS MOBILIS	590-617								
PSRFA_BACSU	SURFACTIN SYNTHETASE SUBUNIT A	BACILLUS SUBTILIS	158-186	244-271							
PSRPI_ECOLI	SIGNAL RECOGNITION PARTICLE PROTEIN	ESCHERICHIA COLI	301-328								
PSRPI_MYCMY	SIGNAL RECOGNITION PARTICLE PROTEIN	MYCOPLASMA MYCOIDES	21-65	107-141	394-428						
PSSAT_PASHA	SEROTYPE-SPECIFIC ANTIGEN I PRECURSOR	PASTEURELLA HAEMOLYTICA	151-178	358-385	465-518	529-570	860-904				
PSBAB STRSA	ADHESIN B PRECURSOR	STREPTOCOCCUS PARASANGUIS	32-59								
PSBB_ECOLI	ADHESIN B PRECURSOR	STREPTOCOCCUS SANGUIS	21-59	101-128							
PSBB_ECOLI	SINGLE-STRAND BINDING PROTEIN	ESCHERICHIA COLI	68-95								
PSBB_PROMI	SINGLE-STRAND BINDING PROTEIN	PROTEUS MIRABILIS	63-104								
PSBB_SERMA	SINGLE-STRAND BINDING PROTEIN	SERRA TIA MARCESCENS	61-104								
PSBP STRSA	AGGLUTININ RECEPTOR PRECURSOR	STREPTOCOCCUS SANGUIS	131-173	178-287	295-483	565-592	676-710	1081-1131			
PSBAV STRAV	STREPTAVIDIN PRECURSOR	STREPTONOCYTES AVIDINII	125-152								
PSIA_ECOLI	STREPTOTHRICIN ACETYLTRANSFERASE	ESCHERICHIA COLI	66-93								
PSICI STRAU	STAPHYLOCOAGULASE PRECURSOR	STAPHYLOCOCCUS AUREUS	90-119	172-199	280-311						
PSICL STRAU	STAPHYLOCOAGULASE PRECURSOR	STAPHYLOCOCCUS AUREUS	90-117	264-291							
PSIC_CLOBE	L-TRANS-TRANS CONTROL PROTEIN	CLOSTRIDIUM BEEUINGKII	47-74								
PSIPA_ECOLI	STPA PROTEIN	ESCHERICHIA COLI	36-63								
PSIRI STRGR	INOSANINE-PHOSPHATE AMIDINOTRANSFERASE I	STREPTONOCYTES GRISEUS	183-210								
PSIRP STRQK	STREPTOKINASE C PRECURSOR	STREPTOCOCCUS EQUIMILILIS	209-236	281-308							
PSIRP STRPY	STREPTOKINASE A PRECURSOR	STREPTOCOCCUS PYOGENES	209-236								
PSIRP STRSP	STREPTOKINASE G PRECURSOR	STREPTOCOCCUS SP	209-236	281-308							
PSUBI_BACSU	MINOR EXTRACELLULAR PROTEASE EPR PREC	BACILLUS SUBTILIS	435-462	522-563	605-639						
PSUBI_BACSU	BACILLOPEPTIDASE F PRECURSOR	BACILLUS SUBTILIS	40-67	89-116	121-148	554-597					
PSUBI_SALTY	SULFATE-BINDING PROTEIN	SALMONELLA TYPHIMURUM	37-74								
PSUBI_STRPY	SULFATE-BINDING PROTEIN PRECURSOR	SYNECHOCOCUS SP	61-94								
PSUBI_STRYJ	SULFATE-BINDING PROTEIN PRECURSOR	SYNECHOCYSTIS SP	64-91								
PSUBI_BACLI	SUBTILISIN CARLSBERG PRECURSOR	BACILLUS LICHENIFORMIS	191-222								
PSUBI_BACMS	SUBTILISIN	BACILLUS MESENTERICUS	91-118								
PSUBI_BACSP	SUBTILISIN PRECURSOR	BACILLUS SP	36-63	250-277							
PSUBI_BACSD	SUBTILISIN ARYLACCHARITICUS PRECURSOR	BACILLUS SUBTILIS	197-224								
PSUBI_BACSU	SUBTILISIN I PRECURSOR	BACILLUS SUBTILIS	86-117								
PSUBI_BACST	SUBTILISIN J PRECURSOR	BACILLUS STEAROTHERMOPHILUS	197-224								
PSUBI_BACSU	SUBTILISIN E PRECURSOR	BACILLUS SUBTILIS	197-224								
PSUBI_BACSU	MINOR EXTRACELLULAR PROTEASE VMP PREC	BACILLUS SUBTILIS	55-108	613-654	741-768						
PSUCC_ECOLI	SUCCINYL-COA SYNTHETASE BETA	ESCHERICHIA COLI	62-89								
PSUCP_AGRVI	SUCROSE PHOSPHORYLASE	AGROBACTERIUM VITIS	449-476								
PSULA_ENTAE	CELL DIVISION INHIBITOR	ENTEROBACTER AEROGES	112-139								
PSYA_ECOLI	ALANYL-TRNA SYNTHETASE	ESCHERICHIA COLI	357-287	725-752	790-821						
PSYD_ECOLI	ASPARTYL-TRNA SYNTHETASE	ESCHERICHIA COLI	310-357								
PSYE_BACST	GLUTAMYL-TRNA SYNTHETASE	BACILLUS STEAROTHERMOPHILUS	49-76								
PSYE_BACSU	GLUTAMYL-TRNA SYNTHETASE	BACILLUS SUBTILIS	49-76	351-386							
PSYE_THETH	GLUTAMYL-TRNA SYNTHETASE	THERMUS AQUATICUS	405-432								
PSYFA_BACSU	PHENYLALANYL-TRNA SYNTHETASE A CHAIN	BACILLUS SUBTILIS	7-34								
PSYFB_BACSU	PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN	BACILLUS SUBTILIS	340-367	407-441							
PSYFB_ECOLI	PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN	ESCHERICHIA COLI	546-573	607-634	744-771						
PSYOB_ECOLI	GLYCYL-TRNA SYNTHETASE BETA CHAIN	ESCHERICHIA COLI	354-381	487-514							
PSYH_STRQK	HISTIDYL-TRNA SYNTHETASE	STREPTOCOCCUS EQUIMILILIS	378-403								
PSYI_METH	ISOLEUCYL-TRNA SYNTHETASE	METHANOBACTERIUM THERMAUTOTROPHICUM	1010-1037								

PCGENE	10717814	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PSY1_ECOLI	LYSYL-TRNA SYNTHETASE	ESCHERICHIA COLI	281-310								
PSY2_ECOLI	LYSYL-TRNA SYNTHETASE, HEAT INDUCIBLE	ESCHERICHIA COLI	45-72	283-310							
PSY3_ECOLI	LEUCYL-TRNA SYNTHETASE	ESCHERICHIA COLI	220-247								
PSY4_ECOLI	METHIONYL-TRNA SYNTHETASE	BACILLUS STEAROTHERIOPHILUS	69-99								
PSY5_ECOLI	PROLYL-TRNA SYNTHETASE	ESCHERICHIA COLI	87-124								
PSY6_ECOLI	GLUTAMINYL-TRNA SYNTHETASE	ESCHERICHIA COLI	541-568								
PSY7_ECOLI	SYRD PROTEIN	PSEUDOMONAS SYRINGAE	394-421								
PSY8_ECOLI	ARGINYL-TRNA SYNTHETASE	ESCHERICHIA COLI	460-483								
PSY9_ECOLI	THREONYL-TRNA SYNTHETASE	BACILLUS SUBTILIS	500-574								
PSY10_ECOLI	VALYL-TRNA SYNTHETASE	BACILLUS STEAROTHERIOPHILUS	401-428	605-639							
PSY11_ECOLI	VALYL-TRNA SYNTHETASE	ESCHERICHIA COLI	603-630	809-843							
PSY12_ECOLI	TRYPHANYL-TRNA SYNTHETASE	BACILLUS STEAROTHERIOPHILUS	300-327	882-912	924-951						
PSY13_ECOLI	TYROSYL-TRNA SYNTHETASE 1	BACILLUS SUBTILIS	204-231	239-266							
PSY14_ECOLI	TYROSYL-TRNA SYNTHETASE 2	BACILLUS SUBTILIS	81-115	375-409							
PSY15_ECOLI	TYROSYL-TRNA SYNTHETASE	BACILLUS CALDOTENAX	69-96								
PSY16_ECOLI	ENZYME ECOR1240 I IN PROTEIN	ESCHERICHIA COLI	295-322	372-416							
PSY17_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	126-167	405-432	485-512						
PSY18_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	30-57	624-651	702-736	768-795	843-870	966-1000			
PT11_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	158-263								
PT12_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	154-181								
PT13_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	279-306								
PT14_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	278-312								
PT15_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	249-283								
PT16_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	279-306								
PT17_ECOLI	ENZYME ECOR1240 R PROTEIN	SALMONELLA POTSDAM	396-423								
PT18_ECOLI	ENZYME ECOR1240 R PROTEIN	SALMONELLA TYPHIMURUM	194-221	276-304	402-429						
PT19_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	138-166	265-295	406-440	639-682	687-728	926-934			
PT20_ECOLI	ENZYME ECOR1240 R PROTEIN	ACINETOBACTER CALCOACETICUS	49-76								
PT21_ECOLI	ENZYME ECOR1240 R PROTEIN	BACILLUS SUBTILIS	1-43	123-223	236-280						
PT22_ECOLI	ENZYME ECOR1240 R PROTEIN	BACILLUS SUBTILIS	1-45	338-384	401-440	532-559					
PT23_ECOLI	ENZYME ECOR1240 R PROTEIN	CITROBACTER FREUNDII	35-62								
PT24_ECOLI	ENZYME ECOR1240 R PROTEIN	HERPETOSSIPHON AURANTIACUS	176-215								
PT25_ECOLI	ENZYME ECOR1240 R PROTEIN	HERPETOSSIPHON AURANTIACUS	243-273								
PT26_ECOLI	ENZYME ECOR1240 R PROTEIN	DESULFOVIBRIO DESULFURICANS	85-122								
PT27_ECOLI	ENZYME ECOR1240 R PROTEIN	STREPTOCOCCUS PNEUMONIAE	213-240								
PT28_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	2-29								
PT29_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	333-360								
PT30_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	128-155	214-241							
PT31_ECOLI	ENZYME ECOR1240 R PROTEIN	FLAVOBACTERIUM ORKANOITIS	302-336								
PT32_ECOLI	ENZYME ECOR1240 R PROTEIN	HAEMOPHILUS INFLUENZAE	6-38	40-96							
PT33_ECOLI	ENZYME ECOR1240 R PROTEIN	HAEMOPHILUS INFLUENZAE	77-125								
PT34_ECOLI	ENZYME ECOR1240 R PROTEIN	HAEMOPHILUS INFLUENZAE	23-50								
PT35_ECOLI	ENZYME ECOR1240 R PROTEIN	HAEMOPHILUS INFLUENZAE	97-138								
PT36_ECOLI	ENZYME ECOR1240 R PROTEIN	KLERSIELLA PNEUMONIAE	18-45	178-203							
PT37_ECOLI	ENZYME ECOR1240 R PROTEIN	MORAXELLA BOVIS	15-61	187-215	225-232						
PT38_ECOLI	ENZYME ECOR1240 R PROTEIN	MORAXELLA BOVIS	3-30	158-185	337-364						
PT39_ECOLI	ENZYME ECOR1240 R PROTEIN	MORAXELLA BOVIS	105-131								
PT40_ECOLI	ENZYME ECOR1240 R PROTEIN	METHANOBACTERIUM THERMOPHILICUM	117-144	231-258							
PT41_ECOLI	ENZYME ECOR1240 R PROTEIN	NEISSERIA GONORRHOEAE	532	41-68	395-446						
PT42_ECOLI	ENZYME ECOR1240 R PROTEIN	STREPTOCOCCUS SANGUIS	206-243	258-288							
PT43_ECOLI	ENZYME ECOR1240 R PROTEIN	STAGELLA SONNEI	70-102								
PT44_ECOLI	ENZYME ECOR1240 R PROTEIN	SHAPYLOCOCCUS AUREUS	144-181								
PT45_ECOLI	ENZYME ECOR1240 R PROTEIN	SALMONELLA INFANTIS	61-88								
PT46_ECOLI	ENZYME ECOR1240 R PROTEIN	SERRATIA MARCESCENS	147-181								
PT47_ECOLI	ENZYME ECOR1240 R PROTEIN	THERMUS AQUATICUS	203-237								
PT48_ECOLI	ENZYME ECOR1240 R PROTEIN	ESCHERICHIA COLI	37-71	236-296	378-405						
PT49_ECOLI	ENZYME ECOR1240 R PROTEIN	BACILLUS CEREUS	62-89	256-283							



PCGENE	1071171.4	Prokaryotic Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILENAME	PROTEIN	ORGANISM	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PTHER_BACTH	THERMOLYSIN	BACILLUS THERMOPROTEOLYTICUS	86-113								
PTHER_THERVU	THERMITASE	THERMOACTINOMYCES VULGARIS	131-161								
PTHIC_ECOLI	THIC PROTEIN	ESCHERICHIA COLI	212-263	301-318							
PTHIO_ECOLI	THIO PROTEIN	ESCHERICHIA COLI	138-165								
PTHIS_SULAC	THERMOPHILIN PRECURSOR	SULFOLOBUS ACIDOCALDARIUS	135-172	199-213							
PTHIC_BRELA	THREONINE SYNTHASE	BREVIDACTERIUM LACTOFERMENTUM	288-315								
PTHTR_SACER	PUTATIVE THIOSULFATE SULFURTRANSFERASE	SACCHAROPOLYSPORA ERYTHRAEA	68-96								
PTIG_ECOLI	TRIGGER FACTOR	ESCHERICHIA COLI	184-171								
PTNPA_TREPA	TREPONEMAL MEMBRANE PROTEIN A PRECURSOR	TREPONEMA PALLIDUM	236-266								
PTNPB_TREPA	TREPONEMAL MEMBRANE PROTEIN B PRECURSOR	TREPONEMA PALLIDUM	44-71								
PTNPB_TREPH	TREPONEMAL MEMBRANE PROTEIN B PRECURSOR	TREPONEMA PHAGEDENIS	41-68								
PTNAB_ECOLI	LOW AFFINITY TRYPTOPHAN PEMEASE	ESCHERICHIA COLI	74-108								
PTNPA_STAUAU	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	52-79	322-349							
PTNP7_ENTFA	TRANSPOSASE	ENTEROCOCCUS FAECALIS	59-97	111-138							
PTNPA_STAUAU	TRANSPOSASE A	STAPHYLOCOCCUS AUREUS	151-178								
PTNPB_STAUAU	TRANSPOSASE B	STAPHYLOCOCCUS AUREUS	589-625								
PTNPI_BACTU	TNP1 RESOLVASE	BACILLUS THURINGIENSIS	7-62	65-92	174-201						
PTNSB_ECOLI	TRANSPOSON TN7 TRANSPOSITION PROTEIN TNSB	ESCHERICHIA COLI	99-126	510-537							
PTNSC_ECOLI	TRANSPOSON TN7 TRANSPOSITION PROTEIN TNSC	ESCHERICHIA COLI	32-59	314-341							
PTNSD_ECOLI	TRANSPOSON TN7 TRANSPOSITION PROTEIN TNSD	ESCHERICHIA COLI	339-366								
PTNSE_ECOLI	TRANSPOSON TN7 TRANSPOSITION PROTEIN TNSE	ESCHERICHIA COLI	403-490								
PTOD1_PSEPU	TOLUENE 1,2-DIOXYGENASE ALPHA SUBUNIT	PSEUDOMONAS PUTIDA	36-63								
PTOD2_PSEPU	TOLUENE 1,2-DIOXYGENASE BETA SUBUNIT	PSEUDOMONAS PUTIDA	119-153								
PTODA_PSEPU	TOLUENE 1,2-DIOXYGENASE SYSTEM	PSEUDOMONAS PUTIDA	179-213								
PTOD1_PSEPU	TODF PRODUCT HYDRATASE	PSEUDOMONAS PUTIDA	143-170								
PTOLA_ECOLI	TOLA PROTEIN	ESCHERICHIA COLI	101-138								
PTOLC_ECOLI	OUTER MEMBRANE PROTEIN TOLC PRECURSOR	ESCHERICHIA COLI	144-178	184-211	239-266	348-375	383-443				
PTOP1_SYNP7	DNA TOPOISOMERASE I	SYNECHOCOCCUS SP	203-230								
PTORA_ECOLI	TRIMETHYLAMINE-N-OXIDE REDUCTASE	ESCHERICHIA COLI	707-824								
PTOX1_BORPE	PERTUSSIS TOXIN SUBUNIT 1 (S1) PRECURSOR	BORDETELLA PERTUSSIS	179-206								
PTOX2_BORPE	PERTUSSIS TOXIN SUBUNIT 2 (S2) PRECURSOR	BORDETELLA PERTUSSIS	58-85								
PTOXA_CLODI	TOXIN A	CLOSTRIDIUM DIFFICILE	20-48	99-159	204-231	342-369	373-414	847-962	966-994	997-1024	1348-1402
PTOXA_PSEAB	EXOTOXIN A PRECURSOR	PSEUDOMONAS AERUGINOSA	470-497								
PTOXD_CLODI	TOXIN B	CLOSTRIDIUM DIFFICILE	38-72	133-163	199-241	825-869	923-950	1334-1388	1403-1433	1506-1565	1716-1747
PTOX5_VIBCH	TRANSMEMBRANE REGULATORY PROTEIN TOX5	VIBRIO CHOLERAE	13-40								
PTPF1_TREPA	ANTIGEN TPF1	TREPONEMA PALLIDUM	106-143								
PTPIS_ECOLI	TRIOSEPHOSPHATE ISOMERASE	ESCHERICHIA COLI	83-110								
PTPIS_MORSP	TRIOSEPHOSPHATE ISOMERASE	MORAXELLA SP	139-166								
PTPR_FORGI	THIOL PROTEINASE PRECURSOR	PORPHYROMONAS GINGIVALIS	117-144								
PTRM_AGR13	TRYPTOPHAN 2-MONOOXYGENASE	AGROBACTERIUM TUMEFACIENS	239-266	501-529							
PTRM_AGR14	TRYPTOPHAN 2-MONOOXYGENASE	AGROBACTERIUM TUMEFACIENS	239-266	501-529							
PTRM_PSESS	TRYPTOPHAN 2-MONOOXYGENASE	PSEUDOMONAS SYRINGAE	41-68								
PTRA1_STAUAU	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	58-113								
PTRA2_STAUAU	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	11-38	58-113							
PTRA3_ECOLI	TRANSPOSASE	ESCHERICHIA COLI	721-755								
PTRA3_RHME	TRANSPOSASE	RHIZOBIUM MELILOTI	179-206								
PTRA3_STAUAU	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	33-60	68-95							
PTRA4_ECOLI	TRANSPOSASE	ESCHERICHIA COLI	181-208	308-340	720-734						
PTRA4_SHRO	TRANSPOSASE	SHIGELLA SONNEI	51-78	200-227	231-238						
PTRA7_ECOLI	TRANSPOSASE	ESCHERICHIA COLI	729-756								
PTRA9_MYCTU	PUTATIVE TRANSPOSASE	MYCOBACTERIUM TUBERCULOSIS	159-186								
PTRA9_BACTB	IS321B PROBABLE TRANSPOSASE	BACILLUS THURINGIENSIS	281-308	419-446							
PTRA9_BACTB	IS321C PROBABLE TRANSPOSASE	BACILLUS THURINGIENSIS	281-308	419-446							
PTRA9_STAUAU	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	4-31	45-72							
PTROX_BACTB	IS321 PROBABLE TRANSPOSASE	BACILLUS THURINGIENSIS	281-308	419-446							
PTRA_BACTU	TRANSPOSASE	BACILLUS THURINGIENSIS	93-127	509-539							

PGCENE	10717244	Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
ELANAP	PROTEIN	ORGANISMI	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
PTPA_PSEAE	TRANSPORSE	PSEUDOMONAS AERUGINOSA	127-134	721-755										
PTRB1_ECOLI	TRAB PROTEIN	ESCHERICHIA COLI	113-143											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	12-39											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	70-97											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	1006-1033											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	1102-1149											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	844-931											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	207-348											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	362-403	477-508										
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	280-307											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	5-32	105-132										
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	91-88	630-657	831-853	865-895								
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	195-222	318-345										
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	155-209	397-424	882-914	1330-1377								
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	155-209	397-424	882-914	1330-1377								
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	47-74	328-371										
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	36-63											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	5-32											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	107-137											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	115-142	226-253										
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	220-247											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	241-275											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	176-203											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	79-113											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	76-103	318-345										
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	172-199											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	83-117											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	77-104	164-191										
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	56-83											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	229-256											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	205-232											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	148-175											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	346-376											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	223-250	260-294										
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	205-232											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	3-29											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	33-60											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	165-226											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	142-191											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	145-179											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	139-166											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	191-218											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	143-183	298-328										
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	9-36	34-81										
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	12-39											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	4-31											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	5-32											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	9-43											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	5-32											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	147-174											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	83-119											
PTRD1_ECOLI	TRD1 PROTEIN	ESCHERICHIA COLI	184-221											



PCGENE	101112844	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PTV1_SALT	TRAY PROTEIN	SALMONELLA TYPHIMURUM	30-57						
PTV2_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	80-107						
PTV3_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	126-153						
PTV4_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	29-63	102-129					
PTV5_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	232-252						
PTV6_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	81-113						
PTV7_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	57-91	107-134					
PTV8_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	117-147	514-561	1019-1051				
PTV9_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	106-143						
PTV10_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	244-271	312-342					
PTV11_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	329-370						
PTV12_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	483-510						
PTV13_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	139-173						
PTV14_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	75-109						
PTV15_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	69-96						
PTV16_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	276-303	316-343					
PTV17_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	276-303	316-343					
PTV18_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	204-231						
PTV19_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	30-57						
PTV20_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	130-384						
PTV21_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	13-42						
PTV22_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	72-99						
PTV23_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	72-99						
PTV24_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	13-40	483-517					
PTV25_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	62-99						
PTV26_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	17-44						
PTV27_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	57-84						
PTV28_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	20-47						
PTV29_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	44-98	150-223	276-303				
PTV30_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	56-83						
PTV31_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	56-83						
PTV32_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	527-554	871-898					
PTV33_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	579-606	619-646	614-718	922-949			
PTV34_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	33-60						
PTV35_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	342-372	311-338					
PTV36_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	37-64	333-362					
PTV37_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	280-307						
PTV38_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	182-209						
PTV39_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	177-211						
PTV40_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	138-172						
PTV41_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	190-227						
PTV42_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	190-227						
PTV43_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	32-59	212-239					
PTV44_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	32-59	212-239					
PTV45_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	32-59	212-239					
PTV46_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	81-108						
PTV47_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	81-108						
PTV48_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	149-176	265-292					
PTV49_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	42-76	113-147	637-684				
PTV50_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	42-69	84-125	637-680				
PTV51_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	42-69	84-125	637-680				
PTV52_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	37-71	107-134	187-214	252-291			
PTV53_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	16-46						
PTV54_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	34-61						
PTV55_SALT	TRAY PROTEIN	STREPTOMYCES GRISEUS	106-137						

PCGENE	10711714	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PVISC_ECOLI	VISC PROTEIN	ESCHERICHIA COLI	47-74							
PVLP1_MYCH	VARIANT SURFACE ANTIGEN A PRECURSOR	MYCOPLASMA HYORUMINIS	74-112							
PV100_BORHE	OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR	BORRELIA HERMSII	54-81							
PV201_BORHE	OUTER MEMBRANE LIPOPROTEIN 7 PRECURSOR	BORRELIA HERMSII	332-359							
PV211_BORHE	OUTER MEMBRANE LIPOPROTEIN 21 PRECURSOR	BORRELIA HERMSII	330-357							
PV212_BORHE	OUTER MEMBRANE LIPOPROTEIN 24 PRECURSOR	BORRELIA HERMSII	47-143							
PV213_BORHE	OUTER MEMBRANE LIPOPROTEIN 25 PRECURSOR	BORRELIA HERMSII	315-316							
PVNF4_AZOVI	NITROGEN FIXATION PROTEIN VNFA	AZOTOBACTER VINELANDII	158-188	218-245						
PVNF6_AZOCH	NITROGENASE VANADIUM-IRON PROTEIN	AZOTOBACTER CIRCOCOCUM MCD 1	68-95							
PVNF6_AZOVI	NITROGENASE VANADIUM-IRON PROTEIN	AZOTOBACTER VINELANDII	68-95	372-403						
PVRP1_SALCH	65 KD VIRULENCE PROTEIN	SALMONELLA CHOLERAE-SUIS	509-516							
PVRP2_SALDU	65 KD VIRULENCE PROTEIN	SALMONELLA DUBLIN	511-538							
PVSD6_SALDU	VIRULENCE PROTEIN VSDE	SALMONELLA DUBLIN	31-36							
PVVB4_VIBVU	CTOLYTRIN SECRETION PROTEIN	VIBRIO VULNIFICUS	10-75							
PWAPA_STRAM	WALL-ASSOCIATED PROTEIN PRECURSOR	STREPTOCOCCUS MUTANS	4-41	313-316						
PWRBA_ECOLI	TRP REPRESSOR BINDING PROTEIN	ESCHERICHIA COLI	89-116							
PXI91_ECOLI	X POLYPEPTIDE	ESCHERICHIA COLI	104-131							
PXI92_ECOLI	X POLYPEPTIDE	ESCHERICHIA COLI	104-131							
PXI93_ECOLI	X POLYPEPTIDE	ESCHERICHIA COLI	104-131							
PXISA_ANASP	EXCISEASE A	ANABAENA SP	4-31	89-116	135-162					
PXP8B_ECOLI	POSSIBLE INTEGRASE/RECOMBINASE XPRB	ESCHERICHIA COLI	268-293							
PXYLA_STAXY	XYLOSE ISOMERASE	STAPHYLOCOCCUS XYLOSUS	411-438							
PXYLK_XLAE	XYLOLASE KINASE	KLEBSIELLA AEROGES	2-29							
PXYLK_LACPE	XYLOLASE KINASE	LACTOBACILLUS PENTOSUS	52-79	211-218	260-287					
PXYLK_STACE	XYLOLASE KINASE	STAPHYLOCOCCUS XYLOSUS	4-31	96-130	209-236	246-273				
PXYLR_BACSU	XYLOSE REPRESSOR	BACILLUS SUBTILIS	73-102	260-287						
PXYLR_LACPE	XYLOSE REPRESSOR	LACTOBACILLUS PENTOSUS	262-289							
PXYLR_STAXY	XYLOSE REPRESSOR	STAPHYLOCOCCUS XYLOSUS	20-64	101-158	181-215	221-235	274-301			
PXYLZ_PSEPU	ELECTRON TRANSFER COMPONENT	PSEUDOMONAS PUTIDA	51-78	104-131						
PXYM_CALSA	PUTATIVE ENDO-1,4-BETA-XYLANASE	CALDOCELLUM SACCHAROLYTICUM	198-235							
PXYNA_BACCI	O-1,4-BETA-XYLANASE PRECURSOR	BACILLUS CIRCULANS	47-74							
PXYNA_BACGS	ENDO-1,4-BETA-XYLANASE PRECURSOR	BACILLUS SUBTILIS	173-200							
PXYNA_BACSU	ENDO-1,4-BETA-XYLANASE PRECURSOR	BACILLUS SUBTILIS	47-74							
PXYNA_CALSA	ENDO-1,4-BETA-XYLANASE A PRECURSOR	CALDOCELLUM SACCHAROLYTICUM	132-159	226-256						
PXYNA_PSEFL	ENDO-1,4-BETA-XYLANASE A PRECURSOR	PSEUDOMONAS FLUORESCENS	33-42							
PXYNB_BACPU	BETA-XYLOSIDASE	BACILLUS PUMILUS	459-486							
PXYNI_CALSA	BETA-XYLOSIDASE	CALDOCELLUM SACCHAROLYTICUM	440-474							
PXYNB_PSEFL	ENDO-1,4-BETA-XYLANASE PRECURSOR	PSEUDOMONAS FLUORESCENS	51-78	251-278	317-344	475-502				
PXYNC_PSEFL	ALPHA-L-ARABINOFURANOSIDASE C PRECURSOR	PSEUDOMONAS FLUORESCENS	51-78	251-278						
PXYNC_STRLI	ENDO-1,4-BETA-XYLANASE C PRECURSOR	STREPTOMYCES LIVIDANS	183-210							
PY14K_HALMO	HYPOTHETICAL 14.9 KD PROTEIN	HALOCOCCUS MORRHUAE	36-43							
PY21K_STOR	HYPOTHETICAL 21.1 KD PROTEIN	STREPTOCOCCUS ORALIS	78-105							
PY36K_METSM	HYPOTHETICAL 36.7 KD PROTEIN	METHANOBREVIBACTER SMITHII	128-163	172-218						
PYAAC_ECOLI	HYPOTHETICAL 34.6 KD PROTEIN	ESCHERICHIA COLI	271-298							
PYAAG_PSEFL	HYPOTHETICAL 31.9 KD PROTEIN	PSEUDOMONAS FLUORESCENS	274-301							
PYAAM_ECOLI	HYPOTHETICAL 39.1 KD PROTEIN	ESCHERICHIA COLI	352-379							
PYAAQ_ECOLI	HYPOTHETICAL 36.6 KD PROTEIN	ESCHERICHIA COLI	355-382							
PYABG_ECOLI	HYPOTHETICAL 34.9 KD PROTEIN	ESCHERICHIA COLI	131-158							
PYABN_ECOLI	HYPOTHETICAL 39.7 KD PROTEIN	ESCHERICHIA COLI	448-480	627-654						
PYAD3_PSEAE	HYPOTHETICAL 21.9 KD PROTEIN	PSEUDOMONAS AERUGINOSA	48-75	150-177						
PYAD3_CLOAB	HYPOTHETICAL 21.6 KD PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	75-109	114-144						
PYAD3_CLOAB	HYPOTHETICAL 36.9 KD PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	132-159	165-196	210-237					
PYADA_YEREN	INVASIN PRECURSOR	YERSINIA ENTEROCOLITICA	21-55							
PYADA_YEBS	INVASIN PRECURSOR	YERSINIA PSEUDOTUBERCULOSIS	196-230	247-274	318-381					
			255-282	297-360						

PCGENE	1071784	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PYADC ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	13-40	101-131							
PYAE8 ECOLI	17 KD PROTEIN	RICKETTSIA RICKETTSII	107-134								
PYAHJ ECOLI	HYPOTHETICAL 29.4 KD PROTEIN	ESCHERICHIA COLI	221-248								
PYAFD ECOLI	HYPOTHETICAL 29.1 KD PROTEIN	ESCHERICHIA COLI	34-71								
PYAF6 ECOLI	HYPOTHETICAL 31.0 KD PROTEIN	ESCHERICHIA COLI	123-150								
PYAHJ ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA FERUGSONII	2-35								
PYAMJ ECOLI	PUTATIVE AMIDASE	SALMONELLA TYPHIMURUM	72-100								
PYATJ ECOLI	HYPOTHETICAL 13.9 KD PROTEIN	SYNECHOCYSTIS SP	26-60								
PYATF ECOLI	HYPOTHETICAL 13.9 KD PROTEIN	MYCOBACTERIUM LEPRAE	23-57	91-138	511-538						
PYATF ECOLI	HYPOTHETICAL 13.9 KD PROTEIN	BACILLUS FIRMUS	211-238								
PYATF ECOLI	HYPOTHETICAL 13.9 KD PROTEIN	MYCOPLASMA GALLISEPTICUM	7-41								
PYATF ECOLI	HYPOTHETICAL 13.9 KD PROTEIN	MYCOPLASMA GALLISEPTICUM	79-56	60-87							
PYATF ECOLI	HYPOTHETICAL 13.9 KD PROTEIN	XANTHOMONAS CANIPESTRIS	68-98	199-226							
PYAHJ ECOLI	HYPOTHETICAL 30 KD VIRULENCE PROTEIN	ESCHERICHIA COLI	49-79								
PYBAH ECOLI	HYPOTHETICAL 34.8 KD PROTEIN	ESCHERICHIA COLI	6-69								
PYBBA ECOLI	HYPOTHETICAL ABC TRANSPORTER	ESCHERICHIA COLI	51-82								
PYBBD ECOLI	HYPOTHETICAL 9.8 KD PROTEIN	ESCHERICHIA COLI	97-124								
PYBBD ECOLI	HYPOTHETICAL 14.1 KD PROTEIN	ESCHERICHIA COLI	14-61								
PYCAE ECOLI	HYPOTHETICAL 24.5 KD PROTEIN	ESCHERICHIA COLI	18-65								
PYCBH ECOLI	HYPOTHETICAL PROTEIN	BACILLUS UNIFORMIS	66-100								
PYCEA ECOLI	HYPOTHETICAL 17.3 KD PROTEIN	BACILLUS LAUTUS	111-138								
PYCEA ECOLI	HYPOTHETICAL 22.9 KD PROTEIN	ESCHERICHIA COLI	52-79								
PYCHH ECOLI	HYPOTHETICAL PROTEIN	ALCALIGENES EUTROPIUS	21-43								
PYCHH ECOLI	HYPOTHETICAL 20.8 KD PROTEIN	ESCHERICHIA COLI	16-43								
PYCHH ECOLI	HYPOTHETICAL 18.6 KD PROTEIN	ESCHERICHIA COLI	7-68	134-166							
PYCHH ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	35-62								
PYCHH ECOLI	HYPOTHETICAL 4.3 KD PROTEIN	ESCHERICHIA COLI	34-81								
PYCHH ECOLI	HYPOTHETICAL 29.1 KD PROTEIN	SYNECHOCOCUS SP	194-221								
PYCHH ECOLI	HYPOTHETICAL 38.0 KD PROTEIN	SYNECHOCOCUS SP	7-34	120-154							
PYCHH ECOLI	HYPOTHETICAL 39.5 KD PROTEIN	SYNECHOCYSTIS SP	272-308								
PYCHH ECOLI	HYPOTHETICAL PROTEIN	MASTIGOCLOADUS LAMINOSUS	2-29								
PYCHH ECOLI	HYPOTHETICAL PROTEIN	PSLEUDANABANA SP	180-407								
PYCHH ECOLI	HYPOTHETICAL 28.1 KD PROTEIN	BACILLUS THURINGIENSIS	42-74	153-180							
PYCHH ECOLI	HYPOTHETICAL PROTEIN PRECURSOR	ESCHERICHIA COLI	32-59								
PYCHH ECOLI	HYPOTHETICAL PROTEIN	BACILLUS SUBTILIS	3-30	59-86							
PYCHH ECOLI	HYPOTHETICAL 68.4 KD PROTEIN	HERPETOSSIPHON AURANTIACUS	12-39	151-178	360-416						
PYCHH ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	12-66	117-144	163-216	233-267	295-339	458-485	676-717	1136-1163	1499-1530
PYCHH ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	80-107								
PYCHH ECOLI	HYPOTHETICAL 16.7 KD PROTEIN	ESCHERICHIA COLI	606-641	683-714	726-753						
PYCHH ECOLI	HYPOTHETICAL 10.8 KD PROTEIN	ESCHERICHIA COLI	373-400	421-452	621-648						
PYCHH ECOLI	HYPOTHETICAL 24.1 KD PROTEIN	ESCHERICHIA COLI	133-174								
PYCHH ECOLI	HYPOTHETICAL 20.5 KD PROTEIN	ESCHERICHIA COLI	96-130								
PYCHH ECOLI	HYPOTHETICAL 18.3 KD PROTEIN	ESCHERICHIA COLI	4-38								
PYCHH ECOLI	HYPOTHETICAL 65.3 KD PROTEIN	BORRELIA BURGDORFERI	333-360	524-551	565-592						
PYCHH ECOLI	HYPOTHETICAL 14.3 KD PROTEIN	SULFOLOBUS SOLEFAVICUS	17-58	71-103							
PYCHH ECOLI	HYPOTHETICAL 16.9 KD PROTEIN	SULFOLOBUS SOLEFAVICUS	11-38								
PYCHH ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	91-120								
PYCHH ECOLI	HYPOTHETICAL 10.7 KD PROTEIN	ESCHERICHIA COLI	50-77								
PYCHH ECOLI	HYPOTHETICAL 38.1 KD PROTEIN	ESCHERICHIA COLI	43-70								
PYCHH ECOLI	HYPOTHETICAL 49.3 KD TRANSPORT PROTEIN	ESCHERICHIA COLI	147-174								
PYCHH ECOLI	HYPOTHETICAL IN DCD REGION	ESCHERICHIA COLI	143-172								
PYCHH ECOLI	HYPOTHETICAL 16.9 KD PROTEIN	ESCHERICHIA COLI	69-106	283-310							
PYCHH ECOLI	HYPOTHETICAL 92.3 KD PROTEIN	ESCHERICHIA COLI	151-178	501-545							
PYCHH ECOLI	HYPOTHETICAL 19.1 KD PROTEIN	ESCHERICHIA COLI	96-123								
PYCHH ECOLI	HYPOTHETICAL 141.0 KD PROTEIN	ESCHERICHIA COLI	343-370								
PYCHH ECOLI	HYPOTHETICAL 138.1 KD PROTEIN	ESCHERICHIA COLI	35-70	102-129							

PCGENE	10117144	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PYH1U_ECOLI	HYPOTHETICAL 43.1 KD PROTEIN	ESCHERICHIA COLI	178-153									
PYH1C_ECOLI	HYPOTHETICAL 31.6 KD PROTEIN	ESCHERICHIA COLI	46-80									
PYH1F_ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	61-88									
PYH1J_ECOLI	HYPOTHETICAL 43.4 KD PROTEIN	ESCHERICHIA COLI	15-42									
PYH1A_ECOLI	HYPOTHETICAL ABC TRANSPORTER	ESCHERICHIA COLI	83-110									
PYH1E_ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	453-480									
PYH1D_ECOLI	HYPOTHETICAL 91.2 KD PROTEIN	ESCHERICHIA COLI	399-433									
PYH1H_ECOLI	HYPOTHETICAL 40.6 KD PROTEIN	ESCHERICHIA COLI	135-202									
PYH1Z_ECOLI	HYPOTHETICAL 30.6 KD PROTEIN	BACILLUS STEAROTHERIOPHILUS	133-160									
PYH1X_BACJA	HYPOTHETICAL PROTEIN	BRADYRHIZOBIUM JAPONICUM	109-150									
PYH1P_BACME	HYPOTHETICAL 37.7 KD PROTEIN	BACILLUS MEGATERIUM	40-67									
PYH1G_ECOLI	HYPOTHETICAL 29.4 KD PROTEIN	ESCHERICHIA COLI	214-241									
PYH1B_ECOLI	HYPOTHETICAL 30.9 KD PROTEIN	ESCHERICHIA COLI	235-252									
PYH1G_ECOLI	HYPOTHETICAL 31.8 KD PROTEIN	ESCHERICHIA COLI	209-236									
PYH1Z_ECOLI	HYPOTHETICAL 32.8 KD PROTEIN	BACILLUS THURINGIENSIS	26-61									
PYH1Z_PSEPU	HYPOTHETICAL 31.4 KD PROTEIN	PSEUDOMONAS PUTIDA	145-172									
PYH1F_ECOLI	HYPOTHETICAL 48.4 KD PROTEIN	ESCHERICHIA COLI	223-264									
PYH1A_BACST	HYPOTHETICAL 35.3 KD PROTEIN	BACILLUS STEAROTHERIOPHILUS	6-33									
PYH1G_BACST	HYPOTHETICAL PROTEIN	BACILLUS STEAROTHERIOPHILUS	182-209									
PYH1N_BACCE	HYPOTHETICAL 15 KD PROTEIN	BACILLUS CEREUS	79-124									
PYH1D_BACSU	HYPOTHETICAL PROTEIN	BACILLUS SUBTILIS	20-47									
PYH1E_BACSU	HYPOTHETICAL 17.1 KD PROTEIN	BACILLUS SUBTILIS	84-111									
PYH1P_BACSU	HYPOTHETICAL 39.0 KD PROTEIN	BACILLUS SUBTILIS	98-125									
PYH1P_CLOAB	HYPOTHETICAL 38.8 KD PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	160-210									
PYH1Z_STRMU	HYPOTHETICAL PROTEIN 2	STREPTOCOCCUS MUTANS	4-40	110-138	235-262							
PYH1B_ECOLI	HYPOTHETICAL 20.6 KD PROTEIN	ESCHERICHIA COLI	20-66									
PYH1C_ECOLI	HYPOTHETICAL 43.2 KD PROTEIN	ESCHERICHIA COLI	69-96									
PYH1F_ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	44-71	138-165								
PYH1B_ECOLI	PROBABLE ABC TRANSPORTER	ESCHERICHIA COLI	176-203									
PYH1G_PSEPU	PROBABLE ABC TRANSPORTER	PSEUDOMONAS PUTIDA	74-101	106-133	147-174							
PYH1G_THIFE	PROBABLE ABC TRANSPORTER	THIOBACILLUS FERROOXIDANS	113-140									
PYH1P_ECOLI	HYPOTHETICAL 35.4 KD PROTEIN	ESCHERICHIA COLI	267-297									
PYH1M_BACSU	HYPOTHETICAL 32.0 KD PROTEIN	BACILLUS SUBTILIS	232-253									
PYH1T_ANASP	HYPOTHETICAL PROTEIN	ANABAENA SP	72-99									
PYH1A_ECOLI	HYPOTHETICAL 16.6 KD PROTEIN	ESCHERICHIA COLI	56-84									
PYH1G_ECOLI	HYPOTHETICAL 15.1 KD PROTEIN	ESCHERICHIA COLI	43-77									
PYH1H_ECOLI	HYPOTHETICAL 14.5 KD PROTEIN	ESCHERICHIA COLI	43-73									
PYH1J_LACLA	HYPOTHETICAL PROTEIN	LACTOCOCCUS LACTIS	167-194									
PYH1B_LACLA	HYPOTHETICAL 30.7 KD PROTEIN	LACTOCOCCUS LACTIS	90-124	132-159								
PYH1B_LACLA	HYPOTHETICAL 30.7 KD PROTEIN	LACTOCOCCUS LACTIS	92-148									
PYH1H_STRAH	HYPOTHETICAL PROTEIN	STAPHYLOCOCCUS AUREUS	77-104	156-183								
PYH1H_VIBGII	HYPOTHETICAL 18.3 KD PROTEIN	VIBRIO CHOLERAE	16-67									
PYH1M_METFE	HYPOTHETICAL 32.2 KD PROTEIN	METHANOTHERMUS FERVIDUS	99-126									
PYH1S_CLOAB	HYPOTHETICAL 11.0 KD PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	106-133									
PYH1S_CLOAB	HYPOTHETICAL 20.6 KD PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	41-85									
PYH1S_CLOAB	HYPOTHETICAL 20.6 KD PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	98-123									
PYH1V_LACIN	HYPOTHETICAL 42.4 KD PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	31-52	208-231	276-310							
PYH1V_LACIN	HYPOTHETICAL PROTEIN	LACTOBACILLUS THELLETICUS	91-120	137-154								
PYH1A_PSESN	HYPOTHETICAL PROTEIN	PSEUDOMONAS SP	217-266									
PYH1J_HALHA	HYPOTHETICAL 38.0 KD PROTEIN	HALOBACTERIUM HALOBUTUM	245-272									
PYH1Z_MYCBU	IS948 HYPOTHETICAL 6.6 KD PROTEIN	MYCOBACTERIUM TUBERCULOSIS	19-46									
PYH1Z_PSEAY	HYPOTHETICAL 42.6 KD PROTEIN	PSEUDOMONAS AMYLODERMOSA	9-26									
PYH1B_ME1M	ISM1 HYPOTHETICAL 48.3 KD PROTEIN	METHANOBREVIBACTER SMITHII	73-100	134-184	338-365							
PYH1Z_HAJHA	HYPOTHETICAL 31 KD PROTEIN	HALOBACTERIUM HALOBUTUM	16-113									
PYH1B_ECOLI	HYPOTHETICAL 34.0 KD PROTEIN	ESCHERICHIA COLI	202-239									
PYH1D_ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	9-43									
PYH1F_ECOLI	HYPOTHETICAL 22.6 KD PROTEIN	ESCHERICHIA COLI	131-158									

PCGENE	101-1214	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PYIBO_ECOLI	HYPOTHETICAL 11.1 KD PROTEIN	ESCHERICHIA COLI	70-97									
PYICC_ECOLI	HYPOTHETICAL 37.2 KD PROTEIN	ESCHERICHIA COLI	143-170									
PYICD_ECOLI	HYPOTHETICAL 31.1 KD PROTEIN	ESCHERICHIA COLI	172-159									
PYICL_ECOLI	HYPOTHETICAL 62.3 KD PROTEIN	ESCHERICHIA COLI	408-435									
PYICN_ECOLI	HYPOTHETICAL 88.1 KD PROTEIN	ESCHERICHIA COLI	122-149									
PYICO_ECOLI	HYPOTHETICAL 18.2 KD PROTEIN	ESCHERICHIA COLI	76-103									
PYIDB_ECOLI	HYPOTHETICAL 49.9 KD PROTEIN	ESCHERICHIA COLI	320-347									
PYIDE_ECOLI	HYPOTHETICAL 11.8 KD PROTEIN	ESCHERICHIA COLI	34-78									
PYIDJ_ECOLI	HYPOTHETICAL 58.9 KD PROTEIN	ESCHERICHIA COLI	86-113	182-209	272-304							
PYIDK_ECOLI	HYPOTHETICAL 13.7 KD PROTEIN	ESCHERICHIA COLI	56-83									
PYIDP_ECOLI	HYPOTHETICAL 62.1 KD PROTEIN	ESCHERICHIA COLI	2-39									
PYIEA_ECOLI	HYPOTHETICAL 27.3 KD PROTEIN	ESCHERICHIA COLI	63-97									
PYIEC_ECOLI	HYPOTHETICAL 49.2 KD PROTEIN	ESCHERICHIA COLI	221-248									
PYIEC_ERWCH	HYPOTHETICAL 60.6 KD PROTEIN	ESCHERICHIA COLI	22-67	270-297								
PYIEG_ECOLI	HYPOTHETICAL 34.8 KD PROTEIN	ERWINIA CHRYSANTHEMI	86-120									
PYIEH_ECOLI	HYPOTHETICAL 46.9 KD PROTEIN	ESCHERICHIA COLI	293-327									
PYIEM_ECOLI	HYPOTHETICAL 24.7 KD PROTEIN	ESCHERICHIA COLI	51-78									
PYIEQ_ECOLI	HYPOTHETICAL 15.9 KD PROTEIN	ESCHERICHIA COLI	73-105									
PYIJC_ECOLI	HYPOTHETICAL 51.5 KD PROTEIN	ESCHERICHIA COLI	201-242	380-407								
PYIJG_ECOLI	HYPOTHETICAL 39.6 KD PROTEIN	ESCHERICHIA COLI	135-202									
PYIGM_ECOLI	HYPOTHETICAL 14.0 KD PROTEIN	ESCHERICHIA COLI	51-92									
PYIGN_ECOLI	HYPOTHETICAL 31.7 KD PROTEIN	ESCHERICHIA COLI	120-154									
PYIQO_ECOLI	HYPOTHETICAL 54.7 KD PROTEIN	ESCHERICHIA COLI	207-234									
PYIGP_ECOLI	HYPOTHETICAL 28.1 KD PROTEIN	ESCHERICHIA COLI	62-94									
PYIGP_ECOLI	HYPOTHETICAL 22.3 KD PROTEIN	ESCHERICHIA COLI	173-200									
PYIIB_ECOLI	HYPOTHETICAL 27.8 KD PROTEIN	ESCHERICHIA COLI	132-159									
PYIIB_ECOLI	HYPOTHETICAL 21.2 KD PROTEIN	ESCHERICHIA COLI	13-40									
PYIHD_ECOLI	HYPOTHETICAL 10.3 KD PROTEIN	ESCHERICHIA COLI	28-55									
PYIHR_ECOLI	HYPOTHETICAL 54.1 KD PROTEIN	ESCHERICHIA COLI	272-306									
PYIHR_ECOLI	HYPOTHETICAL 19.1 KD PROTEIN	ESCHERICHIA COLI	112-139									
PYIHK_ECOLI	HYPOTHETICAL 65.4 KD PROTEIN	ESCHERICHIA COLI	4-31									
PYIHM_ECOLI	HYPOTHETICAL 36.9 KD PROTEIN	ESCHERICHIA COLI	83-110	120-134	297-324							
PYIHO_ECOLI	HYPOTHETICAL 81.8 KD PROTEIN	ESCHERICHIA COLI	612-646									
PYIHP_ECOLI	HYPOTHETICAL 51.1 KD PROTEIN	ESCHERICHIA COLI	337-384									
PYIHV_ECOLI	HYPOTHETICAL 31.9 KD PROTEIN	ESCHERICHIA COLI	72-99									
PYIHX_ECOLI	HYPOTHETICAL 23.3 KD PROTEIN	ESCHERICHIA COLI	9-36									
PYIHZ_ECOLI	HYPOTHETICAL 15.9 KD PROTEIN	ESCHERICHIA COLI	6-33									
PYIIP_ECOLI	HYPOTHETICAL 32.9 KD PROTEIN	ESCHERICHIA COLI	22-63									
PYIUI_ECOLI	HYPOTHETICAL 9.6 KD PROTEIN	ESCHERICHIA COLI	28-71									
PYIUC_ECOLI	HYPOTHETICAL 26.8 KD PROTEIN	ESCHERICHIA COLI	136-163									
PYIUR_ECOLI	HYPOTHETICAL 78.3 KD PROTEIN	ESCHERICHIA COLI	225-263									
PYIUK_ECOLI	HYPOTHETICAL 11.2 KD PROTEIN	ESCHERICHIA COLI	26-53									
PYIUD_ECOLI	HYPOTHETICAL 22.1 KD PROTEIN	ESCHERICHIA COLI	214-241									
PYIUP_ECOLI	HYPOTHETICAL 66.8 KD PROTEIN	ESCHERICHIA COLI	110-137	419-446								
PYINL_LISMO	HYPOTHETICAL 26.8 KD PROTEIN	ESCHERICHIA COLI	7-34									
PYIS1_SHISO	INSERTION ELEMENT IS600	LISTERIA MONOCYTOGENES	62-89									
PYIS1_STRGO	IS110 HYPOTHETICAL 41.6 KD PROTEIN	SHIGELLA SONNEI	135-152									
PYIS7_SHISO	INSERTION ELEMENT IS629	STREPTOMYCES COELICOLOR	66-100									
PYISP_BACP	HYPOTHETICAL 42.1 KD PROTEIN	SHIGELLA SONNEI	312-339									
PYIAG_ECOLI	HYPOTHETICAL 22.6 KD PROTEIN	BACILLUS SP	51-78									
PYIAI_ECOLI	HYPOTHETICAL 20.4 KD PROTEIN	ESCHERICHIA COLI	88-122									
PYIBH_ECOLI	HYPOTHETICAL 78.3 KD PROTEIN	ESCHERICHIA COLI	93-120									
PYIBL_ECOLI	HYPOTHETICAL 9.7 KD PROTEIN	ESCHERICHIA COLI	30-57									
PYIBM_ECOLI	HYPOTHETICAL 26.7 KD PROTEIN	ESCHERICHIA COLI	112-149									
PYIBO_ECOLI	HYPOTHETICAL 15.7 KD PROTEIN	ESCHERICHIA COLI	2-29									
PYICC_ECOLI	HYPOTHETICAL 60.8 KD PROTEIN	ESCHERICHIA COLI	38-65	414-441	451-492							



PCGENE	10717814	Prokaryotic Sequences	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10
FILE NAME	PROTEIN	ORGANISM	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10
PYP1 AGRT4	HYPOTHETICAL PROTEIN 7	AGROBACTERIUM TUMEFACIENS	79-56									
PYP2 LECPN	HYPOTHETICAL PROTEIN	LEGIONELLA PNEUMOPHILA	94-135									
PYP3 ENTFA	HYPOTHETICAL 13 KD PROTEIN	ENTEROCOCCUS FAECALIS	79-106									
PYP4 BACAN	HYPOTHETICAL 21.6 KD PROTEIN	BACILLUS ANTHRACIS	11-47	115-162								
PYP5 ECOLI	HYPOTHETICAL 27.6 KD PROTEIN	ESCHERICHIA COLI	5-32									
PYP6 BACSU	HYPOTHETICAL 27.3 KD PROTEIN	BACILLUS SUBTILIS	184-222									
PYP7 ECOLI	HYPOTHETICAL 12.8 KD PROTEIN	ESCHERICHIA COLI	16-43									
PYP8 STNRP2	HYPOTHETICAL 18.1 KD PROTEIN	SYNECHOCOCCUS SP	34-61									
PYP9 CLOPE	HYPOTHETICAL 19.7 KD PROTEIN	CLOSTRIDIUM PERFRINGENS	7-34	43-77	81-149							
PYP10 CLOPE	HYPOTHETICAL 14.5 KD PROTEIN	CLOSTRIDIUM PERFRINGENS	2-59									
PYP11 CLOPE	HYPOTHETICAL 38.4 KD PROTEIN	CLOSTRIDIUM PERFRINGENS	110-137	263-390	301-340							
PYP12 FSEAE	HYPOTHETICAL 38.5 KD PROTEIN	PSEUDOMONAS AERUGINOSA	22-52									
PYP13 BACSU	HYPOTHETICAL PROCESSING PROTEASE	BACILLUS SUBTILIS	229-356									
PYP14 KLEPN	HYPOTHETICAL PROTEIN	KLEBSIELLA PNEUMONIAE	243-270									
PYP15 PLEBO	HYPOTHETICAL 13.1 KD PROTEIN	PLECTONENIA BORYANUM	27-34									
PYP16 METTF	HYPOTHETICAL 40.7 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	58-85	308-335								
PYP17 METTF	HYPOTHETICAL 23.3 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	3-30									
PYP18 METTF	HYPOTHETICAL 17.3 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	69-117									
PYP19 METTF	HYPOTHETICAL 49.6 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	331-360	389-410								
PYP20 BACSU	HYPOTHETICAL 72.4 KD PROTEIN	BACILLUS SUBTILIS	602-636									
PYP21 METTF	HYPOTHETICAL 40.6 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	58-85	308-335								
PYP22 METTF	HYPOTHETICAL 33.1 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	38-65	154-188								
PYP23 METTF	HYPOTHETICAL 54.1 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	191-220	226-253	381-408							
PYP24 METTF	HYPOTHETICAL 9.7 KD PROTEIN	METHANOBACTERIUM THERMOFORMICICUM	5-78									
PYP25 THEPE	HYPOTHETICAL 18.7 KD PROTEIN	THERMOFILUM PENDENS	82-109									
PYP26 HALCU	HYPOTHETICAL 40 KD GTP-BINDING PROTEIN	HALOBACTERIUM CUTIRUBUM	20-51									
PYP27 SYNRP2	HYPOTHETICAL 24.7 KD PROTEIN	SYNECHOCOCCUS SP	49-76									
PYP28 SALTU	HYPOTHETICAL 40.6 KD PROTEIN	SALMONELLA TYPHIMURIUM	143-190									
PYP29 SALTU	HYPOTHETICAL 51.0 KD PROTEIN	SALMONELLA TYPHIMURIUM	428-455									
PYP30 SALTU	HYPOTHETICAL 20.6 KD PROTEIN	SALMONELLA TYPHIMURIUM	39-56									
PYP31 SALTU	HYPOTHETICAL 36.6 KD PROTEIN	SALMONELLA TYPHIMURIUM	130-157									
PYP32 LACLA	HYPOTHETICAL PROTEIN	LACTOCOCCUS LACTIS	140-167									
PYP33 METVA	HYPOTHETICAL PROTEIN	METHANOCOCCUS VANNIELII	40-93	129-156								
PYP34 SULAC	HYPOTHETICAL 11.6 KD PROTEIN	METHANOCOCCUS VANNIELII	13-40									
PYP35 SULAC	HYPOTHETICAL 11.3 KD PROTEIN	SULFOLOBUS ACIDOCALDARIUS	5-51									
PYP36 BACSU	HYPOTHETICAL 14.3 KD PROTEIN	SULFOLOBUS ACIDOCALDARIUS	17-71									
PYP37 BACSU	HYPOTHETICAL 25.3 KD PROTEIN	BACILLUS SUBTILIS	29-56									
PYP38 BACSU	HYPOTHETICAL 11.4 KD PROTEIN	BACILLUS SUBTILIS	31-30	44-81								
PYP39 YEREN	HYPOTHETICAL YSC OPERON PROTEIN B	YERSINIA ENTEROCOLITICA	90-121	365-399								
PYP40 YEREN	YSC OPERON PROTEIN C PRECURSOR	YERSINIA ENTEROCOLITICA	38-72	242-269								
PYP41 YEREN	YSC OPERON PROTEIN D	YERSINIA ENTEROCOLITICA	28-58									
PYP42 YEREN	YSC OPERON PROTEIN H	YERSINIA ENTEROCOLITICA	28-58									
PYP43 YEREN	YSC OPERON PROTEIN I	YERSINIA ENTEROCOLITICA	49-76									
PYP44 YEREN	YSC OPERON PROTEIN L	YERSINIA ENTEROCOLITICA	49-76									
PYP45 YEREN	YSC OPERON LIPROTEIN J PRECURSOR	YERSINIA ENTEROCOLITICA	99-126									
PYP46 YEREN	YSC OPERON LIPROTEIN J PRECURSOR	YERSINIA ENTEROCOLITICA	99-126									
PYP47 YEREN	YSC OPERON PROTEIN L	YERSINIA ENTEROCOLITICA	41-68									
PYP48 YEREN	YSC OPERON PROTEIN L	YERSINIA ENTEROCOLITICA	41-68									
PYP49 DESAM	HYPOTHETICAL 9.5 KD PROTEIN	SERRATIA MARCESCENS	11-70									
PYP50 DESAM	HYPOTHETICAL 28.3 KD PROTEIN	DESULFOLOBUS AMBIVALENS	68-109									
PYP51 DESAM	HYPOTHETICAL PROTEIN	DESULFOLOBUS AMBIVALENS	65-153									
PYP52 LEPA	HYPOTHETICAL PROTEIN	LEPTOSPIRA INTERROGANS	6-31	60-94								
PYP53 MYLAW	HYPOTHETICAL PROTEIN	MYCOPLASMA MYCOIDES	35-99	185-227	300-327							
PYP54 BACSU	HYPOTHETICAL 19.6 KD PROTEIN	BACILLUS SUBTILIS	72-99									
PYP55 METFE	HYPOTHETICAL PROTEIN	METHANOTHERMUS FERVIDUS	78-105									
PYP56 STRK	HYPOTHETICAL 37.1 KD PROTEIN	STREPTOMYCES FRADIAE	246-273									

PCGENE	10717844	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PLEKHA7	PROTEIN	ORGANISMI	AREA1	AREA2							
PYTDK_BACSU	HYPOTHETICAL 316 KD PROTEIN	BACILLUS SUBTILIS	244-271	779-706							
PYTRF_LEPBI	HYPOTHETICAL 22 KD PROTEIN	LEPTOSPIRA BIFLEXA	84-113								
PYTRP_LACLA	HYPOTHETICAL 133 KD PROTEIN	LACTOCOCCUS LACTIS	76-112								
PYTSJ_BACSU	HYPOTHETICAL 20 KD PROTEIN	BACILLUS SUBTILIS	32-64								
PYTSF_SPHCI	HYPOTHETICAL 238 KD PROTEIN	SPHIROPLASMA CITRI	102-149								
PYX04_BACSU	HYPOTHETICAL 128 KD PROTEIN	BACILLUS SUBTILIS	37-64	63-93							
PYX06_BACSU	HYPOTHETICAL 210 KD PROTEIN	BACILLUS SUBTILIS	142-169								
PYX1J_BACSU	HYPOTHETICAL 260 KD PROTEIN	BACILLUS SUBTILIS	12-51								
PYX1S_BACSU	HYPOTHETICAL 618 KD PROTEIN	BACILLUS SUBTILIS	165-207	262-289							
PYX18_BACSU	HYPOTHETICAL 668 KD PROTEIN	BACILLUS SUBTILIS	3-30	34-61	94-142						
PYX19_BACSU	HYPOTHETICAL 313 KD PROTEIN	BACILLUS SUBTILIS	56-83	85-112							
PYX1D_BACSU	HYPOTHETICAL 212 KD PROTEIN	BACILLUS SUBTILIS	24-58								
PYX1P_ANASP	HYPOTHETICAL 119 KD PROTEIN	ANABAEANA SP	77-104								
PYXYB_CALSA	HYPOTHETICAL 107 KD PROTEIN	CALDOCCELLUM SACCCHAROLYTICUM	9-39								
PYXYC_CALSA	HYPOTHETICAL PROTEIN	CALDOCCELLUM SACCCHAROLYTICUM	41-94								
PYZEI_ECOLI	HYPOTHETICAL 167 KD PROTEIN	ESCHERICHIA COLI	41-78								



TABLE IX

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL HUMAN PROTEINS

FCGENSE	107174x Mail Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PI43F HUMAN	14-3-3 PROTEIN ETA (PROTEIN AS1) (FRAGMENT)	101-115								
PI43S HUMAN	14-3-3 PROTEIN HOMOLOG STRATIFIN	45-72								
PI43T HUMAN	14-3-3 PROTEIN THETA (14-3-3 PROTEIN T-CELL) (H51 PROTEIN)	61-92								
PIA23 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-29(AW.19) A*2901 ALPHA CHAIN	28-55								
PIA24 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-29(AW.19) A*2902 ALPHA CHAIN	87-114								
PIB02 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-7 B*0702 ALPHA CHAIN	87-114								
PIB03 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-13 B*1301 ALPHA CHAIN	87-114								
PIB10 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*3(B.13) B*1302 ALPHA CHAIN	87-114	148-182							
PIB11 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*7(BW.70) B*1303 ALPHA CHAIN	84-115								
PIB12 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-42 B*1504 ALPHA CHAIN	84-115								
PIB13 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN	76-107								
PIB21 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*1501 ALPHA CHAIN	84-115								
PIB22 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*1502 ALPHA CHAIN	84-115								
PIB23 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*1503 ALPHA CHAIN	84-115								
PIB24 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*1504 ALPHA CHAIN	84-115								
PIB26 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*1505 ALPHA CHAIN	76-107								
PIB27 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*1506 ALPHA CHAIN	84-115								
PIB28 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*1507 ALPHA CHAIN	84-115								
PIB29 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-37 B*1701 ALPHA CHAIN	84-115								
PIB32 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-39 B*1902 ALPHA CHAIN	84-115								
PIB33 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4001 ALPHA CHAIN	87-114								
PIB34 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4002 ALPHA CHAIN	60-91								
PIB35 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4003 ALPHA CHAIN	84-115								
PIB36 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4004 ALPHA CHAIN	84-115								
PIB37 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*41 B*4101 ALPHA CHAIN	84-115								
PIB38 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*42 B*4201 ALPHA CHAIN	84-115								
PIB39 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*43 B*4301 ALPHA CHAIN	87-114								
PIB40 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*44(B.12) B*4401 ALPHA CHAIN	84-111								
PIB41 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*44(B.12) B*4402 ALPHA CHAIN	87-114								
PIB42 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*44(B.12) B*4403 ALPHA CHAIN	87-114								
PIB43 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*45(B.12) B*4501 ALPHA CHAIN	84-115								
PIB44 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*46 B*4601 ALPHA CHAIN	87-114								
PIB45 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*47 B*4701 ALPHA CHAIN	88-115								
PIB46 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-48 B*4801 ALPHA CHAIN	84-115								
PIB47 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B.21) B*4901 ALPHA CHAIN	87-114								
PIB48 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*50(B.21) B*5001 ALPHA CHAIN	84-115								
PIB53 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*52(B.5) B*5201 ALPHA CHAIN	87-114								
PIB55 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*53(BW.22) B*5301 ALPHA CHAIN	87-114								
PIB56 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*53(BW.22) B*5302 ALPHA CHAIN	87-114								
PIB57 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*55(BW.22) B*5501 ALPHA CHAIN	87-114								
PIB58 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*55(BW.22) B*5502 ALPHA CHAIN	87-114								
PIB59 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW*56(BW.22) B*5601 ALPHA CHAIN	87-114								
PIC01 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1 CW*0101 ALPHA CHAIN	87-114								
PIC02 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1 CW*0102 ALPHA CHAIN	87-114								
PIC03 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*2 CW*0201 ALPHA CHAIN	87-114								
PIC04 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*2 CW*0202 ALPHA CHAIN	87-114								
PIC06 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*3 CW*0301 ALPHA CHAIN	87-114								
PIC12 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*4 CW*0401 ALPHA CHAIN	87-114								
PIC13 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*4 CW*0402 ALPHA CHAIN	87-114								
PIC14 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*4 CW*0403 ALPHA CHAIN	87-114								
PIC17 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1401 ALPHA CHAIN PRECURSOR	87-114								
P2A6 HUMAN	6971 KD (2-3) POLYADENYLATE SYNTHETASE	593-620								
P2A4A HUMAN	PROTEIN PHOSPHATASE P2A, 65 KD REGULATORY SUBUNIT, ALPHA ISOFORM	12-49	34-81							
P2A4B HUMAN	PROTEIN PHOSPHATASE P2A, 65 KD REGULATORY SUBUNIT, BETA ISOFORM	9-36	41-68							
P2A6A HUMAN	PROTEIN PHOSPHATASE P2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM	177-218								
P411 HUMAN	ERYTHROID PROTEIN 4.1 (BAND 4.1, ERYTHROCYTE FORM)	32-46								

PCGENE	10712124 Motif Search on All Human Protein Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILE NAME	PROTEIN	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
P412_HUMAN	NON-ERYTHROID PROTEIN 4.1 (BAND 4.1, LYMPHOID FORM)	3-30								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	172-200		708-735						
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	318-545								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	381-522								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	311-518								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	222-233								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	22-26								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	72-99								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	98-132		310-337						
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	92-119								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	168-202								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	163-197								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	191-218		365-395						
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	104-134								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	51-80		319-349	1085-1112	1402-1429				
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	428-455								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	92-119		720-747						
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	109-136								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	61-88		119-147	2694-2633					
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	306-333								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	14-51		182-209	668-700					
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	78-108		179-206	313-340					
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	78-115		126-153	676-710					
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	652-689		300-327	1250-1284					
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	48-60								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	46-58								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	43-79		304-331						
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	29-56		70-97						
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	132-149								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	26-53								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	162-189								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	163-190								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	197-238		381-414						
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	36-63								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	79-113								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	59-86								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	49-76								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	492-523		604-648	926-964					
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	213-247								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	173-216		263-290						
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	36-63								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	812-839		1004-1031	1617-1644					
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	1344-1571								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	1811-1838								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	553-580		823-852						
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	810-837								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	162-196								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	40-67		306-333						
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	215-242								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	66-87		626-653						
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	37-78		137-164						
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	16-43		74-104						
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	68-95								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	57-84								
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	585-619		1073-1100	1353-1380	1524-1584	2074-2113	2132-2159	2181-2215	2240-2271
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	2468-2507		2529-2559	2850-3000	3160-3390	3480-3570	3620-3634	4040-4074	4090-4120
P42_HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	4274-4301		4397-4438	4465-4492	4499-4544				

PCGENE	1011714-1 Nucleotide Sequence on All Human Protein Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
BLERANIE	PROTEIN								
PAFC1_HUMAN	APOLIPROTEIN C-II PRECURSOR (APO-CII)	36-63							
PAFC_HUMAN	ADENOMATOUS POLYPOSIS COLI PROTEIN (APC PROTEIN)	145-172	617-651	834-861	1795-1822	2172-2312	2572-2609		
PAPE_HUMAN	APOLIPROTEIN E PRECURSOR (APO-E)	48-81	247-274						
PAPDA_HUMAN	APOLIPROTEIN A PRECURSOR (EC 3.4.21.-) (APO(A)) (LPA(A))	4448-4475							
PAQPI_HUMAN	AQUAPORIN-CHIP (WATER CHANNEL PROTEIN FOR RED BLOOD CELLS AND KIDNEY)	59-73							
PARK1_HUMAN	BETA-ADRENERGIC RECEPTOR KINASE 1 (EC 2.7.1.126) (BETA-ARK-1)	323-553							
PARYL_HUMAN	ARGININOSUCCINATE LYASE (EC 4.3.2.1) (ARGINOSUCCINASE)	69-103							
PARN1_HUMAN	ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR (ARNT PROTEIN) (DIO)	223-230							
PARRC_HUMAN	BETA-ARRESTIN 2	215-242	305-332						
PARRS_HUMAN	ARRESTIN (RETINAL S-ANTIGEN) (48 KD PROTEIN) (S-AG)	299-332							
PARY1_HUMAN	ARYLAMINE N-ACETYLTRANSFERASE, MONOMORPHIC (EC 2.3.1.15) (NNA1)	7-34							
PARY2_HUMAN	ARYLAMINE N-ACETYLTRANSFERASE, POLYMORPHIC (EC 2.3.1.15) (PNA1)	7-34							
PASNS_HUMAN	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (EC 6.3.3.4) (TS11 CELL)	311-338	347-374						
PATCD_HUMAN	CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC RETICULUM TYPE (EC 3.6.1.38)	163-190							
PATCE_HUMAN	CALCIUM-TRANSPORTING ATPASE ENDOPLASMIC RETICULUM TYPE (EC 3.6.1.38)	163-190							
PATF1_HUMAN	TRANSCRIPTION FACTOR ATF-1 (FRAGMENT)	203-230							
PATF3_HUMAN	TRANSCRIPTION FACTOR ATF-3 (FRAGMENT)	30-61							
PATF5_HUMAN	TRANSCRIPTION FACTOR ATF-5 (FRAGMENT)	34-68							
PATF6_HUMAN	TRANSCRIPTION FACTOR ATF-6 (FRAGMENT)	351-394							
PATF7_HUMAN	TRANSCRIPTION FACTOR ATF-7 AND ATF-4-DELTA	129-163							
PB212_HUMAN	ATP SYNTHASE B CHAIN, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34)	114-141							
PB213_HUMAN	NUCLEOLAR PHOSPHOPROTEIN B31 (NUCLEOPHOSMIN) (NUNATRIN)	292-319	345-372						
PB214_HUMAN	BETA-2-ADRENERGIC RECEPTOR	1081-1111							
PB215_HUMAN	ANION EXCHANGE PROTEIN 2 (NON-ERYTHROID BAND 3-LIKE PROTEIN) (BNDIL)	115-142	525-562	609-636					
PB216_HUMAN	B2M PROTEIN	106-140							
PB217_HUMAN	TEXTROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN	120-147	310-337	771-807					
PB218_HUMAN	BASINUCLEIN	178-205							
PB219_HUMAN	TRANSFORMING PROTEIN BCL-2-BETA	33-63							
PB220_HUMAN	B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD)	784-835							
PB221_HUMAN	BREAKPOINT CLUSTER REGION PROTEIN	246-280	504-531						
PB222_HUMAN	BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31)	216-230							
PB223_HUMAN	BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A)	202-229							
PB224_HUMAN	BONE MORPHOGENETIC PROTEIN 3 PRECURSOR (BMP-3)	374-391							
PB225_HUMAN	BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4)	192-219							
PB226_HUMAN	BONE MORPHOGENETIC PROTEIN 7 PRECURSOR (BMP-7) (OSTEOGENIC PROTEIN 1)	284-311							
PB227_HUMAN	BNT1 PROTEIN	168-195							
PB228_HUMAN	BACTERICIDAL PERMEABILITY INCREASING PROTEIN PRECURSOR (BPI) (CAP 37)	10-17							
PB229_HUMAN	BOMBESIN RECEPTOR SUBTYPE 2 (BR2-3)	128-162	333-385						
PB230_HUMAN	BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P42)	26-53							
PB231_HUMAN	BTG1 PROTEIN (B-CELL TRANSLOCATION GENE 1 PROTEIN)	921-948							
PB232_HUMAN	C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLATE)	130-150							
PB233_HUMAN	MHC CLASS II TRANSACTIVATOR CITA	341-368							
PB234_HUMAN	COLLAGEN ALPHA 1(03) CHAIN PRECURSOR	27-54							
PB235_HUMAN	COLLAGEN ALPHA 1(02) CHAIN PRECURSOR	731-750							
PB236_HUMAN	CALBINDIN (VITAMIN D-DEPENDENT CALCIUM-BINDING PROTEIN) (CABP), AVIAN	818-865							
PB237_HUMAN	CADHERIN 3 PRECURSOR (784 ANTIGEN)	93-122	323-350						
PB238_HUMAN	EPITHELIAL-CADHERIN PRECURSOR (E-CADHERIN)	384-411	580-607						
PB239_HUMAN	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)	2-29							
PB240_HUMAN	PLACENTAL-CADHERIN PRECURSOR (P-CADHERIN)	140-167							
PB241_HUMAN	CALGRANULIN A (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 8) (MRP-8)	297-324	467-494						
PB242_HUMAN	CALCITONIN RECEPTOR PRECURSOR (CT-R)	561-588							
PB243_HUMAN	CARTILAGE MATRIX PROTEIN PRECURSOR	502-539							
PB244_HUMAN	CALPAIN 1 LARGE (CATALYTIC) SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED)	674-701							
PB245_HUMAN	CALPAIN 2 LARGE (CATALYTIC) SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED)	13-40							
PB246_HUMAN	CALPAIN P4 LARGE (CATALYTIC) SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED)	111-138	321-355						
PB247_HUMAN	PLACENTAL CALCIUM-BINDING PROTEIN								
PB248_HUMAN	ADENYL CYCLASE-ASSOCIATED PROTEIN (CAP)								

PCGENE	10711714 Mail Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PCALB	PCALB HUMAN	217-244	14-48								AREA 2
PCASB	PCASB HUMAN	14-48									
PCATA	PCATA HUMAN	432-436									
PCATD	PCATD HUMAN	233-282									
PCATH	PCATH HUMAN	41-68									
PCATL	PCATL HUMAN	278-305									
PCATS	PCATS HUMAN	10-57	142-169								
PCBFB	PCBFB HUMAN	24-58	138-165								
PCBGO	PCBGO HUMAN	88-122									
PCBPB	PCBPB HUMAN	69-129	278-305	319-346							
PCBPH	PCBPH HUMAN	335-382									
PCCT1	PCCT1 HUMAN	33-62									
PCCT7	PCCT7 HUMAN	209-240									
PCCG1	PCCG1 HUMAN	1298-1342									
PCD14	PCD14 HUMAN	142-169									
PCD1A	PCD1A HUMAN	32-63	281-308								
PCD1E	PCD1E HUMAN	77-104									
PCD10	PCD10 HUMAN	226-235									
PCD1R	PCD1R HUMAN	226-235									
PCD1S	PCD1S HUMAN	88-119									
PCD14	PCD14 HUMAN	74-108									
PCD17	PCD17 HUMAN	101-128									
PCD1L	PCD1L HUMAN	7-34									
PCD1X	PCD1X HUMAN	328-335	183-217								
PCD1Y	PCD1Y HUMAN	44-71	240-267								
PCD23	PCD23 HUMAN	87-114									
PCD27	PCD27 HUMAN	118-177									
PCD33	PCD33 HUMAN	5-32									
PCD35	PCD35 HUMAN	296-330									
PCD3B	PCD3B HUMAN	568-595									
PCD3C	PCD3C HUMAN	433-460									
PCD3E	PCD3E HUMAN	372-399	493-520	553-607	715-732	767-825	850-884	903-947	963-995	1000-1107	
PCD3F	PCD3F HUMAN	1122-1149	1179-1239	1230-1271	1340-1367	1440-1481	1486-1556	1646-1680	1684-1724	1808-1846	
PCD3G	PCD3G HUMAN	1852-1887	1890-1917	1940-1988	2071-2048	2288-2318	2440-2478	2498-2563			
PCD3H	PCD3H HUMAN	913-940									
PCD3I	PCD3I HUMAN	71-108									
PCD3J	PCD3J HUMAN	158-189	802-829	895-922	1243-1270						
PCD3K	PCD3K HUMAN	216-243									
PCD3L	PCD3L HUMAN	315-349									
PCD3M	PCD3M HUMAN	17-51									
PCD3N	PCD3N HUMAN	56-97	220-257	451-478							
PCD3O	PCD3O HUMAN	112-139									
PCD3P	PCD3P HUMAN	787-814	943-970								
PCD3Q	PCD3Q HUMAN	121-148									
PCD3R	PCD3R HUMAN	123-157									
PCD3S	PCD3S HUMAN	9-50									
PCD3T	PCD3T HUMAN	36-98	323-350	367-394							
PCD3U	PCD3U HUMAN	93-120	430-457								
PCD3V	PCD3V HUMAN	66-93									
PCD3W	PCD3W HUMAN	29-56	93-148								
PCD3X	PCD3X HUMAN	242-276	591-620	837-867							
PCD3Y	PCD3Y HUMAN	1292-1319									
PCD3Z	PCD3Z HUMAN	298-342	537-564	970-997	1270-1304						
PCD4	PCD4 HUMAN	367-398									
PCD4A	PCD4A HUMAN	225-261									
PCD4B	PCD4B HUMAN										
PCD4C	PCD4C HUMAN										
PCD4D	PCD4D HUMAN										
PCD4E	PCD4E HUMAN										
PCD4F	PCD4F HUMAN										
PCD4G	PCD4G HUMAN										
PCD4H	PCD4H HUMAN										
PCD4I	PCD4I HUMAN										
PCD4J	PCD4J HUMAN										
PCD4K	PCD4K HUMAN										
PCD4L	PCD4L HUMAN										
PCD4M	PCD4M HUMAN										
PCD4N	PCD4N HUMAN										
PCD4O	PCD4O HUMAN										
PCD4P	PCD4P HUMAN										
PCD4Q	PCD4Q HUMAN										
PCD4R	PCD4R HUMAN										
PCD4S	PCD4S HUMAN										
PCD4T	PCD4T HUMAN										
PCD4U	PCD4U HUMAN										
PCD4V	PCD4V HUMAN										
PCD4W	PCD4W HUMAN										
PCD4X	PCD4X HUMAN										
PCD4Y	PCD4Y HUMAN										
PCD4Z	PCD4Z HUMAN										
PCD5	PCD5 HUMAN										
PCD5A	PCD5A HUMAN										
PCD5B	PCD5B HUMAN										
PCD5C	PCD5C HUMAN										
PCD5D	PCD5D HUMAN										
PCD5E	PCD5E HUMAN										
PCD5F	PCD5F HUMAN										
PCD5G	PCD5G HUMAN										
PCD5H	PCD5H HUMAN										
PCD5I	PCD5I HUMAN										
PCD5J	PCD5J HUMAN										
PCD5K	PCD5K HUMAN										
PCD5L	PCD5L HUMAN										
PCD5M	PCD5M HUMAN										
PCD5N	PCD5N HUMAN										
PCD5O	PCD5O HUMAN										
PCD5P	PCD5P HUMAN										
PCD5Q	PCD5Q HUMAN										
PCD5R	PCD5R HUMAN										
PCD5S	PCD5S HUMAN										
PCD5T	PCD5T HUMAN										
PCD5U	PCD5U HUMAN										
PCD5V	PCD5V HUMAN										
PCD5W	PCD5W HUMAN										
PCD5X	PCD5X HUMAN										
PCD5Y	PCD5Y HUMAN										
PCD5Z	PCD5Z HUMAN										
PCD6	PCD6 HUMAN										
PCD6A	PCD6A HUMAN										
PCD6B	PCD6B HUMAN										
PCD6C	PCD6C HUMAN										
PCD6D	PCD6D HUMAN										
PCD6E	PCD6E HUMAN										
PCD6F	PCD6F HUMAN										
PCD6G	PCD6G HUMAN										
PCD6H	PCD6H HUMAN										
PCD6I	PCD6I HUMAN										
PCD6J	PCD6J HUMAN										
PCD6K	PCD6K HUMAN										
PCD6L	PCD6L HUMAN										
PCD6M	PCD6M HUMAN										
PCD6N	PCD6N HUMAN										
PCD6O	PCD6O HUMAN										
PCD6P	PCD6P HUMAN										
PCD6Q	PCD6Q HUMAN										
PCD6R	PCD6R HUMAN										
PCD6S	PCD6S HUMAN										
PCD6T	PCD6T HUMAN										
PCD6U	PCD6U HUMAN										
PCD6V	PCD6V HUMAN										
PCD6W	PCD6W HUMAN										
PCD6X	PCD6X HUMAN										
PCD6Y	PCD6Y HUMAN										
PCD6Z	PCD6Z HUMAN										
PCD7	PCD7 HUMAN										
PCD7A	PCD7A HUMAN										
PCD7B	PCD7B HUMAN										
PCD7C	PCD7C HUMAN										
PCD7D	PCD7D HUMAN										
PCD7E	PCD7E HUMAN										
PCD7F	PCD7F HUMAN										
PCD7G	PCD7G HUMAN										
PCD7H	PCD7H HUMAN										
PCD7I	PCD7I HUMAN										
PCD7J	PCD7J HUMAN										
PCD7K	PCD7K HUMAN										
PCD7L	PCD7L HUMAN										
PCD7M	PCD7M HUMAN										
PCD7N	PCD7N HUMAN										
PCD7O	PCD7O HUMAN										
PCD7P	PCD7P HUMAN										
PCD7Q	PCD7Q HUMAN										
PCD7R	PCD7R HUMAN										
PCD7S	PCD7S HUMAN										
PCD7T	PCD7T HUMAN										
PCD7U	PCD7U HUMAN										
PCD7V	PCD7V HUMAN										
PCD7W	PCD7W HUMAN										
PCD7X	PCD7X HUMAN										
PCD7Y	PCD7Y HUMAN										
PCD7Z	PCD7Z HUMAN										

PCGENE	1071214.4 Motif Search on All Human Protein Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
FILE NAME	PROTEIN	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
PC01_HUMAN	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.1.1)	353-380							
PC02_HUMAN	CYTOCHROME P450 VII (CHOLESTEROL 7-ALPHA-MONOXYGENASE)	263-290	146-173						
PC03_HUMAN	CYTOCHROME P450 IIC17 (EC 1.14.14.1) (P450-3AC) (FRAGMENT)	109-136							
PC04_HUMAN	CYTOCHROME P450 IIE1 (EC 1.14.14.1) (P450-9) (ETHANOL INDUCIBLE)	231-258							
PC05_HUMAN	CARBAMOYL-PHOSPHATE SYNTHASE (AMMONIA) MITOCHONDRIAL PRECURSOR	112-146	420-447						
PC06_HUMAN	MITOCHONDRIAL CARNITINE PALMITOYLTRANSFERASE II PRECURSOR	410-437							
PC07_HUMAN	CYTOCHROME P450 IIC17 (EC 1.14.14.1) (P450-C17) (ESTEROID 17-ALPHA-)	226-257							
PC08_HUMAN	CYTOCHROME P450 IIC17 (EC 1.14.14.1) (P450-C17) (ESTEROID 17-ALPHA-)	234-271							
PC09_HUMAN	COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR)	986-1013							
PC10_HUMAN	COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN)	94-125							
PC11_HUMAN	CAMP RESPONSE ELEMENT BINDING PROTEINS A AND B (CREB-A AND CREB-B)	68-126	179-420	633-678	724-754	763-790			
PC12_HUMAN	CAMP RESPONSE ELEMENT BINDING PROTEIN CRE-BP1	380-414							
PC13_HUMAN	C-REACTIVE PROTEIN PRECURSOR	60-87	150-177						
PC14_HUMAN	CLEAVAGE SIGNAL-1 PROTEIN (CS-1)	203-233							
PC15_HUMAN	MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (M-CSF)	143-170							
PC16_HUMAN	CLEAVAGE STIMULATION FACTOR, 30 KD SUBUNIT (CSTF 30 KD SUBUNIT) (CF-1)	6-33							
PC17_HUMAN	ALPHA-CATENIN (CADHERIN-ASSOCIATED PROTEIN)	681-718							
PC18_HUMAN	ALPHA-CATENIN RELATED PROTEIN (CATENIN ALPHA-2)	680-717							
PC19_HUMAN	GAP JUNCTION BETA-2 PROTEIN (CONNEXIN 26) (CX26)	108-139							
PC20_HUMAN	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 32) (CX32) (GAP JUNCTION 28 K)	117-144							
PC21_HUMAN	GAP JUNCTION ALPHA-4 PROTEIN (CONNEXIN 37) (CX37)	88-115							
PC22_HUMAN	CYTOCHROME B5	3-42							
PC23_HUMAN	GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN)	80-107	126-153	352-396					
PC24_HUMAN	GUANYLATE CYCLASE SOLUBLE, ALPHA-2 CHAIN (EC 4.6.1.2)	106-133							
PC25_HUMAN	RETINAL GUANYL CYCLASE PRECURSOR (EC 4.6.1.2)	824-851							
PC26_HUMAN	CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)	293-320							
PC27_HUMAN	CYSTATIN A (STEIN A) (CYSTATIN AS)	27-58							
PC28_HUMAN	PROTO-ONCOGENE DBL PRECURSOR (CONTAINS: MCF2)	233-283							
PC29_HUMAN	DESNOPLAXIN I AND II (DPI AND DPII) (FRAGMENT)	153-180							
PC30_HUMAN	ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (EC 1.2.1.5)	31-58							
PC31_HUMAN	DYSTROPHIN	86-116	318-365	484-511	753-780	976-1003	1012-1039	1201-1228	1364-1394
PC32_HUMAN	DNA J PROTEIN HOMOLOG	183-185	318-365	484-511	753-780	976-1003	1012-1039	1201-1228	1364-1394
PC33_HUMAN	DNA LIGASE (EC 6.3.1.1) (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))	45-76							
PC34_HUMAN	DNA POLYMERASE ALPHA (EC 2.7.7.7)	130-157	355-392	732-759					
PC35_HUMAN	DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7)	25-74	1009-1037	1100-1127					
PC36_HUMAN	DIPYRIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION)	729-756							
PC37_HUMAN	DEOXYRIBONUCLEASE I PRECURSOR (EC 3.1.2.1) (DNASE I)	29-77	114-148						
PC38_HUMAN	DESMOCOLLIN JARIB PRECURSOR (DESMOSOMAL GLYCOPROTEIN II AND III)	44-71							
PC39_HUMAN	DESMOGLEIN 1 PRECURSOR (DESMOSOMAL GLYCOPROTEIN I) (DGI)	80-107	355-398						
PC40_HUMAN	DESMOGLEIN 3 PRECURSOR (DESMOSOMAL GLYCOPROTEIN I) (DGI)	13-42	271-298	497-531					
PC41_HUMAN	DIVEGENT UPSTREAM PROTEIN (DUP)	211-248	325-352						
PC42_HUMAN	VEGFA RELATED PROTEIN EAR-1	584-618							
PC43_HUMAN	EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2)	523-550							
PC44_HUMAN	ELONGATION FACTOR I BETA (EF-1-BETA)	44-78							
PC45_HUMAN	ELONGATION FACTOR I DELTA (EF-1-DELTA)	105-132							
PC46_HUMAN	EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112)	84-118							
PC47_HUMAN	EPIDERMAL GROWTH FACTOR RECEPTOR, KIDNEY (EGF) (UROGASTRONE)	64-91	440-467						
PC48_HUMAN	ETS-RELATED TRANSCRIPTION FACTOR E1-1	47-74							
PC49_HUMAN	ENDOPLASMIC RETICULUM PRECURSOR (94 KD GLUCOSE-REGULATED PROTEIN) (GRP94) (GRP96)	551-588							
PC50_HUMAN	RETROVIRUS-RELATED ENV POLYPEPTIDE	382-420	246-273						
PC51_HUMAN	IG EPSILON CHAIN C REGION	161-188							
PC52_HUMAN	PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72)	35-62	67-94	240-283					
PC53_HUMAN	DNA EXCISION REPAIR PROTEIN ERCC-1	58-85	142-169	458-485					
PC54_HUMAN	DNA EXCISION REPAIR PROTEIN ERCC-1	240-270							

PCGENE	1071784 Motif Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN									
PERC3 HUMAN	EXCISION REPAIR PROTEIN ERCC-4	160-209	919-971							
PESTR HUMAN	ESTROGEN RECEPTOR (ER)	431-488								
PET2 HUMAN	ENDOTHELIN-2 PRECURSOR (ET-2)	133-160								
PET3 HUMAN	ENDOTHELIN-3 PRECURSOR (ET-3)	182-209								
PEVA HUMAN	EVIA PROTEIN PRECURSOR	29-46								
PEZB1 HUMAN	EZB1 (P11) (GYTOVILIN) (VILIN-2)	119-146	331-392	402-429	512-539					
PFAS HUMAN	COAGULATION FACTOR V PRECURSOR	2101-2137								
PFAB HUMAN	COAGULATION FACTOR VIII PRECURSOR (PROCOAGULANT COMPONENT)	871-908	1007-1034	1194-1210						
PFAG HUMAN	COAGULATION FACTOR IX PRECURSOR (EC 3.4.21.22) (CHRISTMAS FACTOR)	271-298								
PFAB1 HUMAN	FATTY ACID-BINDING PROTEIN, INTESTINAL	98-125								
PFAS1 HUMAN	APOTOSIS-MEDIATING SURFACE ANTIGEN FAS PRECURSOR (APO-1 ANTIGEN)	23-50	249-301	306-333						
PFCE2 HUMAN	LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE)	81-115								
PFCEA HUMAN	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR ALPHA-SUBUNIT (FCER)	140-174								
PFGR2 HUMAN	FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC 2.1.1.117)	310-337								
PFIBA HUMAN	FIBRINOGEN ALPHA CHAIN PRECURSOR	131-165	427-457							
PFIBB HUMAN	FIBRINOGEN BETA CHAIN PRECURSOR	149-186								
PFIBG HUMAN	FIBRINOGEN GAMMA-A CHAIN PRECURSOR	59-93	123-160							
PFIBH HUMAN	FIBRINOGEN GAMMA-B CHAIN (FIBRINOGEN GAMMA)	59-93	123-160							
PFINC HUMAN	FIBRONECTIN PRECURSOR	2168-2199								
PFLI1 HUMAN	FLI-1 ONCOGENE (EBOS TRANSCRIPTION FACTOR)	172-209								
PFMO2 HUMAN	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 2 (EC 1.14.13.8)	162-193								
PFOS HUMAN	P53-C-FOS PROTO-ONCOGENE PROTEIN	184-218	236-283	301-328						
PFR1 HUMAN	FOS-RELATED ANTIGEN 1	133-168								
PFR2 HUMAN	FOS-RELATED ANTIGEN 2	149-180								
PFRH HUMAN	FERRITIN HEAVY CHAIN	7-34								
PFRL HUMAN	FERRITIN LIGHT CHAIN	3-33								
PFSLR HUMAN	FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R)	164-195								
PFUCO HUMAN	TISSUE ALPHA-L-FUCOSIDASE PRECURSOR (EC 3.2.1.51) (ALPHA-L-FUCOSIDASE)	308-333								
PFUMH HUMAN	FUMARATE HYDATASE, MITOCHONDRIAL (EC 4.2.1.2) (FUMARASE)	424-451								
PGS2 HUMAN	PUTATIVE LYMPHOCYTE GAG SWITCH PROTEIN	56-83								
PGI9P HUMAN	PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, HEAVY CHAIN (PKCSH)	146-173								
PGH1P HUMAN	GLUCOSE-4-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9) (PHOSPHOGLUCOSE)	16-50								
PGI2 HUMAN	MAJOR GASTROINTESTINAL TUMOR-ASSOCIATED PROTEIN GA733-2 PRECURSOR	181-215								
PGAT2 HUMAN	GALACTOKINASE 2 (EC 2.7.1.6)	294-281								
PGAA1 HUMAN	GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-1 SUBUNIT PRECURSOR (GABA(A) 210-237)	210-237								
PGAA3 HUMAN	GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-3 SUBUNIT PRECURSOR (GABA(A) 211-255)	211-255								
PGAS3 HUMAN	GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR)	74-105								
PGBO1 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 1	22-49								
PGBO2 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 2	22-49								
PGBAK HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(K), ALPHA SUBUNIT (GQ) (ALPHA-3)	22-49								
PGBAS HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (ADENYLATE)	7-34								
PGBAY HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(Y), ALPHA SUBUNIT (ALPHA-11)	93-122								
PGBBJ HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(Y), ALPHA SUBUNIT (ALPHA-11)	93-122								
PGBPL HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(Y), ALPHA SUBUNIT (ALPHA-11)	65-92								
PGBP2 HUMAN	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 2 (GUANINE NUCLEOTIDE-)	110-137	235-282	289-316						
PGBT2 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-2 SUBUNIT (TRANSDUCIN)	22-49								
PGCF HUMAN	GC-RICH SEQUENCE DNA-BINDING FACTOR (GC) (TRANSCRIPTION FACTOR 9)	200-227	293-320	367-394	396-423	647-674				
PGCHI HUMAN	GTP CYCLOHYDROLASE I (EC 3.5.4.16)	163-192								
PGCRA HUMAN	GLUCOCORTICOID RECEPTOR, ALPHA (GR)	167-194								
PGCRB HUMAN	GLUCOCORTICOID RECEPTOR, BETA (GR)	167-194								
PGCSP HUMAN	GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2)	460-487								
PGDN HUMAN	GLIA DERIVED NEURIN (GDN) (PROTEINASE NEURIN)	83-110								
PGELS HUMAN	GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF)	701-728								
PGFAP HUMAN	GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE	189-216	349-376	384-411						
PGLAS HUMAN	N-ACETYL GLUCOSAMINE-6-ASULFATASE PRECURSOR (EC 3.1.6.14) (G6S)	170-221								
PGLPK HUMAN	GLYCEROL KINASE (EC 2.7.1.30) (ATP-GLYCEROL 1-PHOSPHOTRANSFERASE)	78-112	231-278							
POLY1 HUMAN	SERINE HYDROXYMETHYL TRANSFERASE, CYTOSOLIC (EC 2.1.2.1) (SERINE)	32-59	344-371							

PCGENE	10217164.Nc01 Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ELK1	PROTEIN									
PGY17	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL (EC 2.1.2.1) (SERINE)	417-444								
PGK7	78 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN	564-591	598-625							
PGK2	GLYCINE RECEPTOR ALPHA-2 CHAIN PRECURSOR	142-169	341-368							
PGRAV	GRAVIN (FRAGMENT)	9-43	61-88							
PGRFR	GROWTH HORMONE-RELEASING HORMONE RECEPTOR PRECURSOR (GHRH RECEPT	128-155								
PGTH	GLUTATHIONE S-TRANSFERASE HA SUBUNIT 2 (EC 2.3.1.18) (GTH2) (CLASS-	64-91								
PGTFA	GLTASE-ACTIVATING PROTEIN (GAP) (GAS P21 PROTEIN ACTIVATOR)	474-501	1012-1047							
PGTBI	GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN	274-301								
PGTBJ	GLUCOSE TRANSPORTER TYPE 3, BRAIN	272-299								
PGTRA	GLUCOSE TRANSPORTER TYPE 4, INSULIN-RESPONSIVE	290-317								
PHIO	HISTONE H1	44-89								
PHIA	HISTONE H1A (H1.1)	71-104								
PHIB	HISTONE H1B (H1.4)	70-101								
PHIC	HISTONE H1C (H1.3)	71-102								
PHID	HISTONE H1D (H1.2)	70-101								
PHIT	HISTONE H1T	74-105								
PHZBO	HISTONE H2B.1	20-47								
PHZBZ	HISTONE H2B.2	20-47								
PHZB	HISTONE H2B (H2B.1 A)	20-47								
PHZ3	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ3) ALPHA CHAIN PRECURSOR	142-169								
PHZK	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-W4) BETA CHAIN PRECURSOR	56-83								
PHBP	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(W4) BETA CHAIN PRECURSOR	50-77								
PHBQ	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(W2) BETA CHAIN PRECURSOR	50-77								
PHB3	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, SB BETA CHAIN (FRAGMENT)	16-43								
PHBG	HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1 (HBGF-1) (ACIDIC FIBROBLAST	102-129								
PHBQJ	INT-3 PROTO-ONCOGENE PROTEIN PRECURSOR (HBGF-3)	61-91								
PHBG	FIBROBLAST GROWTH FACTOR-4 PRECURSOR (FGF-4) (HBGF-4) (HST-2)	41-75	159-186							
PHBI	P59 PROTEIN (HSP BINDING IMMUNOPHILIN) (HBI) (POSSIBLE PEPTIDYL-PROLYL	264-312								
PHEM4	URICOPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.73) (URICOPORPHYRINOGEN-III	74-118								
PHBP2	HEPARIN COFACTOR II PRECURSOR (HC-II) (PROTEASE INHIBITOR LEUSEPIN 2)	169-196								
PHBP3	SERINE PROTEASE HEPSEN (EC 3.4.21.-)	22-49								
PHBXA	BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL-	356-383								
PHBXB	BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL-BETA-	388-415								
PHMX1	HOMEOBOX PROTEIN MSX-1 (HOX-7)	178-212								
PHNFA	HEPATOCYTE NUCLEAR FACTOR 1-ALPHA (HNF-1A) (LIVER SPECIFIC	2-29								
PHOT	HEMB OXYGENASE 1 (EC 1.14.99.3) (HO-1)	197-224								
PHPTD	4-HYDROXYPHENYLPIRUVATE DIOXYGENASE (EC 1.13.11.27) (4HPPD)	306-333								
PHRX	ZINC FINGER PROTEIN HBX	521-548	914-974	1637-1666	2215-2286	2289-2316	3317-3344	3448-3475		
PHS1	HEMATOPOIETIC LINEAGE CELL SPECIFIC PROTEIN	43-70								
PHS9A	HEAT SHOCK PROTEIN HSP 90-ALPHA (HSP 86)	443-470	640-674							
PHSER	HEAT-STABLE ENTEROTOXIN RECEPTOR PRECURSOR (GC-C) (INTESTINAL	511-545								
PHSF1	HEAT SHOCK FACTOR PROTEIN 1 (HSF 1) (HEAT SHOCK TRANSCRIPTION FACTOR	113-140	168-209							
PHSF2	HEAT SHOCK FACTOR PROTEIN 2 (HSF 2) (HEAT SHOCK TRANSCRIPTION FACTOR	117-198								
PHY21	IG HEAVY CHAIN PRECURSOR V-J REGION (ARH-77)	67-108								
PHYT	IG HEAVY CHAIN V-III REGION (GAL)	47-74								
PHX11	HOMEOBOX PROTEIN HOX-11 (TCL-3 PROTO-ONCOGENE)	262-289								
PHX87	HOMEOBOX PROTEIN HOX-87 (HOX-2C) (RH0.C1)	115-162								
PIAPP	ISLET AMYLOID POLYPEPTIDE	53-80								
PIBP3	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3)	181-210								
PICI	PLASMA PROTEASE C1 INHIBITOR PRECURSOR (C1 INH)	231-278								
PICQ2	INTERCELLULAR ADHESION MOLECULE-2 PRECURSOR (ICAM-2)	57-84								
PIDB	INSULIN-DEGRADING ENZYME (EC 3.4.99.45) (INSULINASE) (INSULIN	474-504	907-941							
PIFA1	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)	222-259	322-349							
PIF4B	INTRINSIC FACTOR PRECURSOR (IF) (GASTRIC INTRINSIC FACTOR)	149-176	406-433							
PIF	INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN) (ERYTHROID	308-349								
PUBA	INTERLEUKIN-1 ALPHA PRECURSOR (IL-1 ALPHA) (HEMATOPOIETIN-1)	86-107	183-210							
PLIA	INTERLEUKIN-1 RECEPTOR, TYPE 1 PRECURSOR (IL-1R1) (P80)	76-110	172-199							



FCGENE	1021784.Neill/ Search on All Human Protein Sequences	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10
FILE NAME	PROTEIN	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10
PILIR1 HUMAN	INTERLEUKIN-1 RECEPTOR, TYPE I PRECURSOR (IL-1R1) (P80)	437-467									
PILIR2 HUMAN	INTERLEUKIN-1 RECEPTOR, TYPE II PRECURSOR (IL-1R2)	159-186									
PILIR3 HUMAN	INTERLEUKIN-3 RECEPTOR ALPHA CHAIN PRECURSOR (IL-3R-ALPHA)	87-114									
PILIR4 HUMAN	INTERLEUKIN-4 RECEPTOR (IL-4) (B-CELL STIMULATORY FACTOR 2) (BSF-2)	112-139									
PILIR5 HUMAN	INTERFERON ALPHA-1 PRECURSOR	94-121									
PILIR6 HUMAN	INTERFERON ALPHA-2 PRECURSOR	90-117	164-191	300-327	508-535						
PILIR7 HUMAN	INTERFERON BETA PRECURSOR (FIBROBLAST)	88-129									
PILIR8 HUMAN	INTERFERON-INDUCED 17 KD PROTEIN (CONTAINS INTERFERON-INDUCED 15 KD)	83-121									
PILIR9 HUMAN	INTERFERON-INDUCED 36 KD PROTEIN (IFI-36K)	51-78	216-245	393-430							
PILIR10 HUMAN	INSULIN RECEPTOR PRECURSOR (EC 2.7.1.112) (IR)	592-619									
PILIR11 HUMAN	INVLUCIN	119-146	229-273	326-363	386-430						
PILIR12 HUMAN	ID-MYO-INOSITOL-TRISPHOSPHATE 3-KINASE A (EC 2.7.1.127) (INOSITOL)	121-162									
PILIR13 HUMAN	PLASMA SERINE PROTEASE (PROTEIN C) INHIBITOR PRECURSOR (PCI)	90-117	206-233								
PILIR14 HUMAN	INTERPHOTORECEPTOR RETINOID-BINDING PROTEIN PRECURSOR (IRBP)	670-697									
PILIR15 HUMAN	INTERFERON REGULATORY FACTOR 2 (IRF-2)	157-193									
PILIR16 HUMAN	75 KD INOSITOL-1,4,5-TRISPHOSPHATE 4-PHOSPHATASE PRECURSOR	235-262									
PILIR17 HUMAN	PLATELET MEMBRANE GLYCOPROTEIN IIA PRECURSOR (GPIIa) (COLLAGEN RECEPTOR)	1579-606	900-927								
PILIR18 HUMAN	FIBRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-F)	250-284	657-695	765-792							
PILIR19 HUMAN	FIBRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-E) (CD49F)	884-911	944-974								
PILIR20 HUMAN	LEUKOCYTE ADHESION GLYCOPROTEIN LFA-1 ALPHA CHAIN PRECURSOR (LEUKOC)	256-283	310-341	795-822							
PILIR21 HUMAN	CELL SURFACE GLYCOPROTEIN MAC-1 ALPHA SUBUNIT PRECURSOR (CR-3 ALPHA)	1044-1078									
PILIR22 HUMAN	VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V)	230-264									
PILIR23 HUMAN	FIBRONECTIN RECEPTOR BETA SUBUNIT PRECURSOR (INTEGRIN BETA-1) (CD29)	218-245	334-399								
PILIR24 HUMAN	CELL SURFACE ADHESION GLYCOPROTEINS LFA-1, CR3 AND P150.95, BETA-	319-366	705-732								
PILIR25 HUMAN	PLATELET MEMBRANE GLYCOPROTEIN IIIa PRECURSOR (GPIIb) (INTEGRIN BETA-3)	324-351									
PILIR26 HUMAN	INTEGRIN BETA-4 SUBUNIT PRECURSOR (GPIIb)	342-369									
PILIR27 HUMAN	INTEGRIN BETA-5 SUBUNIT PRECURSOR	724-751									
PILIR28 HUMAN	INTEGRIN BETA-6 SUBUNIT PRECURSOR	311-318	332-393								
PILIR29 HUMAN	INTEGRIN BETA-8 SUBUNIT PRECURSOR	162-199	606-717								
PILIR30 HUMAN	INTER-ALPHA-TRYPsin INHIBITOR COMPLEX COMPONENT II PRECURSOR	134-161	435-452	772-818							
PILIR31 HUMAN	KERATIN, TYPE I CYTOSKELETAL 10 (CYTOKERATIN 10) (K10)	154-187	196-227	337-399	428-462						
PILIR32 HUMAN	KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13)	112-142									
PILIR33 HUMAN	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14)	122-152	306-335	391-424							
PILIR34 HUMAN	KERATIN, TYPE I CYTOSKELETAL 15 (CYTOKERATIN 15) (K15)	112-141									
PILIR35 HUMAN	KERATIN, TYPE I CYTOSKELETAL 16 (CYTOKERATIN 16) (K16)	308-339									
PILIR36 HUMAN	KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17)	122-152	302-346	393-431							
PILIR37 HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18)	87-114	231-298	337-385							
PILIR38 HUMAN	KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19)	88-118	317-362	370-397							
PILIR39 HUMAN	KERATIN, TYPE I CYTOSKELETAL 1 (CYTOKERATIN 1) (K1)	196-226	346-384	390-467							
PILIR40 HUMAN	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (FRAGMENT)	215-248	364-405	461-488							
PILIR41 HUMAN	KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (K5 KD)	42-73	126-153	189-248							
PILIR42 HUMAN	KERATIN, TYPE II CYTOSKELETAL 6 (CYTOKERATIN 6) (K6) (K6B KERATIN)	183-246	332-373								
PILIR43 HUMAN	KERATIN, TYPE II CYTOSKELETAL 8 (CYTOKERATIN 8) (K8)	178-239	325-366	422-449							
PILIR44 HUMAN	KERATIN, TYPE II CYTOSKELETAL 36 KD (K6A KERATIN) (FRAGMENT)	140-167									
PILIR45 HUMAN	6-PHOSPHOFRUCTOKINASE, MUSCLE TYPE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE)	140-167									
PILIR46 HUMAN	6-PHOSPHOFRUCTOKINASE, LIVER TYPE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE)	49-80	128-159								
PILIR47 HUMAN	PHOTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL (EC 2.7.1.112) (P150)	498-525									
PILIR48 HUMAN	IG KAPPA CHAIN C REGION	37-85									
PILIR49 HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE-LIKE X-LINK)	380-414									
PILIR50 HUMAN	CAMP-DEPENDENT PROTEIN KINASE TYPE I-ALPHA REGULATORY CHAIN	179-208									
PILIR51 HUMAN	CAMP-DEPENDENT PROTEIN KINASE TYPE I-BETA REGULATORY CHAIN	172-204									
PILIR52 HUMAN	CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN	175-202	290-317								
PILIR53 HUMAN	NUCLEAR FACTOR KAPPA-B SUBUNIT-1 (NF-KAPPA-B P105 SUBUNIT)	329-370									
PILIR54 HUMAN	CREATINE KINASE, B CHAIN (EC 2.7.3.2)	301-328									
PILIR55 HUMAN	TYROSINE PROTEIN KINASE ECK PRECURSOR (EC 2.7.1.112) (EPITHELIAL CELL)	466-493									
PILIR56 HUMAN	PHOTO-ONCOGENE TYROSINE-PROTEIN KINASE FER (EC 2.7.1.112) (P94-FER)	219-246	564-591								

ECGENE	10111244 Motif Search on All Human Protein Sequences	ARKA.1	ARKA.2	ARKA.3	ARKA.4	ARKA.5	ARKA.6	ARKA.7	ARKA.8	ARKA.9
FILE NAME	PROTEIN	ARKA.1	ARKA.2	ARKA.3	ARKA.4	ARKA.5	ARKA.6	ARKA.7	ARKA.8	ARKA.9
PKFES_HUMAN	PRO-ONCOGENE TYROSINE-PROTEIN KINASE FES/FPS (EC 2.7.1.112) (C-FES)	101-145	295-322							ARKA.9
PKFLT_HUMAN	RECEPTOR-RELATED TYROSINE KINASE FLT PRECURSOR (EC 2.7.1.112)	208-235	319-333							
PKFMS_HUMAN	MACROPHAGE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (CSF-1-R)	293-320								
PKFYN_HUMAN	PRO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN)	199-233								
PKOPB_HUMAN	CGMP-DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37)	17-34								
PKHEK_HUMAN	TYROSINE KINASE HEK RECEPTOR PRECURSOR (EC 2.7.1.112)	646-673								
PKNH_HUMAN	KINESIN HEAVY CHAIN	125-155	425-452	471-542	633-680	689-716	872-899			
PKKIT_HUMAN	KIT PRO-ONCOGENE TYROSINE KINASE PRECURSOR (EC 2.7.1.112)	235-263								
PKMET_HUMAN	HEPATOCYTE GROWTH FACTOR RECEPTOR PRECURSOR (MET PRO-ONCOGENE)	898-975								
PKNH_HUMAN	KININOGEN, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR)	505-532								
PKP35_HUMAN	GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE P35GTA (EC 2.7.1.1)	81-108								
PKP48_HUMAN	INTERFERON-INDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE	149-179	191-235	285-312						
PKP78_HUMAN	POTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.1)	582-609								
PKPCL_HUMAN	PROTEIN KINASE C, ETA TYPE (EC 2.7.1.1) (RPKC-ETA) (PKC-L)	318-345								
PKPT1_HUMAN	SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1 (EC 2.7.1.1)	149-176	209-233							
PKPY1_HUMAN	PYRUVATE KINASE, M1 (MUSCLE) ISOZYME (EC 2.7.1.40) (CYTOSOLIC THYROID)	243-289								
PKPY2_HUMAN	PYRUVATE KINASE, M2 ISOZYME (EC 2.7.1.40)	243-289								
PKPYR_HUMAN	PYRUVATE KINASE, ISOZYME R (EC 2.7.1.40)	2-29								
PKRET_HUMAN	PRO-ONCOGENE TYROSINE-PROTEIN KINASE RET (EC 2.7.1.112)	183-217								
PKROS_HUMAN	ROS PRO-ONCOGENE TYROSINE KINASE (EC 2.7.1.112) (FRAGMENT)	137-203								
PKSRC_HUMAN	PRO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC)	143-170								
PKUP7_HUMAN	LUPUS KU AUTOANTIGEN PROTEIN P70 (70 KD SUBUNIT OF KU ANTIGEN)	235-279								
PKUP8_HUMAN	LUPUS KU AUTOANTIGEN PROTEIN P86 (86 KD SUBUNIT OF KU ANTIGEN)	238-292								
PKYES_HUMAN	PRO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112) (P61-YES)	209-243								
PLAM1_HUMAN	LAMIN B1	32-66	117-144	152-193	214-241	397-424	480-507	510-539		
PLAM2_HUMAN	LAMIN A (70 KD LAMIN)	32-66	114-165	292-343						
PLAMC_HUMAN	LAMIN C	32-66	114-165	292-343						
PLAR_HUMAN	LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48)	935-969								
PLA_HUMAN	LUPUS LA PROTEIN (SIOGREN SYNDROME TYPE B ANTIGEN (SS-B))	191-222	295-342							
PLCAT_HUMAN	PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)	131-158								
PLDH9_HUMAN	L-LACTATE DEHYDROGENASE H CHAIN (EC 1.1.1.27) (LDH-B)	81-108	302-329							
PLDH9_HUMAN	L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A)	225-252								
PLDLR_HUMAN	LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR	480-510								
PLECH_HUMAN	ASIALOGLYCOPROTEIN RECEPTOR 1 (HEPATIC LECTIN II) (ASGPR)	62-96								
PLEND_HUMAN	P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GNP-140) (PADGEM)	32-59	87-116							
PLGUL_HUMAN	LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE)	83-117								
PLIF_HUMAN	LEUKAEMIA INHIBITORY FACTOR PRECURSOR (LIF) (DIFFERENTIATION-)	93-122								
PLIN1_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	152-179	232-263	298-338	671-698	874-901	1035-1066			
PLIPO_HUMAN	TRIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.3) (LIPASE, GASTRIC)	158-185								
PLIPS_HUMAN	HORMONE SENSITIVE LIPASE (EC 3.1.1.3) (HSL)	305-332								
PLKHA_HUMAN	LEUKOTRIENE A-4 HYDROLASE (EC 3.2.2.6) (LTA-4 HYDROLASE) (LEUKOTRIENE	42-83	290-324							
PLKHA_HUMAN	LAMININ A CHAIN PRECURSOR	1318-1345	1741-1771	1785-1812	1874-1851	1884-1921	1965-1999	2026-2039	2091-2118	
PLMB1_HUMAN	LAMININ B1 CHAIN PRECURSOR	1267-1314	1364-1394	1397-1631	1651-1714	1722-1781				
PLMB2_HUMAN	LAMININ B2 CHAIN PRECURSOR	1105-1135	1513-1547							
PLMB7_HUMAN	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2)	135-182								
PLOX3_HUMAN	ARACHIDONATE 12-LIPOXYGENASE (EC 1.11.1.3) (12-LOX)	341-368								
PLP33_HUMAN	ARACHIDONATE 5-LIPOXYGENASE (EC 1.11.1.34) (5-LIPOXYGENASE) (5-LO)	50-87								
PLP33_HUMAN	LACTASE-PHLOZIN HYDROLASE PRECURSOR (EC 3.2.1.62)	776-803								
PLP3B_HUMAN	PROTEIN-TYROSINE PHOSPHATASE BETA PRECURSOR (EC 2.7.1.60)	140-167	589-637							
PLP3G_HUMAN	PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (PTP-BETA)	1081-1108								
PLP3Z_HUMAN	PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR (EC 3.1.3.48) (PTP-ZETA)	553-587								
PLSHR_HUMAN	LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LHCG-R)	166-174	448-480							
PLV3B_HUMAN	IG LAMBDA CHAIN V-H REGION (NET)	61-88								
PLYAG_HUMAN	LYSOSOMAL ALPHA-GLUCOSIDASE PRECURSOR (EC 3.2.1.20) (ACID MALTASE)	183-212								
PLYAG_HUMAN	MITOCHONDRIAL 2-OXOGLUTARATE CARRIER PROTEIN (OGCP)	50-77								
PLMAC3_HUMAN	GALLACTOSE-SPECIFIC LECTIN (MAC-2 ANTIGEN) (G2-BINDING PROTEIN) (S1 KD	219-246								
PLMAN9_HUMAN	MAN(9)-ALPHA-MANNOSIDASE (EC 3.2.1.1)	414-441								

PCGENE	107178x4 Ncift Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN									
PMANA_HUMAN	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.1.1.9) (PHOSPHOMANNOSE ISOMERASE)	60-87								AREA 2
PMANR_HUMAN	MACROPHAGE MANNOSE RECEPTOR PRECURSOR	248-284	1147-1182							
PMAP2_HUMAN	MICROTUBULE-ASSOCIATED PROTEIN 2 (FRAGMENT)	434-478								
PMAP4_HUMAN	MICROTUBULE-ASSOCIATED PROTEIN 4	408-449								
PMAX_HUMAN	MAX PROTEIN	117-144								
PMDM2_HUMAN	MDM2 PROTEIN (P53-ASSOCIATED PROTEIN)	235-288								
PMDR1_HUMAN	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)	561-595								
PMERL_HUMAN	MERLIN (SCHWANNOMIN)	377-407	532-566							
PMERO_HUMAN	MEROSIN HEAVY CHAIN (LAMININ CHAIN A3) (FRAGMENT)	71-103	139-173	431-458	791-818					
PMGMT_HUMAN	METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (EC 2.1.1.63) (6-O-)	91-118								
PMKLP_HUMAN	MITOTIC KINESIN-LIKE PROTEIN-1	207-224	319-346	510-537	549-608					
PMKLT_HUMAN	MELANIN-CONCENTRATING HORMONE PRECURSOR	8-35								
PMKX1_HUMAN	MIXED LINEAGE KINASE 1 (EC 2.1.1-) (FRAGMENT)	130-157	321-348							
PMASA_HUMAN	METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE	393-420								
PMOES_HUMAN	MOESIN (MEMBRANE-ORGANIZING EXTENSION SPIKE PROTEIN)	119-146	331-403							
PMPCP_HUMAN	MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR	286-313								
PMPI3_HUMAN	M-PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48)	72-99								
PMPKK_HUMAN	DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE (EC 2.7.1.1-)	19-50								
PMPL1_HUMAN	CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (CI MAN-6)	1569-1596	2437-2478							
PMRCP_HUMAN	MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN	396-423	507-548							
PMSTR_HUMAN	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN	18-63								
PMKRE_HUMAN	MACROPHAGE SCAVENGER RECEPTOR TYPES I AND II (MACROPHAGE ACETYLATED	173-204	230-260							
PMATM_HUMAN	DNA (CYTOSINE-3)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA	387-414	601-628							
PMITF1_HUMAN	MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (MTTF1)	181-212								
PMOTA_HUMAN	METHYLMALONYL-COA MUTASE PRECURSOR (EC 5.4.99.3) (MCM)	468-519								
PMO2_HUMAN	INTERFERON-REGULATED RESISTANCE GTP-BINDING PROTEIN MXA (INTERFERON-108-150									
PMO3_HUMAN	INTERFERON-REGULATED RESISTANCE GTP-BINDING PROTEIN MBX (P78-RELATED	431-489	670-697							
PMYBA_HUMAN	MYB-RELATED PROTEIN A (FRAGMENT)	619-646								
PMYBB_HUMAN	MYB-RELATED PROTEIN B	87-117								
PMYCN_HUMAN	N-MYC PROTO-ONCOGENE PROTEIN	263-300	413-461							
PMYC_HUMAN	MYC PROTO-ONCOGENE PROTEIN	193-422								
PMYF4_HUMAN	MYOGENIC FACTOR MYF-4 (MYOGENIN)	119-146								
PMYF3_HUMAN	MYOGENIC FACTOR MYF-3	121-148								
PMYF2_HUMAN	MYELIN P2 PROTEIN	70-110								
PMYF1_HUMAN	MYELIN P1 PROTEIN	43-70								
PMYF7_HUMAN	MYELIN PROTEOLIPID PROTEIN (PLP) (LIPOPHILIN) (CONTAINS: MYELIN	38-23								
PMYSA_HUMAN	MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM (FRAGMENT)	48-75								
PMYSB_HUMAN	MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM	1541-1582	1640-1681	1683-1710	1801-1838					
PMYSE_HUMAN	MYOSIN HEAVY CHAIN, FAST SKELETAL MUSCLE, EMBRYONIC	46-73	860-903	932-1077	1119-1146	1193-1235	1267-1340	1364-1411	1483-1597	1641-1675
PMYSP_HUMAN	MYOSIN HEAVY CHAIN, PERINATAL CARDIAC MUSCLE (FRAGMENT)	1707-1734	1822-1858							
PMYS3_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (FRAGMENT)	50-77	95-125	141-188	215-272	403-483	507-552	586-624	685-726	784-818
PMYS5_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (FRAGMENT)	823-907	946-987	1049-1076						
PMYS6_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (FRAGMENT)	133-160	193-280	304-349	423-460	468-526	581-608	645-681	743-798	808-835
PMY1_HUMAN	MYELIN TRANSCRIPTION FACTOR 1 (MYT1) (FRAGMENT)	640-678								
PMY2_HUMAN	SODIUM/CALCIUM EXCHANGER PRECURSOR (NA+/CA2+-EXCHANGE PROTEIN)	492-519	594-621	705-735						
PMY3_HUMAN	NEURAL CELL ADHESION MOLECULE, PHOSPHATIDYLINOSITOL-LINKED ISOFORM	235-282								
PMY4_HUMAN	NEUTROPHIL CYTOSOL FACTOR 1 (NCF-47K) (47 KD AUTOSOMAL CHRONIC	234-261	310-337							
PMY5_HUMAN	NEUTROPHIL NADPH OXIDASE FACTOR (P67-PHOX)	532								
PMY6_HUMAN	DNA-BINDING PROTEIN NEFA PRECURSOR	50-77	82-112	143-195						
PMY7_HUMAN	NEPILYSIN (EC 3.4.24.11) (NEUTRAL ENDOPEPTIDASE) (NEP)	170-216	644-671							
PMY8_HUMAN	NEUROFIBROMIN (NEUROFIBROSIS-RELATED PROTEIN NF-1) (FRAGMENT)	1145-1172	1388-1422	1639-1666						
PMY9_HUMAN	NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)	91-128	431-490							
PMY10_HUMAN	NEUROFILAMENT TRIPLET L PROTEIN (68 KD NEUROFILAMENT PROTEIN) (NF-L)	92-126	441-468							
PMY11_HUMAN	NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M)	338-365								
PMY12_HUMAN	SUBSTANCE-P RECEPTOR (SPR) (NK-1 RECEPTOR) (NK-1R)	166-193								
PMY13_HUMAN	NATURAL KILLER CELLS PROTEIN 4 PRECURSOR									

FCGENE	1071784 NcRef Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PKCKR_HUMAN	PKCKR RECOGNITION PROTEIN (NATURAL-KILLER CELLS CYCLOPHILIN-)	187-214	448-475	555-599	701-742	816-841	1080-1131		
PKGGA_HUMAN	PKGGA AND NKG2-B TYPE II INTEGRAL MEMBRANE PROTEINS	28-55							
PNOST_HUMAN	NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I)	389-416							
PNOS1_HUMAN	NITRIC-OXIDE SYNTHASE, ENDOTHELIAL (EC 1.14.13.39) (EC-NOS) (NOS)	389-416	1116-1146	1292-1319					
PNTG1_HUMAN	SODIUM- AND CHLORIDE-DEPENDENT GABA TRANSPORTER 1	131-158							
PNTR_HUMAN	NEUROTENSIN RECEPTOR (NT-R)	57-84							
PNTRSE_HUMAN	SODIUM-DEPENDENT SEROTONIN TRANSPORTER (5HT TRANSPORTER) (SHT)	71-98							
PNNTA_HUMAN	SODIUM- AND CL-ORDE-DEPENDENT TAURINE TRANSPORTER	120-147							
PNM2A_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3)	202-240							
PNM2M_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3)	184-191	372-399						
PNM2N_HUMAN	NUCLEOBINDIN PRECURSOR	46-73	360-387						
PNM2L_HUMAN	NUCLEOBINDIN (PROTEIN C23)	462-508							
PNM2R_HUMAN	PUTATIVE NEUROPEPTIDE Y RECEPTOR TYPE 1 (NPY1-R) (FB23) (NPYRL)	115-142							
PNM2T_HUMAN	ORNITHINE AMINOTRANSFERASE PRECURSOR (EC 2.6.1.1) (ORNITHINE--OXO-	98-128							
PNM2A_HUMAN	OCTAMER-BINDING TRANSCRIPTION FACTOR 3A (OCT-3A)	179-173							
PNM2B_HUMAN	OCTAMER-BINDING TRANSCRIPTION FACTOR 3B (OCT-3B)	37-78							
PNM2C_HUMAN	LOWE'S OCULOCECEREBRORETAL SYNDROME PROTEIN	704-715							
PNM2D_HUMAN	LIPOMIDE ACTIN-TRANSFERASE COMPONENT (E2) PRECURSOR OF BRANCHED-CHAIN	100-127	375-402						
PNM2E_HUMAN	DHAPOLIPOMIDE ACETYLTRANSFERASE COMPONENT (E3) OF PYRUVATE	72-99							
PNM2F_HUMAN	OLIGODENDROCYTE-MYELIN GLYCOPROTEIN PRECURSOR (OMG)	51-80							
PNM2G_HUMAN	BLUE-SENSITIVE OPSIN (BLUE CONE PHOTORECEPTOR PIGMENT)	220-247							
PNM2H_HUMAN	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT)	90-117	239-266						
PNM2I_HUMAN	RED-SENSITIVE OPSIN (RED CONE PHOTORECEPTOR PIGMENT)	90-117	239-266						
PNM2J_HUMAN	ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (EC 2.1.3.1)	170-204							
PNM2K_HUMAN	OSTEONECTIN PRECURSOR (BASEMENT MEMBRANE PROTEIN BM-40)	173-207							
PNM2L_HUMAN	OXYSTEROL-BINDING PROTEIN	89-123	190-217	290-317	517-604				
PNM2M_HUMAN	OXYTOCIN RECEPTOR (OT-R)	350-377							
PNM2N_HUMAN	RETINOBLASTOMA-ASSOCIATED PROTEIN-LIKE 107 KD HOMOLOG (P107)	159-186	422-449						
PNM2O_HUMAN	DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1	19-40	637-664						
PNM2P_HUMAN	PLECKSTIN (P17)	398-325							
PNM2Q_HUMAN	PROLYL-4-HYDROXYLASE ALPHA SUBUNIT PRECURSOR (EC 1.14.11.2)	29-69	191-218						
PNM2R_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN)	72-99	271-298	361-407					
PNM2S_HUMAN	PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SUBUNIT (PI3-KINASE	12-39	428-476	386-613	688-715				
PNM2T_HUMAN	PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR	72-104							
PNM2U_HUMAN	PAIRED BOX PROTEIN FAX-3 (B-CELL SPECIFIC TRANSCRIPTION FACTOR)	157-187							
PNM2V_HUMAN	PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)	38-65							
PNM2W_HUMAN	PLATELET ENDOTHELIAL CELL ADHESION MOLECULE PRECURSOR (PECAN-1)	685-719							
PNM2X_HUMAN	PROENKEPHALIN A PRECURSOR	142-176							
PNM2Y_HUMAN	EOSINOPHIL PEROXIDASE PRECURSOR (EC 1.11.1.7) (EPO) (FRAGMENT)	308-335							
PNM2Z_HUMAN	PERFORIN 1 PRECURSOR (P1) (LYMPHOCYTE PORE FORMING PROTEIN) (PFP)	411-418							
PNM2A_HUMAN	PLATELET BASIC PROTEIN PRECURSOR (PBP) (CONTAINS: CONNECTIVE-TISSUE	21-55							
PNM2B_HUMAN	CARILAGE-SPECIFIC PROTEOGLYCAN CORE PROTEIN PRECURSOR (CSPC)	72-100							
PNM2C_HUMAN	LARGE FIBROBLAST PROTEOGLYCAN PRECURSOR (VEBICAN) (CHONDROITIN	64-98	1390-1417	1553-1580					
PNM2D_HUMAN	15-HYDROXYPROSTAGLANDIN DEHYDROGENASE (NADH) (EC 1.1.1.147) (PGDH)	87-118							
PNM2E_HUMAN	BETA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112)	294-321	334-384	465-495					
PNM2F_HUMAN	ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR	64-94	347-395	461-488	524-551	986-1018			
PNM2G_HUMAN	PROSTAGLANDIN G/H SYNTHASE PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE)	331-358							
PNM2H_HUMAN	BONE/CARTILAGE PROTEOGLYCAN PRECURSOR (BIGLYCAN) (PG-S1)	100-127							
PNM2I_HUMAN	PHENYLALANINE-4-HYDROXYLASE (EC 1.14.16.1) (PAH) (PHE-4-	239-266							
PNM2J_HUMAN	PROHIBITIN	41-68							
PNM2K_HUMAN	PHOSPHUCIN (1) KD PHOTOTRANSLOCING PROTEIN (MEKA PROTEIN)	184-225							
PNM2L_HUMAN	GLYCOCEN PHOSPHORYLASE, LIVER FORM (EC 2.4.1.1)	116-143							
PNM2M_HUMAN	GLYCOCEN PHOSPHORYLASE, MUSCLE FORM (EC 2.4.1.1)	532-559							
PNM2N_HUMAN	GLYCOCEN PHOSPHORYLASE, BRAIN FORM (EC 2.4.1.1)	531-560							
PNM2O_HUMAN	1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2	908-935							

PCGENE	101-1784	NCBI Search on All Human Protein Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PILECAN	PROTEIN		371-400								
PIPLX	HUMAN	1-3-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2	371-400								
PLASL	HUMAN	FLAOGLOBIN (DESOMOLAKIN III)	507-514								
PLSL	HUMAN	L-PLASTIN (FIBRIN)	510-561								
PLSL	HUMAN	T-PLASTIN (FIBRIN)	3-33								
PM22	HUMAN	PERIPHERAL MYELIN PROTEIN 22 (PMP-22)	81-111								
PM22	HUMAN	PHOSPHOGLYCERATE MUTASE, BRAIN FORM (EC 5.4.2.1) (PGAM-B) (EC 5.4.2.4)	81-111								
PM22	HUMAN	PHOSPHOGLYCERATE MUTASE, MUSCLE FORM (EC 5.4.2.1) (PGAM-M)	531-585								
PM22	HUMAN	PROBABLE TRANSCRIPTION FACTOR PML-1	531-585								
PM22	HUMAN	PROBABLE TRANSCRIPTION FACTOR PML-X	101-130								
PM22	HUMAN	AUTOANTIGEN PM-SCL	14-51								
PM22	HUMAN	DNA-BINDING PROTEIN PO-GA	182-209	610-637	667-699						
PM22	HUMAN	RETROVIRUS-RELATED POLYPROTEIN (REVERSE TRANSCRIPTASE)	774-804								
PM22	HUMAN	RETROVIRUS-RELATED POLYPROTEIN (FRAGMENT)	78-118	171-203							
PM22	HUMAN	OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION)	189-216								
PM22	HUMAN	PROSTATIC ACID PHOSPHATASE PRECURSOR (EC 3.1.3.3)	235-269								
PM22	HUMAN	RED CELL ACID PHOSPHATASE 1, ISOZYME 5 (EC 3.1.3.2) (ACP1)	26-53								
PM22	HUMAN	NAD(+)-ADP-RIBOSYLTRANSFERASE (EC 2.4.2.30) (POLY (ADP-RIBOSE))	699-729	972-1003							
PM22	HUMAN	PROTEASOMAL COMPONENT C2 (EC 3.4.99.46) (MACROPAIN SUBUNIT C2)	39-66								
PM22	HUMAN	PROTEASOMAL COMPONENT C3 (EC 3.4.99.46) (MACROPAIN SUBUNIT C3)	34-61								
PM22	HUMAN	PROTEASOMAL COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9)	201-261								
PM22	HUMAN	PROGESTERONE RECEPTOR (PR) (FORMS A AND B)	846-890								
PM22	HUMAN	VITAMIN K-DEPENDENT PROTEIN S (BLOOD CLOTTING) PRECURSOR	337-371								
PM22	HUMAN	VITAMIN K-DEPENDENT PROTEIN Z PRECURSOR	29-56								
PM22	HUMAN	PSORIN	63-92								
PM22	HUMAN	PULMONARY SURFACTANT-ASSOCIATED PROTEIN D PRECURSOR (PSP-D) (SP-D)	224-231								
PM22	HUMAN	PARATHYROID HORMONE PRECURSOR (PARATHYRIN)	86-113								
PM22	HUMAN	PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.49) (PTP-1B)	136-177								
PM22	HUMAN	T-CELL PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.49) (TCPTP)	59-86	138-178							
PM22	HUMAN	PROTEIN-TYROSINE PHOSPHATASE 1C (EC 3.1.3.49) (PTP-1C) (HEMATOPOIETIC)	227-261	512-580							
PM22	HUMAN	PROTEIN-TYROSINE PHOSPHATASE 2C (EC 3.1.3.49) (PTP-2C) (PTP-1D)	41-68	218-245							
PM22	HUMAN	PROTEIN-TYROSINE PHOSPHATASE G1 (EC 3.1.3.49) (PTPG1)	618-645	695-722							
PM22	HUMAN	PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE	368-395								
PM22	HUMAN	PENTAXIN-RELATED PROTEIN PTK3 PRECURSOR	74-101								
PM22	HUMAN	PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (EC 6.3.4.13) (GARS) (GLYCINAMIDE)	801-830								
PM22	HUMAN	MULTIFUNCTIONAL PROTEIN ADEH1 (PHOSPHORIBOSYLAMINOIMIDAZOLE-)	391-418								
PM22	HUMAN	ADENYLOSUCCLATE LYASE (EC 4.3.2.2) (ADENYLOSUCCLATE) (ASL)	204-231								
PM22	HUMAN	UREIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE)	120-150								
PM22	HUMAN	GTP SYNTHASE (EC 6.3.4.2) (UTP-AMMONIA LIGASE) (CTP SYNTHETASE)	86-113	300-334							
PM22	HUMAN	PREGNANCY ZONE PROTEIN PRECURSOR	315-354	990-1024	1162-1189	1405-1432					
PM22	HUMAN	TRANSCRIPTION FACTOR IIF, ALPHA SUBUNIT (TIF, ALPHA SUBUNIT)	474-501								
PM22	HUMAN	RAS-RELATED PROTEIN RAB-4	38-65								
PM22	HUMAN	RAS-RELATED PROTEIN RAB-6	123-150								
PM22	HUMAN	RADIX	308-335	414-463	510-537						
PM22	HUMAN	RAS-RELATED PROTEIN RAB-11 (RAB11) (YLB)	131-178								
PM22	HUMAN	RETINOLACTONIA BINDING PROTEIN 1 (RBBP-1) (PRB-BINDING PROTEIN E1F-1)	139-156	161-222							
PM22	HUMAN	RENIN PRECURSOR, RENAL (EC 3.4.21.15) (ANGIOTENSINOGENASE)	116-163								
PM22	HUMAN	RESTIN (CYTOPLASMIC LINKER PROTEIN-170 ALPHA-2) (CLIP-170)	190-217	333-370	445-472	571-619	744-771	784-832	1023-1050	1088-1139	1157-1184
PM22	HUMAN	REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A)	1216-1306								
PM22	HUMAN	TRANSFORMING PROTEIN (RPT) (RET FINGER PROTEIN)	208-235	423-455							
PM22	HUMAN	BLOOD GROUP RH(D) POLYPEPTIDE	182-217								
PM22	HUMAN	RIBOPHORIN I PRECURSOR	361-388								
PM22	HUMAN	RIBOPHORIN II PRECURSOR	81-108	496-530							
PM22	HUMAN	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M1 CHAIN (EC 1.17.4.1)	142-172	361-388							
PM22	HUMAN	60S RIBOSOMAL PROTEIN L23 (EPSTEIN-BARR VIRUS SMALL RNA ASSOCIATED)	42-69	370-400							
PM22	HUMAN	60S RIBOSOMAL PROTEIN L26	78-112								
PM22	HUMAN	60S RIBOSOMAL PROTEIN L28	155-89	101-137							

PCGENE	1071784 Nucleotide Search on All Human Protein Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PRLA9	PROTEIN									
PRLA9	60S RIBOSOMAL PROTEIN L9	146-192								
PRLA9	60S ACIDIC RIBOSOMAL PROTEIN P0 (L10E)	138-163								
PRLA9	32 KD RO PROTEIN (SIOGREN SYNDROME TYPE A ANTIGEN (SS-A))	190-233	218-265							
PRLA9	60 KD RO PROTEIN (SIOGREN SYNDROME TYPE A ANTIGEN (SS-A))	192-245								
PROL	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C1C2 (HNRNP C1 AND HNRNP C2)	16-43								
PROL	HETEROGENEOUS RIBONUCLEOPROTEIN L (HNRNP L)	501-528								
PROL	HETEROGENEOUS RIBONUCLEOPROTEIN U	630-657								
PRPB1	DNA-DIRECTED RNA POLYMERASE II 215 KD POLYPEPTIDE	269-296	665-720	879-906	1314-1341	1371-1398				
PRPB1	DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	626-667	1008-1035							
PRPB1	DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	242-274								
PRPB1	RETINOIC ACID RECEPTOR RXR-ALPHA	318-352								
PRPB1	RETINOIC ACID RECEPTOR RXR-BETA ISOFORM 1	378-403								
PRPB1	RETINOIC ACID RECEPTOR RXR-BETA ISOFORM 2	396-423								
PRPB1	40S RIBOSOMAL PROTEIN S12	60-87								
PRPB1	40S RIBOSOMAL PROTEIN S16	89-116								
PRPB1	40S RIBOSOMAL PROTEIN S15	26-53								
PRPB1	40S RIBOSOMAL PROTEIN S17A	14-41								
PRPB1	40S RIBOSOMAL PROTEIN S17 (S1)	73-100								
PRPB1	40S RIBOSOMAL PROTEIN S18	136-163								
PRPB1	RAS-LIKE PROTEIN TC21	231-350								
PRPB1	UT SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN)	13-47								
PRPB1	UT SMALL NUCLEAR RIBONUCLEOPROTEIN B	17-44								
PRPB1	RYANODINE RECEPTOR, SKELETAL MUSCLE	134-188	493-532	866-893	2750-2777	2820-2847	3304-3331	3359-3356	3912-3939	4021-4048
PS10A	5-100 PROTEIN, ALPHA CHAIN	12-54								
PS10B	5-100 PROTEIN, BETA CHAIN	14-56								
PS10B	5-100D PROTEIN	31-38								
PS10B	ADENOSYLHOMOCYSTEINASE (EC 3.1.1.1) (S-ADENOSYL-L-HOMOCYSTEINE)	389-416								
PS10B	DNA-BINDING PROTEIN SA TB1	709-736								
PS10B	SQUAMOUS CELL CARCINOMA ANTIGEN (SCCA) (PROTEIN T4-A)	78-105								
PS10B	STEM CELL FACTOR PRECURSOR (SCF)	74-101								
PS10B	SEMOGELIN I PROTEIN PRECURSOR (SGI) (CONTAINS: SEMINAL BASIC)	64-98	176-226	288-329	334-368					
PS10B	SEMOGELIN II PRECURSOR (SGII)	71-98	183-226	304-355	405-439	539-575				
PS10B	SET PROTEIN	38-65	154-181							
PS10B	SECRETOGRAFIN I PRECURSOR (CHROMOGRAFIN B)	144-178								
PS10B	SECRETOGRAFIN II PRECURSOR (CHROMOGRAFIN C)	234-281	290-317	334-361						
PS10B	BONE SIALOPROTEIN II PRECURSOR (BSP II)	84-113	155-193	256-283						
PS10B	POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF1L	231-258	345-372							
PS10B	SKI-RELATED ONCOGENE SNON	414-441								
PS10B	SPECTRIN ALPHA CHAIN	193-220	370-621	653-712	1099-1126	1461-1502	1882-1909	1988-2022	2120-2154	2223-2250
PS10B	SPECTRIN BETA CHAIN, ERYTHROCYTE	2346-2373								
PS10B	SEPIA TERN REDUCTASE (EC 1.1.1.13) (SPR)	90-124	316-330	486-520	648-675	987-1021	1027-1083	1287-1324	1347-1374	1834-1861
PS10B	SERUM RESPONSE FACTOR (SRF)	72-104	480-507							
PS10B	SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT (SR-ALPHA)	76-110								
PS10B	SOMATOSTATIN RECEPTOR TYPE 1	289-316								
PS10B	STATIN (PHOSPHOPROTEIN P19) (ONCOPROTEIN P19) (LEUKEMIA-ASSOCIATED)	47-74								
PS10B	SUCRASE-ISOMALTAZE, INTESTINAL (EC 3.2.1.48) (EC 3.2.1.10)	1748-1775								
PS10B	SYNAPTOSOMAL	31-67								
PS10B	ASPARTYL-TRNA SYNTHETASE ALPHA-2 SUBUNIT (EC 6.1.1.12) (ASPARTATE--	44-71								
PS10B	MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE (CONTAINS: GLUTAMYL-TRN	174-201	740-771							
PS10B	HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.2) (HISTIDINE--TRNA LIGASE)	380-442	468-502							
PS10B	ISNAPTOSOMAL (P19)	140-167	250-277							
PS10B	THREONYL-TRNA SYNTHETASE (EC 6.1.1.3) (THREONINE--TRNA	497-524	658-685							
PS10B	VALYL-TRNA SYNTHETASE (EC 6.1.1.9) (VALINE--TRNA LIGASE) (VALRS)	230-257	413-440							
PS10B	TRYPTOPHAN-TRNA SYNTHETASE (EC 6.1.1.2) (TRYPTOPHAN--TRNA LIGASE)	93-127	196-223							
PS10B	TRANSCRIPTION INITIATION FACTOR IE-BETA CHAIN (TIFIE-BETA)	34-68								
PS10B	TRANSCRIPTION FACTOR AP-4 (FRAGMENT)	169-196	245-272							

FCGNE	1071784 Motif Search on All Human Protein Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILENAME	PROTEIN									
PTAPB_HUMAN	TRANSCRIPTION FACTOR JUN-B	296-323								
PTAPD_HUMAN	TRANSCRIPTION FACTOR JUN-D	291-323								
PTAUT_HUMAN	MICROTUBULE-ASSOCIATED PROTEIN TAU	278-305								
PTAU2_HUMAN	MICROTUBULE-ASSOCIATED PROTEIN TAU, FETAL	211-238								
PTCOI_HUMAN	TRANSCOBALAMIN 1 PRECURSOR	201-241	310-337							
PTCPI_HUMAN	T-COMPLEX PROTEIN 1 (TCP-1)	316-343								
PTDIT_HUMAN	DNA NUCLEOTIDYL-LEUTRANSFERASE (EC 2.7.7.3) (TERMINAL ADDITION ENZYME)	61-95								
PTKEK_HUMAN	RECEPTOR TYROSINE KINASE TEB PRECURSOR (EC 2.7.1.112) (IINK-6)	644-678	909-996	1007-1016						
PTFIB_HUMAN	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB)	135-162								
PTFEJ_HUMAN	TRANSCRIPTION FACTOR E1 (FRAGMENT)	43-70	122-149	178-226						
PTFSI_HUMAN	TRANSCRIPTION ELONGATION FACTOR 3-II	29-36								
PTF_HUMAN	TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III)	148-175								
PTGFI_HUMAN	TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1)	148-185								
PTGFI_HUMAN	TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2) (GLI 103H AS11)	241-270								
PTGFA_HUMAN	TRANSFORMING GROWTH FACTOR ALPHA PRECURSOR (TGF-ALPHA) (EGF-LIKE TGF)	27-114								
PTGLK_HUMAN	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE K (EC 2.3.2.13)	238-285								
PTHBS_HUMAN	THROMBOSPONDIN PRECURSOR	110-165	284-314							
PTHIK_HUMAN	3-KETOACYL-CoA THIOLEASE PEROXISOMAL PRECURSOR (EC 2.3.1.16) (BETA-)	185-212								
PTKND_HUMAN	PROTACHININ BETA PRECURSOR (CONTAINS: SUBSTANCE P, NEUROKININ A)	11-38								
PTLEI_HUMAN	TRANSUDIN-LIKE ENHANCER PROTEIN 1	626-653								
PTLEJ_HUMAN	TRANSUDIN-LIKE ENHANCER PROTEIN 2	94-125								
PTLEA_HUMAN	TRANSUDIN-LIKE ENHANCER PROTEIN 4 (FRAGMENT)	304-331								
PTOPA_HUMAN	DNA TOPOISOMERASE II, ALPHA ISOZYME (EC 5.99.1.3)	19-46	501-532							
PTOPB_HUMAN	DNA TOPOISOMERASE II, BETA ISOZYME (EC 5.99.1.3)	35-65	616-647							
PTPMI_HUMAN	TROPOMYOSIN, FIBROBLAST ISOFORM TM1	16-74	82-116							
PTPNA_HUMAN	TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE	16-43	47-74	82-116	147-174	191-237	243-277			
PTPAB_HUMAN	TROPOMYOSIN BETA CHAIN, SKELETAL MUSCLE	32-116	191-240							
PTPMC_HUMAN	TROPOMYOSIN ALPHA CHAIN, CARDIAC MUSCLE	16-74	82-116	193-277						
PTPMF_HUMAN	TROPOMYOSIN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TM10) (TME1)	37-116	210-240	243-270						
PTPMG_HUMAN	TROPOMYOSIN, FIBROBLAST NON-MUSCLE TYPE (TM10PL)	46-80	111-138	158-199	207-234					
PTPMI_HUMAN	TROPOMYOSIN, CYTOSKELETAL TYPE (TM10NM)	46-80	111-138	172-199						
PTPAS_HUMAN	TROPOMYOSIN ALPHA CHAIN, SMOOTH MUSCLE (FRAGMENT)	25-59	147-178							
PTPPI_HUMAN	TRIPETIDYL-PEPTIDASE II (EC 3.4.14.10) (TPP II) (TRIPETIDYL)	133-187	1004-1031	1160-1187						
PTPR_HUMAN	TPR ONCOGENE (FRAGMENT)	82-147								
PTR36_HUMAN	TREB36 PROTEIN	18-45	242-269							
PTRER_HUMAN	THYROTROPIN-RELEASING HORMONE RECEPTOR (TRH-R) (THYROLIBERIN)	349-383								
PTRUC_HUMAN	TROPONIN I, CARDIAC MUSCLE	36-63								
PTRKA_HUMAN	HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112)	66-93	117-148							
PTRSR_HUMAN	TRANSFERRIN RECEPTOR PROTEIN (TR) (ANTIGEN CD71) (T9)	188-215	366-393							
PTSHR_HUMAN	THYROTROPIN RECEPTOR PRECURSOR (TSH-R)	87-117	420-447							
PTTK_HUMAN	PROTEIN KINASE TKX (EC 2.7.1.1)	170-197	324-359	510-544	549-583					
PTTK2_HUMAN	NON-RECEPTOR TYROSINE KINASE TYR2 (EC 2.7.1.112)	150-177								
PUBAI_HUMAN	UBIQUITIN-ACTIVATING ENZYME E1 (A159 PROTEIN)	448-475								
RUBFI_HUMAN	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UBF-1)	227-254								
RUDPO_HUMAN	UDP-GLUCURONOSYLTRANSFERASE PRECURSOR, MICROSMAL (EC 2.4.1.17)	227-254								
PUDPO_HUMAN	RECEPTOR TYROSINE KINASE UFO PRECURSOR (EC 2.7.1.112)	488-522								
PUSFI_HUMAN	UPSTREAM STIMULATORY FACTOR 1	251-295								
PVATC_HUMAN	VACUOLAR ATP SYNTHASE SUBUNIT C (EC 3.6.1.34) (V-ATPASE C SUBUNIT)	47-74	117-147							
PVILI_HUMAN	VILIN	318-372	427-461	712-744						
PVIDE_HUMAN	VIMENTIN	119-146	233-260							
PVINC_HUMAN	VINCULIN	108-135								
PVPRI_HUMAN	RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-)	95-174								
PWEEI_HUMAN	WEE1-LIKE PROTEIN KINASE (EC 2.7.1.113)	334-388								
PWTI_HUMAN	WILMS TUMOR PROTEIN (WT1)	247-274								
PXBPT_HUMAN	X-BOX BINDING PROTEIN-1 (XBP-1) (TREB3 PROTEIN)	97-115								
PXPAC_HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS (XERODERMA PIGMENTOSUM)	180-211								
PXPCC_HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM)	134-168	701-728							

PCGENE	10711744	Moif Search on All Human Protein Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILENAME	PROTEIN		AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PXPDC_HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM)	264-291		715-766	1047-1081						
PXPDC_HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-G CELLS (XERODERMA PIGMENTOSUM)	83-110									
PXRCC_HUMAN	DNA-REPAIR PROTEIN XPRC1	23-57									
PZNI0_HUMAN	ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN KOX1) (FRAGMENT)	29-56									
PZNI0_HUMAN	ZINC FINGER PROTEIN 40 (HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER)	17-62		307-334	1071-1078	1469-1500	2013-2037	2146-2180			
PZNI0_HUMAN	ZINC FINGER PROTEIN 45 (URC1744) (FRAGMENT)	1-30		201-228							
PZNI0_HUMAN	ZINC FINGER PROTEIN 46 (ZINC FINGER PROTEIN KUP)	121-149									



## TABLE X

Search Results Summary for PCTLZIP,  
P1CTLZIP, and P2CTLZIP Motifs



PHEMA MUMPM	133-146		PHEMA IABAN	221-237		PHEMA CVHOC	381-408
PHEMA MUMPR	133-148		PHEMA IABUD	234-260		PHEMA IAAIC	322-339
PHEMA MUMPS	133-148		PHEMA IACKA	234-260		PHEMA IABAN	308-323
PHEMA P11HW	345-380		PHEMA IACKG	231-247		PHEMA IABUD	320-337
PHEMA P12H	65-80		PHEMA IACKV	230-246		PHEMA IACKA	320-337
PHEMA P12HT	65-80		PHEMA IADA1	234-260		PHEMA IACKG	316-333
PHEMA RINDK	388-383		PHEMA IADA3	237-263		PHEMA IACKP	302-319
PHEMA SV6	7-84		PHEMA IADCC	234-260		PHEMA IACKQ	302-319
PHEMA SV6CM	7-84		PHEMA IADH1	221-237		PHEMA IACKG	319-330
PHEMA SV6CP	7-84		PHEMA IADH2	221-237		PHEMA IACKV	316-332
PHEMA SV6LN	7-84		PHEMA IADH3	221-237		PHEMA IADA1	320-337
PVENV DHV11	42-57		PHEMA IADH4	221-237		PHEMA IADA3	322-339
PVP77 CAPVK	89-104		PHEMA IADH6	221-237		PHEMA IADCZ	320-337
PVRJ8 VACC0	72-87		PHEMA IADH6	221-237		PHEMA IADH1	308-323
PVG01 BPP22	242-267		PHEMA IADH7	221-237		PHEMA IADH2	308-323
PVG01 HBVEB	168-184		PHEMA IADM2	237-263		PHEMA IADH3	308-323
PVG01 H8V11	210-226	317-332	PHEMA IADNZ	204-260		PHEMA IADH4	308-323
PVG06 BPT4	184-198		PHEMA IAE6	221-237		PHEMA IADH6	308-323
PVG07 BPT4	885-800		PHEMA IAE7	237-263		PHEMA IADH7	308-323
PVG08 HBV11	134-149		PHEMA IAFPR	230-246		PHEMA IADM2	322-339
PVG10 BPPH2	183-188		PHEMA IAHAL	230-262		PHEMA IADNZ	320-337
PVG10 BPPZA	183-188		PHEMA IAHAR	235-261		PHEMA IADU3	322-339
PVG10 H8V8A	106-124		PHEMA IAHCB	230-246		PHEMA IAE6	308-323
PVG16 BPP1	81-88		PHEMA IAHCB	230-246		PHEMA IAE7	322-339
PVG18 BPT4	468-483		PHEMA IAHCD	230-246		PHEMA IAFPR	316-332
PVG26 BPT4	87-112		PHEMA IAHDE	230-246		PHEMA IAGRE	320-337
PVG28 HBV11	20-35		PHEMA IAHFO	235-262		PHEMA IAGU2	320-337
PVG30 BPPH8	11-84		PHEMA IAHK6	235-262		PHEMA IAGUA	319-336
PVG30 BPOX2	22-37		PHEMA IAHK7	235-262		PHEMA IAHAL	321-338
PVG30 HBV8A	106-123		PHEMA IAHLE	230-246		PHEMA IAHCB	316-332
PVG37 BPT2	1263-1288		PHEMA IAHLO	230-246		PHEMA IAHCB	316-332
PVG37 HBV11	284-289		PHEMA IAHMI	235-262		PHEMA IAHCB	316-332
PVG66 HBV11	22-37	143-168	PHEMA IAHNM	235-262		PHEMA IAHDE	316-332
PVG66 HBV11	288-283		PHEMA IAHRO	235-262		PHEMA IAHFO	321-338
PVG68 HBV11	102-117		PHEMA IAH8A	235-262		PHEMA IAHK6	321-338
PVG68 HBV11	287-282		PHEMA IAH8P	230-246		PHEMA IAHK7	321-338
PVG68 HBV11	518-533		PHEMA IAH8W	230-246		PHEMA IAHLE	316-332
PVG8 BPPH2	234-249		PHEMA IAHTE	230-262		PHEMA IAHLO	316-332
PVG8 BPPZA	234-249		PHEMA IAHTO	235-262		PHEMA IAHMI	321-338
PVG8 BPPV1R	67-72		PHEMA IAHUR	235-262		PHEMA IAHNM	321-338
PVG8 BPPHX	234-249		PHEMA IAKIE	235-261		PHEMA IAHPR	316-332
PVG12 CVBF	284-278		PHEMA IALEN	235-261		PHEMA IAHRO	321-338
PVG12 CVBL9	284-278		PHEMA IAMAA	235-264		PHEMA IAH8A	321-338
PVG12 CVBLY	284-278		PHEMA IAMAB	237-283		PHEMA IAH8P	316-332
PVG12 CVBM	284-278		PHEMA IAMAO	237-263		PHEMA IAH8W	316-332
PVG12 CVBQ	284-278		PHEMA IAME1	237-263		PHEMA IAHTE	321-338
PVG12 CVBV	284-278		PHEMA IAME2	237-263			

PVQL2 CVPF3	442-467		PHEMA JAME9	221-237				PHEMA IAHTO	321-338	
PVQL2 CVPPU	440-466	604-619	PHEMA JAMIN	86-101				PHEMA IAHRU	321-338	
PVQL2 CVPR8	218-233		PHEMA JANT6	237-263			231-247	PHEMA IAJAP	317-334	
PVQL2 CVPRM	218-233		PHEMA JAQU7	221-237				PHEMA IAMAA	318-338	
PVQL2 IBV6	1066-1071		PHEMA IARUD	234-260				PHEMA IAMAB	324-341	
PVQL2 IBV8	1066-1070		PHEMA IABE2	234-260				PHEMA IAMAO	322-338	
PVQL2 IBVD2	1066-1071		PHEMA IASH2	234-260				PHEMA IAME1	322-338	
PVQL2 IBVK	1066-1070		PHEMA IASTA	230-246				PHEMA IAME2	322-338	
PVQL2 IBVM	1066-1070		PHEMA IATAI	235-261				PHEMA IAME9	300-323	
PVQLB HSB8A	701-716		PHEMA IATKM	234-260				PHEMA IAMIN	318-333	
PVQLB PRVIF	203-216		PHEMA IATKO	233-246				PHEMA IANT6	322-339	
PVQLC HSBVC	476-480		PHEMA IATKR	230-246				PHEMA IAPIL	320-337	
PVQLC HSE4	444-469		PHEMA IATKW	228-245				PHEMA IAGU7	306-323	
PVQLC HSEB	427-442		PHEMA IAUDD	237-263				PHEMA IARUD	320-337	
PVQLC PRVIF	446-461		PHEMA IAU89	235-261				PHEMA IABE2	320-337	
PVQLD H8V11	78-84		PHEMA IAVI7	236-264				PHEMA IASH2	321-338	
PVQLD H8V2	78-84		PHEMA IAXIA	235-261				PHEMA IASTA	315-332	
PVQLF BR8VA	286-280		PHEMA IAZCO	237-263				PHEMA IATKM	320-337	
PVQLF BR8VC	286-280		PHEMA IAZH2	221-237				PHEMA IAUDD	322-339	380-387
PVQLF BR8VR	286-280		PHEMA IAZH3	221-237				PHEMA IAVI7	323-340	
PVQLF HR8V1	286-280		PHEMA IAZUK	237-263				PHEMA IAZCO	322-339	
PVQLF HR8VA	286-280		PHEMA INBAA	116-131	286-310			PHEMA IAZH2	306-323	
PVQLF HR8VL	286-280		PHEMA INBBE	123-139	303-318			PHEMA IAZH3	306-323	
PVQLF HR8VR	286-280		PHEMA INBBO	116-132	283-308			PHEMA IAZUK	322-339	
PVQLF MUMPS	8-84		PHEMA INBEN	123-139	301-316			PHEMA MUMPM	101-118	
PVQLI VZVD	278-283		PHEMA INBFU	108-124	288-301			PHEMA MUMPR	101-118	
PVQLM HANTB	800-816		PHEMA INBGL	118-136	288-311			PHEMA MUMPS	101-118	
PVQLM FTFV	743-768		PHEMA INBHK	116-132	283-308			PHEMA NDVA	93-110	
PVQLM 8E0UR	801-816		PHEMA INBIB	108-124	288-303			PHEMA NDVB	93-110	
PVQLM 8E0U8	800-915		PHEMA INBID	120-136	289-314			PHEMA NDVD	93-110	
PVQLY LA88G	426-441		PHEMA INBLE	123-139	302-317			PHEMA NDVH	93-110	
PVQLY LA88J	427-442		PHEMA INBMO	113-129	282-307			PHEMA NDVI	93-110	
PVQLY MOPEI	426-440		PHEMA INBME	116-132	288-311			PHEMA NDVM	93-110	
PVM33 REOVD	621-636		PHEMA INBNA	108-124	288-303			PHEMA NDVQ	93-110	
PVM3A HP808	386-386		PHEMA INBOR	123-139	301-310			PHEMA NDVTQ	93-110	
PVM3A HPBV9	187-202		PHEMA INB81	123-139	301-316			PHEMA NDVV	93-110	
PVM3A WHV1	378-383		PHEMA INB9J	118-136	298-313			PHEMA PHODV	38-63	
PVM3A WHV59	383-398		PHEMA INBUS	116-132	294-309			PHEMA PI1HW	486-503	
PVM3A WHV7	383-398		PHEMA INBVI	116-132	286-311			PHEMA PI3B	111-128	
PVM3A WHV8	383-398		PHEMA INBVK	123-139	303-318			PHEMA PI3H4	111-128	
PVM3A WHV81	383-398		PHEMA INBYB	108-124	286-301			PHEMA PI3HA	111-128	
PVM3A WHVW6	234-249		PHEMA MUMPM	133-148				PHEMA PI3HT	111-128	
PVMT2 IAKIN	26-40		PHEMA MUMPR	133-148				PHEMA PI3HU	111-128	
PVMT2 IABAN	26-40		PHEMA MUMPB	133-148				PHEMA PI3HV	111-128	
PVMT2 IAFOW	26-40		PHEMA PI1HW	345-360				PHEMA PI3HW	111-128	
PVMT2 IAFPR	26-40		PHEMA PI2H	85-91				PHEMA PI3HX	111-128	
PVMT2 IAFPW	26-40		PHEMA PI2HT	85-91				PHEMA PI4HA	50-67	







[illegible]



## TABLE XI

Search Results Summary for P3CTLZIP, P4CTLZIP,  
P5CTLZIP, and P6CTLZIP Motifs



PVM01 VACCV	83-101	126-144	PVGL2 CVN4	980-1018		PVENY THGV	356-376		PHEMA P12H	13-34	
PVM1 REOVD	227-245		PVGL2 CVN4S	847-868		PVQ01 VACCC	280-318		PHEMA P12HT	13-34	
PVM1 REOVL	227-246		PVGL2 CVN4H	868-877		PVQ01 VACCV	237-257		PHEMA 8V8	7-28	378-400
PVMAT HRSVA	44-82		PVGL2 CVPF8	84-03	1030-1067	PVQ01 VARV	280-318		PHEMA 8V6CM	7-28	378-400
PVMAT NDVA	180-208		PVGL2 CVPPU	84-83	1030-1066	PVQ00 VACCC	31-61		PHEMA 8V6CP	7-28	378-400
PVMAT NDVB	180-208		PVGL2 CVPRD	814-833		PVQ06 VARV	31-61		PHEMA 8V6LN	7-28	378-400
PVMP CAMVC	183-201		PVGL2 CVPRM	814-833		PVQ09 BPPF1	25-45		PVQ01 H8VEB	188-180	
PVMP CAMVD	183-201		PVGL2 FIPV	1041-1080		PVQ12 H8V11	151-171		PVQ01 H8V11	588-610	
PVMP CAMVE	183-201		PVGL2 IBV8	588-607	771-700	PVQ22 H8V11	300-320		PVQ23 H8V11	314-336	
PVMP CAMVN	183-201		PVGL2 IBV8	588-607	770-788	PVQ39 H8V11	648-668	870-990	PVQ37 BPOX2	66-86	
PVMP CAMVW	183-201		PVGL2 IBVD2	588-607	770-788	PVQ61 H8V11	28-49		PVQ43 H8V11	167-178	
PVMP CAMVW	183-201		PVGL2 IBV8	588-607	770-788	PVQ63 H8V11	336-356		PVQ66 H8V11	288-309	
PVMP CAMVD	180-188		PVGL2 IBVM	588-607	770-788	PVQ65 H8V11	117-137		PVQ66 H8V8A	86-108	
			PVGLB HCMVA	708-725		PVQ74 H8V8A	124-144		PVQ56 H8V11	1155-1176	
			PVGLB HCMVT	707-720		PVGL2 IBV8	328-348		PVQ68 H8V8A	288-287	
			PVGLB H8V8U	117-138		PVGL2 IBV8	327-347		PVQ60 H8V11	30-51	
			PVGLB LTV8	260-275		PVGL2 IBVD2	328-348		PVQ63 H8V11	238-269	
			PVGLB LTVS	268-285		PVGL2 IBVD3	328-348		PVQF1 IBV8	1856-1877	
			PVGLB LTVT	288-285		PVGL2 IBV8	327-347		PVQH3 HCMVA	167-178	
			PVGLC H8V11	3-84	487-488	PVGL2 IBVM	327-347	378-388	PVGL2 CVBF	1259-1280	
			PVGLC H8V1K	3-84	407-488	PVGL2 IBVU2	310-330		PVGL2 CVBL9	1259-1280	
			PVGLC H8V8C	475-484		PVGLB EBV	732-782		PVGL2 CVBLV	1259-1280	
			PVGLQ CHAV	438-456		PVGLB HCMVA	760-770		PVGL2 CVBM	1259-1280	
			PVGLQ RABVH	372-381		PVGLB HCMVT	751-771		PVGL2 CVBQ	1259-1280	
			PVGLI H8VEB	44-83		PVGLB H8V23	78-88		PVGL2 CVB8V	1259-1280	
			PVGLI VZVD	278-287		PVGLB H8V2H	78-88		PVGL2 CVM4	1317-1338	
			PVGLM BUNGE	117-136		PVGLB H8V29	85-86		PVGL2 CVMA5	1266-1280	
			PVGLM PHV	152-171		PVGLB H8V8U	72-82		PVGL2 CVNMJH	1178-1187	
			PVGLM PTPV	887-1016		PVGLB H8V82	278-288		PVGLB H8V11	83-104	
			PVGLM PUUMH	155-174		PVGLB H8V8A	83-83		PVGLB H8V1F	82-103	
			PVGLM PUUMS	155-174		PVGLB MCMV8	738-758		PVGLB H8V1K	82-103	
			PVGLM RVFV	830-849		PVGLF P13H4	283-303		PVGLB H8V1P	83-104	
			PVGLM RVFVZ	830-849		PVGLQ RABVE	454-474		PVGLB MCMV9	135-158	
			PVGLM UUK	865-874		PVGLQ RABVH	454-474		PVGLC PRVIF	446-467	
			PVGLY LYCVW	89-108		PVGLQ RABVP	454-474		PVGLF COVO	338-357	
			PVQNB CPMV	1106-1104		PVGLQ RABV8	454-474		PVGLF MEAG8	224-245	
			PVQ3 REOVD	521-540		PVGLQ RABVT	454-474		PVGLF MEAG1	227-248	
			PVME1 CVBM	171-180		PVGLH MCMV8	670-680		PVGLF MEAGY	224-245	
			PVME1 CVH22	138-155		PVGLM BUNL7	1325-1346		PVGLF MUMPM	446-467	
			PVME1 CVPF8	174-183		PVGLM BUN8H	1325-1346		PVGLF MUMPR	446-467	
			PVME1 CVPPU	174-183		PVGLM BUNYV	988-1018		PVGLF MUMPS	446-467	
			PVME1 CVPRM	174-183		PVGLM HANTB	988-1018		PVGLF PHODV	305-328	
			PVME1 CVTKE	171-180		PVGLM HANTH	1000-1020		PVGLF P11HC	460-471	
						PVGLM HANTL	1001-1021		PVGLF P12H	460-471	
						PVGLM HANTV	1001-1021		PVGLF P12HQ	460-471	
						PVGLM RVFVZ	1156-1178		PVGLF P12HT	460-471	
						PVGLM SEOUR	1000-1020		PVGLF P13B	405-420	453-474

						PVGLM 6E0U9	999-1019	PVGLF PJH4	463-474	
						PVGLM ULK	926-945	PVGLF RINDK	220-241	
						PVGLY LYCYA	12-32	PVGLF RINDL	220-241	
						PVGLY LYCYW	12-32	PVGLF 8END6	400-481	
						PVGLY PIARV	12-32	PVGLF 8ENDF	400-481	
						PVGNB CPMV	141-161	PVGLF 8ENDH	400-481	
						PVMAT MUUPS	310-330	PVGLF 8ENDJ	400-481	
						PVMAT NDVA	308-329	PVGLF 8ENDZ	400-481	
						PVMAT NDVB	308-329	PVGLF 8V41	463-474	
						PVMAT PIHT	308-328	PVGLF 8V6	448-467	
						PVMAT PI4HA	312-332	PVGLH HCMVA	081-712	
						PVMAT PI4HB	312-332	PVGLH HCMVT	080-711	
						PVMAT 9V41	308-328	PVGLH H8VE4	304-326	
						PVMAT 8V6	308-328	PVGLH H8VE8	287-318	
						PVME1 BV0	74-84	PVGLH H8V8A	058-079	
						PVME1 BV8	74-84	PVGLH H8V2	2-23	
						PVME1 BV82	74-84	PVGLH H8V23	2-23	
						PVME1 BVK	74-84	PVGLM BUNGE	187-218	
						PVMSA HP808	201-221	PVGLM BUNL7	180-211	
						PVMSA HP806	208-228	PVGLM BUNSH	180-211	
						PVMSA HP8HE	283-313	PVGLM BUNYW	183-214	
						PVMSA WHV1	207-227	PVGLY LA86G	237-268	
						PVMSA WHV50	212-232	PVGLY LA86J	238-269	
						PVMSA WHV7	212-232	PVGP8 EBV	67-88	
						PVMSA WHV8	212-232	PVM01 VACC	281-302	
						PVMSA WHV81	212-232	PVM01 VACC	230-251	
						PVMSA WHV8	03-83	PVMAT H88VA	189-180	
								PVMAT RINDK	200-221	239-260
								PVMAT TRTV	122-143	
								PVME1 CVHOC	64-85	
								PVMSA HP8DB	201-222	
								PVMSA HP8VO	70-91	
								PVMSA HP8V2	244-265	
								PVMSA HP8V4	244-265	
								PVMSA HP8V6	244-265	
								PVMSA HP8VA	233-264	
								PVMSA HP8VD	70-91	
								PVMSA HP8V1	233-264	
								PVMSA HP8VJ	233-264	
								PVMSA HP8VL	233-264	
								PVMSA HP8VN	70-91	
								PVMSA HP8VO	233-264	
								PVMSA HP8VP	244-265	
								PVMSA HP8VR	244-265	
								PVMSA HP8V8	70-91	
								PVMSA HP8VW	233-264	
								PVMSA HP8VY	233-264	



TABLE XII

Search Results Summary for P7CTLZIP,  
P8CTLZIP, and P9CTLZIP Motifs



PHEMA IAV17	38-60	PVQL2 IBVK	196-218	PVQL8 H9VMD	588-813			
PHEMA IAX31	37-68	PVQL2 IBVM	196-218	PVQL8 ILTV6	587-821			
PHEMA IAZCO	37-68	PVQL2 IBVU1	178-201	PVQL8 ILTV9	607-831			
PHEMA IAZH2	21-43	PVQL2 IBVU2	178-201	PVQL8 ILTVT	607-831			
PHEMA IAZH3	21-43	PVQL2 IBVU3	178-201	PVQL8 H9V11	413-437			
PHEMA IAZUK	37-68	PVQL8 HCMVA	535-558	PVQL8 VZVD	468-483			
PHEMA PHODV	38-68	PVQL8 HCMVT	630-559	PVQLF 9V6	401-426			
PHEMA P12H	65-87	PVQL8 H9V6A	483-508	PVQL8 HCMVA	574-588			
PHEMA P12HT	65-87	PVQL8 HCMVB	508-509	PVQL8 HCMVT	673-587			
PVFF7 CAPVK	89-111	PVQLC H9V11	407-480	PVQL8 H9V11	443-467	803-827		
PVFF8 VACC8	72-84	PVQLC H9V1K	407-480	PVQL8 H9V1E	443-467	803-827		
PVGG1 H9V1	317-339	PVQLC H9V2	435-458	PVQL8 BUNL7	31-55			
PVGG3 VACC8	80-72	PVQLC H9V23	438-459	PVQL8 BUNSH	31-55			
PVGG3 VARV	50-72	PVQL8 BUNL7	1387-1410	PVQL8 HANTH	684-718			
PVGG4 VACC8	11-33	PVQL8 BUNSH	1387-1410	PVQL8 RVFV	344-368			
PVGG4 VARV	11-33	PVQL8 UUK	905-989	PVQL8 RVFVZ	344-368			
PVGG9 H9V1	88-110	PVQLY JUNIN	12-35	PVQL8 UUK	501-585			
PVGG9 H9V1	173-185	PVQLY LAS80	12-35	PVQL8 CMV	311-335			
PVGG9 H9V1	20-42	PVQLY LAR9J	12-35	PVGP2 EBV	657-081			
PVGG8 H9V6A	71-83	PVQLY LYCVA	12-35	PVGP3 EBV	654-078			
PVGG8 H9V6A	288-288	PVQLY LYCVM	12-35	PVM1 REOV	280-304			
PVGG8 H9V1	267-289	PVQLY MOPEI	12-35	PVM1 REOVL	280-304			
PVGG8 BPV4	42-84	PVQLY TACV	12-35	PVM21 REOVL	108-192			
PVGG8 H9V1	83-78	PVQLY TACV6	12-35	PVM22 REOVL	188-192			
PVGG8 H9V1	1347-1389	PVQLY TACV7	12-35	PVM2 REOVJ	188-192			
PVGG8 H9V1	80-82	PVQLY TACV7	12-35	PVM2 REOVL	188-192			
PVGL2 IBV8	1058-1077	PVQL8 CMV	741-704	PVMAT MEAS1	67-111			
PVGL2 IBV8	1058-1077	PVM1 REOVL	324-347	PVMAT 86PVB	314-338			
PVGL2 IBV2	1058-1077	PVM1 REOVL	464-477	PVME1 CVBM	137-101			
PVGL2 IBVK	1058-1077	PVMAT MUMPB	227-250	PVME1 CVHOC	137-101			
PVGL2 IBVM	1058-1077	PVMSA HPB08	288-281	PVME1 CVTKE	137-101			
PVGL8 H9V6U	117-139	PVMSA HPB0C	231-254	PVME1 IBV8	74-88			
PVGL8 H9V82	746-767	PVMSA HPB0U	288-282	PVME1 IBVB	74-88			
PVGLC H9VMB	388-421	PVMSA HPB0V	238-259	PVME1 IBVB2	74-88			
PVGLC H9VMD	388-420	PVMSA HPBHE		PVME1 IBVK	74-88			
PVGLC H9VMM	265-287			PVMSA HPB08	271-285			
PVGLF BR8VA	484-508			PVMSA WHV1	200-283			
PVGLF BR8VR	484-508			PVMSA WHV69	274-288			
PVGLF HR8V1	484-508			PVMSA WHV7	274-288			
PVGLF HR8VA	484-508			PVMSA WHV8	274-288			
PVGLF HR8VL	484-508			PVMSA WHV8I	274-288			
PVGLF HR8VR	484-508			PVMSA WHVW8	125-149			
PVGLF TRV	452-474							
PVGL8 H9V	77-89							
PVGL8 VMBVO	400-428							





## TABLE XIII

SEARCH RESULTS SUMMARY FOR P12LZIPC MOTIF







PCGENE	PICT2IP	All Viruses (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PE1BL ADEN1	E1B PROTEIN, LARGE T-ANTIGEN	CANINE ADENOVIRUS TYPE 2	101-122								
PE1BL ADEN2	E1B PROTEIN, SMALL T-ANTIGEN	TUPAIA ADENOVIRUS	75-101								
PE1BS ADE01	E1B PROTEIN, SMALL T-ANTIGEN	CANINE ADENOVIRUS TYPE 2	55-77								
PE10 ADE02	EARLY E1B 10.4 KD PROTEIN PRECURSOR	MOUSE ADENOVIRUS TYPE 1	118-138								
PE10 ADE03	EARLY E1B 10.4 KD PROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 2	3-21	314-60							
PE10 ADE07	EARLY E1B 10.4 KD PROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 3	3-21	31-60							
PE11 ADE02	EARLY E1A 11.6 KD GLYCOPROTEIN	HUMAN ADENOVIRUS TYPE 2	3-24								
PE11 ADE03	EARLY E1A 11.6 KD GLYCOPROTEIN	HUMAN ADENOVIRUS TYPE 2	27-53								
PE11 ADE05	EARLY E1A 10.5 KD GLYCOPROTEIN	HUMAN ADENOVIRUS TYPE 3	19-45								
PE11 ADE07	EARLY E1A 10.5 KD GLYCOPROTEIN	HUMAN ADENOVIRUS TYPE 3	20-46								
PE14 ADE05	EARLY E1A 14.5 KD PROTEIN	HUMAN ADENOVIRUS TYPE 3	36-62								
PE14 ADE07	EARLY E1A 14.5 KD PROTEIN	HUMAN ADENOVIRUS TYPE 3	108-173								
PE15 ADE03	EARLY E1B 14.5 KD PROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 3	52-72								
PE15 ADE07	EARLY E1B 14.5 KD PROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 3	52-72								
PE16 ADE03	EARLY E1B 14.5 KD GLYCOPROTEIN	HUMAN ADENOVIRUS TYPE 3	102-135								
PE21 ADE03	EARLY E1B 20.5 KD GLYCOPROTEIN	HUMAN ADENOVIRUS TYPE 3	146-167								
PE21 ADE07	EARLY E1B 20.5 KD GLYCOPROTEIN	HUMAN ADENOVIRUS TYPE 3	146-167								
PE21 ADE01	EARLY E1B 22.2 KD GLYCOPROTEIN	CANINE ADENOVIRUS TYPE 1 (STRAIN GLAXO)	155-177								
PE10L ADE01	EARLY E1B 17.7 KD GLYCOPROTEIN	MOUSE ADENOVIRUS TYPE 1	105-127								
PE11 ADE03	PROBABLE EARLY E1A 11 KD PROTEIN	HUMAN ADENOVIRUS TYPE 2	56-77								
PE11 ADE05	PROBABLE EARLY E1A 11 KD PROTEIN	HUMAN ADENOVIRUS TYPE 3	56-77								
PE14 ADE01	PROBABLE EARLY E1A 11 KD PROTEIN	HUMAN ADENOVIRUS TYPE 2	61-80								
PE14 ADE02	EARLY E1A 14 KD PROTEIN	HUMAN ADENOVIRUS TYPE 2	80-106								
PEAD E1V	EARLY ANTIGEN PROTEIN D	EPSTEIN-BARR VIRUS (STRAIN 955-8)	263-286								
PEAR E1V	EARLY ANTIGEN PROTEIN R	EPSTEIN-BARR VIRUS (STRAIN 955-8)	159-184								
PEB2 E1V	EARLY ANTIGEN PROTEIN R	EPSTEIN-BARR VIRUS (STRAIN 955-8)	176-141								
PEB2 E1V	EARLY ANTIGEN PROTEIN R	EPSTEIN-BARR VIRUS (STRAIN 955-8)	113-131	662-683							
PE1T1 VARV	EARLY TRANSCRIPTION FACTOR 70 KD SUBUNIT	VARICELLA VIRUS	21-41								
PENY1 FR5FV	ENV POLYPROTEIN PRECURSOR	FRIEND SPLEEN FOCUS-FORMING VIRUS	380-407								
PENY2 FR5FV	ENV POLYPROTEIN PRECURSOR	FRIEND SPLEEN FOCUS-FORMING VIRUS	380-407								
PENY AVB3	ENV POLYPROTEIN	AVIAN RETROVIRUS 821.0	206-235								
PENY AVISU	ENV POLYPROTEIN	AVIAN RETROVIRUS 821.0	98-117								
PENY BAEVM	ENV POLYPROTEIN	ABOON ENDOGENOUS VIRUS (STRAIN UR2)	170-190	202-224							
PENY BIV06	ENV POLYPROTEIN PRECURSOR	BOVINE IMMUNODEFICIENCY VIRUS (ISOLATE 106)	47-68	178-201	434-450	525-546					
PENY BIV27	ENV POLYPROTEIN PRECURSOR	BOVINE IMMUNODEFICIENCY VIRUS (ISOLATE 127)	47-68	147-168	207-230	403-479	554-575				
PENY BLVAF	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (AMERICAN ISOLATE FLK)	303-327								
PENY BLVAU	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (AUSTRALIAN ISOLATE)	303-327								
PENY BLVB2	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (AMERICAN ISOLATE YDM)	303-327								
PENY BLVB3	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (BELGIUM ISOLATE LB285)	303-327								
PENY BLV1	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (BELGIUM ISOLATE LB359)	303-327								
PENY FENY1	ENV POLYPROTEIN PRECURSOR	BOVINE LEUKEMIA VIRUS (JAPANESE ISOLATE BLV-1)	303-327								
PENY FENY8	ENV POLYPROTEIN PRECURSOR	FELINE ENDOGENOUS VIRUS ECE1	30-47	225-246	630-651						
PENY FLV03	ENV POLYPROTEIN PRECURSOR	FELINE LEUKEMIA VIRUS (CLONE CFE-6)	30-47	225-246	630-651						
PENY FLV04	ENV POLYPROTEIN PRECURSOR	FELINE LEUKEMIA VIRUS (STRAIN AGLASGOW-1)	318-55	624-645							
PENY FLV18	ENV POLYPROTEIN PRECURSOR	FELINE LEUKEMIA VIRUS (STRAIN LAMBDA-B1)	9-29	447-468	605-626						
PENY FLV5A	ENV POLYPROTEIN PRECURSOR	FELINE LEUKEMIA VIRUS (STRAIN SARNA)	467-485	625-646							
PENY FOAMV	ENV POLYPROTEIN	HUMAN SPUMARETROVIRUS (FOAMY VIRUS)	444-465	602-623							
PENY FSV0A	ENV POLYPROTEIN PRECURSOR	FELINE SARCOMA VIRUS (STRAIN GARDNER-ANNSTEIN)	153-174	235-275	300-325	481-496	710-727	864-887	924-951	957-978	
PENY FSV0B	ENV POLYPROTEIN PRECURSOR	FELINE SARCOMA VIRUS (STRAIN GA)	467-488	625-646							
PENY FSV0M	ENV POLYPROTEIN PRECURSOR	FELINE SARCOMA VIRUS (STRAIN SM)	447-468	605-626							
PENY FSV1	ENV POLYPROTEIN PRECURSOR	FELINE SARCOMA VIRUS (STRAIN SMO)	450-471	608-629							
PENY QALV	ENV POLYPROTEIN PRECURSOR	FELINE SARCOMA VIRUS (STRAIN SMOYER-THEILEN)	467-488								
PENY HV1B1	GP160 PRECURSOR	GIBBON APE LEUKEMIA VIRUS	519-540								
PENY HV1B2	GP160 PRECURSOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BIII0 ISOLATE)	498-520								
PENY HV1B3	GP160 PRECURSOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BIII0 ISOLATE)	493-515								
PENY HV1B4	GP160 PRECURSOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BIII0 ISOLATE)	494-516								
PENY HV1B5	GP160 PRECURSOR	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BIII0 ISOLATE)	503-525								













FCGENE	PICT121P	All Viruses (No Bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PIC18	PROTEIN	VIRUS									
PIEMA_P1H1U	HEXAAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TEX95/05/82)	111-128	272-299	324-340						
PIEMA_P1H1V	HEXAAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TEX97/07/78)	111-128	272-299	324-340						
PIEMA_P1H1W	HEXAAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN WAS10/04/79)	111-128	272-299	324-340						
PIEMA_P1H1X	HEXAAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN WAS10/11/73)	111-128	272-299	324-340						
PIEMA_P1H1A	HEXAAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIBA)	50-67								
PIEMA_P1H1B	HEXAAGGLUTININ-NEURAMINIDASE	RINDERPEST VIRUS (STRAIN KABETE O)	368-383								
PIEMA_P1H1C	HEXAAGGLUTININ-NEURAMINIDASE	RINDERPEST VIRUS (STRAIN L)	4-30								
PIEMA_P1H1D	HEXAAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN 2, HOST MUTANTS)	122-142								
PIEMA_P1H1E	HEXAAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN HUSINUI)	122-142								
PIEMA_P1H1F	HEXAAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN HARRIS)	322-342								
PIEMA_P1H1G	HEXAAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN HV)	322-342								
PIEMA_P1H1H	HEXAAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN Z)	322-342								
PIEMA_P1H1I	HEXAAGGLUTININ-NEURAMINIDASE	SIMIAN VIRUS 41	55-73								
PIEMA_P1H1J	HEXAAGGLUTININ-NEURAMINIDASE	SIMIAN VIRUS 5 (STRAIN WJ)	7-28								
PIEMA_P1H1K	HEXAAGGLUTININ-NEURAMINIDASE	SIMIAN VIRUS 5 (ISOLATE CANIN/CPI)	7-28								
PIEMA_P1H1L	HEXAAGGLUTININ-NEURAMINIDASE	SIMIAN VIRUS 5 (ISOLATE CANIN/CPI)	7-28								
PIEMA_P1H1M	HEXAAGGLUTININ-NEURAMINIDASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	173-192								
PIEMA_P1H1N	HEXAAGGLUTININ-NEURAMINIDASE	VACCINIA VIRUS (STRAIN TIAN TAN)	173-192								
PIEMA_P1H1O	HEXAAGGLUTININ-NEURAMINIDASE	VACCINIA VIRUS (STRAIN WR)	173-192								
PIEMA_P1H1P	HEXAAGGLUTININ-NEURAMINIDASE	VACCINIA VIRUS	173-194								
PIEMA_P1H1Q	HEXAAGGLUTININ-NEURAMINIDASE	HUMAN ADENOVIRUS TYPE 2	38-61								
PIEMA_P1H1R	HEXAAGGLUTININ-NEURAMINIDASE	HUMAN ADENOVIRUS TYPE 3	27-48								
PIEMA_P1H1S	HEXAAGGLUTININ-NEURAMINIDASE	HUMAN ADENOVIRUS TYPE 5	38-61								
PIEMA_P1H1T	HEXAAGGLUTININ-NEURAMINIDASE	HUMAN ADENOVIRUS TYPE 41	38-61								
PIEMA_P1H1U	HEXAAGGLUTININ-NEURAMINIDASE	MOUSE ADENOVIRUS TYPE 1	36-52								
PIEMA_P1H1V	HEXAAGGLUTININ-NEURAMINIDASE	HUMAN ADENOVIRUS TYPE 7, AND 3	92-117								
PIEMA_P1H1W	HEXAAGGLUTININ-NEURAMINIDASE	CANINE ADENOVIRUS TYPE 2	52-77								
PIEMA_P1H1X	HEXAAGGLUTININ-NEURAMINIDASE	TUPAIA ADENOVIRUS	60-82								
PIEMA_P1H1Y	HEXAAGGLUTININ-NEURAMINIDASE	COWPOX VIRUS	517-533								
PIEMA_P1H1Z	HEXAAGGLUTININ-NEURAMINIDASE	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	64-83								
PIEMA_P1H2A	HEXAAGGLUTININ-NEURAMINIDASE	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	169-190								
PIEMA_P1H2B	HEXAAGGLUTININ-NEURAMINIDASE	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	60-77								
PIEMA_P1H2C	HEXAAGGLUTININ-NEURAMINIDASE	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	239-260								
PIEMA_P1H2D	HEXAAGGLUTININ-NEURAMINIDASE	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	2-29								
PIEMA_P1H2E	HEXAAGGLUTININ-NEURAMINIDASE	SOYBEAN CHLOROTIC MOTTLE VIRUS	92-119								
PIEMA_P1H2F	HEXAAGGLUTININ-NEURAMINIDASE	EPSTEIN-BARR VIRUS (STRAIN B91-8)	101-123								
PIEMA_P1H2G	HEXAAGGLUTININ-NEURAMINIDASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	156-176								
PIEMA_P1H2H	HEXAAGGLUTININ-NEURAMINIDASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	8-29								
PIEMA_P1H2I	HEXAAGGLUTININ-NEURAMINIDASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN ANGELOTTI)	8-29								
PIEMA_P1H2J	HEXAAGGLUTININ-NEURAMINIDASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN F)	8-29								
PIEMA_P1H2K	HEXAAGGLUTININ-NEURAMINIDASE	BOVINE HERPESVIRUS TYPE 2 (STRAIN BN9)	12-37								
PIEMA_P1H2L	HEXAAGGLUTININ-NEURAMINIDASE	EQUINE HERPESVIRUS TYPE 1	37-56								
PIEMA_P1H2M	HEXAAGGLUTININ-NEURAMINIDASE	HERPESVIRUS SAIMIRI (STRAIN 11)	27-49								
PIEMA_P1H2N	HEXAAGGLUTININ-NEURAMINIDASE	MURINE CYTOMEGALOVIRUS (STRAIN SN111)	126-144								
PIEMA_P1H2O	HEXAAGGLUTININ-NEURAMINIDASE	VARICELLA-ZOSTER VIRUS (STRAIN INDIANA-FUNKIAUSER / BECKER)	285-307								
PIEMA_P1H2P	HEXAAGGLUTININ-NEURAMINIDASE	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	69-88								
PIEMA_P1H2Q	HEXAAGGLUTININ-NEURAMINIDASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	668-684								
PIEMA_P1H2R	HEXAAGGLUTININ-NEURAMINIDASE	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN 17)	711-729								
PIEMA_P1H2S	HEXAAGGLUTININ-NEURAMINIDASE	HERPES SIMPLEX VIRUS (STRAIN INDIANA-FUNKIAUSER / BECKER)	82-102								
PIEMA_P1H2T	HEXAAGGLUTININ-NEURAMINIDASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN F)	211-227								
PIEMA_P1H2U	HEXAAGGLUTININ-NEURAMINIDASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	81-98								
PIEMA_P1H2V	HEXAAGGLUTININ-NEURAMINIDASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB42)	708-735								
PIEMA_P1H2W	HEXAAGGLUTININ-NEURAMINIDASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN KENTUCKY A)	708-735								
PIEMA_P1H2X	HEXAAGGLUTININ-NEURAMINIDASE	MAREK'S DISEASE HERPESVIRUS (STRAIN GA)	488-506								
PIEMA_P1H2Y	HEXAAGGLUTININ-NEURAMINIDASE	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	547-563								

















PCGENE	PICTLZIP	PROTEIN	All Viruses (No Bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN											
PPOLN FCV6	NON-STRUCTURAL POLYPROTEIN		FELINE CALICIVIRUS (STRAIN CF168 FIV)	443-469	748-766	902-927	1066-1088					AREA2
PPOLN FCV7	NON-STRUCTURAL POLYPROTEIN		FELINE CALICIVIRUS (STRAIN JAPANESE F4)	300-326								
PPOLN FCV9	NON-STRUCTURAL POLYPROTEIN		FELINE CALICIVIRUS (STRAIN F9)	171-186	262-283	919-945	1224-1242	1378-1399	1545-1564			
PPOLN HEV6	NON-STRUCTURAL POLYPROTEIN		HEPATITIS E VIRUS (STRAIN BURMA)	250-266	1274-1291							
PPOLN HEV7	NON-STRUCTURAL POLYPROTEIN		HEPATITIS E VIRUS (STRAIN MEXICO)	250-266	1272-1289							
PPOLN HEV8	NON-STRUCTURAL POLYPROTEIN		HEPATITIS E VIRUS (STRAIN MYANMAR)	250-266	1274-1291							
PPOLN HEV9	NON-STRUCTURAL POLYPROTEIN		HEPATITIS E VIRUS (STRAIN PAKISTAN)	249-263	1273-1290							
PPOLN MIDV	NON-STRUCTURAL POLYPROTEIN		MIDDLEBURY VIRUS	484-512	628-641	760-770						
PPOLN ONV6	NON-STRUCTURAL POLYPROTEIN		ONYONG-ONYONG VIRUS (STRAIN GULL)	90-107	613-634	2148-2163	2270-2240					
PPOLN RUDV	NON-STRUCTURAL POLYPROTEIN		RABBIT HEMORRHAGIC DISEASE VIRUS	156-180	276-292	279-320	479-502	1310-1353	1429-1455	1471-1499		
PPOLN RUDV	NON-STRUCTURAL POLYPROTEIN		RABBIT HEMORRHAGIC DISEASE VIRUS (STRAIN V-351)	115-135								
PPOLN RAVN	NON-STRUCTURAL POLYPROTEIN		ROSS RIVER VIRUS (STRAIN NB5092)	89-106	611-632	2113-2128	2185-2205					
PPOLN RAVT	NON-STRUCTURAL POLYPROTEIN		RUBELLA VIRUS (STRAIN T48)	782-797	854-874							
PPOLN RUBV	NON-STRUCTURAL POLYPROTEIN		SEMURU FOREST VIRUS	14-37	92-113	263-279	670-694	901-918	1374-1393	2033-2052		
PPOLN SIVD	NON-STRUCTURAL POLYPROTEIN		SINDBIS VIRUS (SUBTYPE OCKELBO / STRAIN HUNSHYN N2-5)	91-108	617-643	2062-2077	2134-2154					
PPOLN SIVD	NON-STRUCTURAL POLYPROTEIN		SINDBIS VIRUS (STRAIN HIRSP)	620-646	1123-1150	1796-1814	2148-2161	2230-2240				
PPOLN EPHV	RNA REPLICASE POLYPROTEIN		EGGPLANT MOSAIC VIRUS	620-646	1123-1150	1744-1763	1790-1812	2146-2161	2230-2240			
PPOLN OTMV	RNA REPLICASE POLYPROTEIN		ONION YELLOW MOSAIC VIRUS	808-833								
PPOLN TYMV	RNA REPLICASE POLYPROTEIN		TURNIP YELLOW MOSAIC VIRUS	707-727	941-962							
PPOLN TYMV	RNA REPLICASE POLYPROTEIN		TURNIP YELLOW MOSAIC VIRUS (AUSTRALIAN ISOLATE)	212-233	416-453	1173-1192						
PPOLN TYMV	RNA REPLICASE POLYPROTEIN		TURNIP YELLOW MOSAIC VIRUS (ISOLATE TYMC)	212-233	416-453	1173-1192						
PPOLN EEEV	STRUCTURAL POLYPROTEIN		EASTERN EQUINE ENCEPHALITIS VIRUS	315-330	213-229	491-507						
PPOLN EEEV	STRUCTURAL POLYPROTEIN		EASTERN EQUINE ENCEPHALITIS VIRUS	315-330	213-229	491-507						
PPOLN EEEV	STRUCTURAL POLYPROTEIN		VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TC-83)	32-48	229-245	504-522						
PPOLN EEEV	STRUCTURAL POLYPROTEIN		VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TRINIDAD DON 32-48)	32-48	229-245	504-522						
PPOLN IBV6	STRUCTURAL POLYPROTEIN		AVIAN INFLUENZA VIRUS (STRAIN AUSTRALIAN C/900-922)	900-922								
PPOLN IBV6	STRUCTURAL POLYPROTEIN		AVIAN INFLUENZA VIRUS (STRAIN CU-1)	900-922								
PPOLN IBV6	STRUCTURAL POLYPROTEIN		AVIAN INFLUENZA VIRUS (STRAIN PIIG-98)	881-903								
PPOLN IBV6	STRUCTURAL POLYPROTEIN		AVIAN INFLUENZA VIRUS (STRAIN STC)	900-922								
PPOLN IBV6	STRUCTURAL POLYPROTEIN		ONYONG-ONYONG VIRUS (STRAIN GULL)	688-708								
PPOLN RAVT	STRUCTURAL POLYPROTEIN		ROSS RIVER VIRUS (STRAIN T48)	1216-1243								
PPOLN RUBV	STRUCTURAL POLYPROTEIN		RUBELLA VIRUS (VACCINE STRAIN IPV77)	281-302								
PPOLN RUBV	STRUCTURAL POLYPROTEIN		RUBELLA VIRUS (VACCINE STRAIN M31)	281-302								
PPOLN RUBV	STRUCTURAL POLYPROTEIN		RUBELLA VIRUS (VACCINE STRAIN RA373)	281-302								
PPOLN SFV	STRUCTURAL POLYPROTEIN		SEMURU FOREST VIRUS	281-302	1041-1060							
PPOLN SIVD	STRUCTURAL POLYPROTEIN		SINDBIS VIRUS (SUBTYPE OCKELBO / STRAIN EDSUN 82-5)	31-52	751-772	780-801						
PPOLN SIVD	STRUCTURAL POLYPROTEIN		SINDBIS VIRUS (STRAINS HRSP AND IRLP)	31-52								
PPOLN WEEV	STRUCTURAL POLYPROTEIN		WESTERN EQUINE ENCEPHALITIS VIRUS	36-51	909-933							
PPOLN BAEV	POL POLYPROTEIN		AVIAN RETICULOENDOTHELIOSIS VIRUS	283-303								
PPOLN BIV6	POL POLYPROTEIN		BABOON ENDOGENOUS VIRUS (STRAIN M7)	526-544	973-993	999-1019	1070-1091					
PPOLN BIV7	POL POLYPROTEIN		BOVINE IMMUNODEFICIENCY VIRUS (ISOLATE 106)	101-119	742-768	868-889						
PPOLN BLV6	POL POLYPROTEIN		BOVINE IMMUNODEFICIENCY VIRUS (ISOLATE 127)	101-119	742-768	868-889						
PPOLN BLV7	POL POLYPROTEIN		BOVINE LEUKEMIA VIRUS (AUSTRALIAN ISOLATE)	487-504								
PPOLN BLV8	POL POLYPROTEIN		BOVINE LEUKEMIA VIRUS (JAPANESE ISOLATE BLV-1)	487-504								
PPOLN CAEV	POL POLYPROTEIN		CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (STRAIN CORK)	393-419	556-671							
PPOLN CAMV	ENZYMATIC POLYPROTEIN		CAULIFLOWER MOSAIC VIRUS (STRAIN CM-1841)	184-204	380-407	471-494						
PPOLN CAMV	ENZYMATIC POLYPROTEIN		CAULIFLOWER MOSAIC VIRUS (STRAIN D19)	175-199	373-402	466-489						
PPOLN CAMV	ENZYMATIC POLYPROTEIN		CAULIFLOWER MOSAIC VIRUS (STRAIN BUC)	184-204	380-407	471-494						
PPOLN CAMV	ENZYMATIC POLYPROTEIN		CAULIFLOWER MOSAIC VIRUS (STRAIN NY8153)	70-97	185-203	381-408	472-495					
PPOLN CERV	ENZYMATIC POLYPROTEIN		CARNATION ETCHED RING VIRUS (STRAIN STRASSBOURG)	184-204	380-407	471-494						
PPOLN COV6	PUTATIVE POLYPROTEIN		CONNELLIA YELLOW MOTTLE VIRUS	161-186	453-478							
PPOLN EIV6	POL POLYPROTEIN		EQUINE INFLUENZA VIRUS (CLONE 1369)	320-343	1266-1311	1606-1622	1641-1665					
PPOLN EIV6	POL POLYPROTEIN		EQUINE INFLUENZA VIRUS (CLONE CL21)	437-456								



PCGENE	FILENAME	FILETYPE	ALL Viruses (No. Bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PROTEIN	PROTEIN	PROTEIN	ALL Viruses (No. Bacteriophages)										
PPOL_SV1	PPOL_SV1	POL POLYPROTEIN	SIMIAN FOAMY VIRUS (TYPE 1)	188-204	335-356	845-869							AREA2
PPOL_SV2	PPOL_SV2	POL POLYPROTEIN	SIMIAN FOAMY VIRUS (TYPE 3 / STRAIN LK)	186-206	317-338	841-871							AREA1
PPOL_SV3	PPOL_SV3	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGM155 ISOLATE)	895-915									
PPOL_SV4	PPOL_SV4	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGM1 ISOLATE)	899-926	900-920								
PPOL_SV5	PPOL_SV5	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (TYO-1 ISOLATE)	726-741	915-935								
PPOL_SV6	PPOL_SV6	POL POLYPROTEIN	CHIMPANZEE IMMUNODEFICIENCY VIRUS	884-911									
PPOL_SV7	PPOL_SV7	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE GH)	680-695	869-896								
PPOL_SV8	PPOL_SV8	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (MM142-83 ISOLATE)	780-807	908-935								
PPOL_SV9	PPOL_SV9	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (K6V ISOLATE)	380-407	712-737	906-933							
PPOL_SV10	PPOL_SV10	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (P2165SMH ISOLATE)	343-370	871-898								
PPOL_SV11	PPOL_SV11	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (MIMC11 ISOLATE)	346-373	874-901								
PPOL_SV12	PPOL_SV12	POL POLYPROTEIN	SQUID MONKEY RETROVIRUS	748-768									
PPOL_SV13	PPOL_SV13	POL POLYPROTEIN	SIMIAN SARCOMA VIRUS	100-130	177-200								
PPOL_SV14	PPOL_SV14	POL POLYPROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	131-155									
PPOL_SV15	PPOL_SV15	POL POLYPROTEIN	SIMIAN RETROVIRUS	743-763									
PPOL_SV16	PPOL_SV16	POL POLYPROTEIN	VISNA LENTIVIRUS (STRAIN 1514)	488-507	651-666	971-991							
PPOL_SV17	PPOL_SV17	POL POLYPROTEIN	VISNA LENTIVIRUS (STRAIN 1514 / CLONE LV1-K51)	488-507	651-666	971-991							
PPOL_SV18	PPOL_SV18	POL POLYPROTEIN	VISNA LENTIVIRUS (STRAIN 1514 / CLONE LV1-K53)	488-507	651-666	971-991							
PPOL_SV19	PPOL_SV19	POL POLYPROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	116-141	153-171	183-210							
PPOL_SV20	PPOL_SV20	POL POLYPROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	116-141	153-171	183-210							
PPOL_SV21	PPOL_SV21	POL POLYPROTEIN	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN G5)	158-175	396-411								
PPOL_SV22	PPOL_SV22	POL POLYPROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	301-323									
PPOL_SV23	PPOL_SV23	POL POLYPROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	79-102									
PPOL_SV24	PPOL_SV24	POL POLYPROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6)	40-61									
PPOL_SV25	PPOL_SV25	POL POLYPROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN GR)	40-61									
PPOL_SV26	PPOL_SV26	POL POLYPROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN GR)	40-61									
PPOL_SV27	PPOL_SV27	POL POLYPROTEIN	HARVEY MURINE SARCOMA VIRUS	49-73									
PPOL_SV28	PPOL_SV28	POL POLYPROTEIN	RASHEED RAT SARCOMA VIRUS	56-80									
PPOL_SV29	PPOL_SV29	POL POLYPROTEIN	CAMPLETTIS SORORENSIS VIRUS	14-36									
PPOL_SV30	PPOL_SV30	POL POLYPROTEIN	VACCINIA VIRUS (STRAIN WR), AND (STRAIN COPEHAGEN)	274-298	316-335	517-535							
PPOL_SV31	PPOL_SV31	POL POLYPROTEIN	VACCINIA VIRUS	274-298	316-335	517-535							
PPOL_SV32	PPOL_SV32	POL POLYPROTEIN	SIMIAN IMMUNODEFICIENCY VIRUS (AGM ISOLATE)	45-72									
PPOL_SV33	PPOL_SV33	POL POLYPROTEIN	AFRICAN SWINE FEVER VIRUS (ISOLATE MALAWI LIL 2001)	139-164	189-210	495-510							
PPOL_SV34	PPOL_SV34	POL POLYPROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)	793-812									
PPOL_SV35	PPOL_SV35	POL POLYPROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	192-212	669-684								
PPOL_SV36	PPOL_SV36	POL POLYPROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	415-410	587-613								
PPOL_SV37	PPOL_SV37	POL POLYPROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	60-85	266-288	668-694							
PPOL_SV38	PPOL_SV38	POL POLYPROTEIN	HERPESVIRUS SAMIRI (STRAIN 11)	136-151									
PPOL_SV39	PPOL_SV39	POL POLYPROTEIN	VACCINIA VIRUS (STRAIN COPEHAGEN)	36-51									
PPOL_SV40	PPOL_SV40	POL POLYPROTEIN	VACCINIA VIRUS (STRAIN WR)	36-51									
PPOL_SV41	PPOL_SV41	POL POLYPROTEIN	VACCINIA VIRUS	36-51									
PPOL_SV42	PPOL_SV42	POL POLYPROTEIN	VACCINIA VIRUS (STRAIN DUMAS)	34-58	221-247	258-280							
PPOL_SV43	PPOL_SV43	POL POLYPROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)	209-236									
PPOL_SV44	PPOL_SV44	POL POLYPROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	44-66	375-392								
PPOL_SV45	PPOL_SV45	POL POLYPROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN KOS)	43-65	245-261	274-291							
PPOL_SV46	PPOL_SV46	POL POLYPROTEIN	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN 331)	41-63	275-289								
PPOL_SV47	PPOL_SV47	POL POLYPROTEIN	BOVINE HERPESVIRUS TYPE 1 (STRAIN 14)	244-266									
PPOL_SV48	PPOL_SV48	POL POLYPROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	61-88	251-273								
PPOL_SV49	PPOL_SV49	POL POLYPROTEIN	HERPESVIRUS SAMIRI (STRAIN 11)	212-239									
PPOL_SV50	PPOL_SV50	POL POLYPROTEIN	SHOPE FIBROMA VIRUS (STRAIN KASZA)	184-206	215-237								
PPOL_SV51	PPOL_SV51	POL POLYPROTEIN	VACCINIA VIRUS (STRAIN COPEHAGEN)	184-206									
PPOL_SV52	PPOL_SV52	POL POLYPROTEIN	VACCINIA VIRUS (STRAIN L-1V7)	184-206									
PPOL_SV53	PPOL_SV53	POL POLYPROTEIN	VACCINIA VIRUS (STRAIN WR)	184-206									















PCGENE	PICTLZIP	FILENAME	PROTEIN	All Viruses (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PUL20 PVNU	UL20	MEMBRANE PROTEIN HOMOLOG	UL20	PSUDORABIES VIRUS (STRAIN NIA-3)	54-76								
PUL20 VZVD	GENE 39	MEMBRANE PROTEIN	UL20	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	201-224								
PUL21 HCMVA	UL21	MEMBRANE PROTEIN	UL21	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	91-110								
PUL21 HSVIT	PROTEIN UL21			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	98-114								
PUL21 HSVIE	PROTEIN UL21			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	98-114								
PUL21 HSVIEB	GENE 40	PROTEIN	UL21	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	110-146								
PUL21 VZVD	GENE 38	PROTEIN	UL21	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	119-142								
PUL23 HCMVA	UL23	MEMBRANE PROTEIN	UL23	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	270-293								
PUL24 EBV	PROTEIN BXB1			EPSTEIN-BARR VIRUS (STRAIN D95-4)	44-67								
PUL24 HCMVA	UL24	MEMBRANE PROTEIN	UL24	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	114-135								
PUL24 HSVI1	PROTEIN UL24			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	206-222								
PUL24 ILTVT	PROTEIN UL24			INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE V83)	147-166								
PUL33 HCMVA	UL33	MEMBRANE PROTEIN	UL33	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	158-179								
PUL33 HSVI1	PROTEIN UL33			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	484-500								
PUL33 HSVIEB	PROTEIN UL33			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	86-101								
PUL33 HSVSA	PROTEIN UL33			EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	89-104								
PUL33 ILTVT	PROTEIN UL33			HERPESVIRUS SAIMIRI (STRAIN 11)	244-263								
PUL37 HCMVA	UL37	MEMBRANE PROTEIN	UL37	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE V83)	320-287								
PUL39 HCMVA	UL39	MEMBRANE PROTEIN	UL39	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	307-324								
PUL39 HCMVA	UL39	MEMBRANE PROTEIN	UL39	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	339-266								
PUL31 EBV	PROTEIN B1F2			EPSTEIN-BARR VIRUS (STRAIN D95-4)	9-32								
PUL31 HCMVA	UL31	MEMBRANE PROTEIN	UL31	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	373-296								
PUL31 HSVI1	PROTEIN UL31			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	410-437								
PUL31 HSVIEB	PROTEIN UL31			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	95-116								
PUL31 HSVSA	PROTEIN UL31			HERPESVIRUS SAIMIRI (STRAIN 11)	104-123								
PUL31 VZVD	GENE 27	PROTEIN	UL31	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	145-161								
PUL32 HSVI1	PROBABLE MAJOR ENV GLYCOPROTEIN UL32			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	117-138								
PUL32 HSVIEB	MAJOR ENVELOPE GLYCOPROTEIN 300			VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	127-143								
PUL32 VZVD	PROBABLE MAJOR ENV GLYCOPROTEIN 26			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	81-108								
PUL33 HCMVA	Q-PROTEIN COUPLED REC HOMOLOG UL33			VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	553-574								
PUL34 HCMVA	UL34	MEMBRANE PROTEIN	UL34	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	76-102								
PUL34 HSVI1	PROTEIN UL34			HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	214-232								
PUL34 HSVIEB	PROTEIN UL34			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	231-275								
PUL34 HSVSA	PROTEIN UL34			EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	249-264								
PUL34 VZVD	GENE 28	PROTEIN	UL34	HERPESVIRUS SAIMIRI (STRAIN 11)	207-229								
PUL34 HCMVA	UL34	MEMBRANE PROTEIN	UL34	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	244-266								
PUL35 HCMVA	UL35	MEMBRANE PROTEIN	UL35	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	229-252								
PUL37 EBV	PROTEIN BOLF1			EPSTEIN-BARR VIRUS (STRAIN D95-4)	143-168								
PUL37 HSVI1	PROTEIN UL37			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	21-36								
PUL37 HSVIEB	GENE 21	PROTEIN	UL37	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	229-252								
PUL37 HSVSA	GENE 61	PROTEIN	UL37	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	414-440								
PUL37 VZVD	GENE 21	PROTEIN	UL37	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	5-20								
PUL38 HCMVA	UL38	MEMBRANE PROTEIN	UL38	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	4-19								
PUL40 HCMVA	UL40	MEMBRANE PROTEIN	UL40	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	904-923								
PUL41 HCMVA	UL41	MEMBRANE PROTEIN	UL41	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	199-220								
PUL43 HSVI1	UL43	MEMBRANE PROTEIN	UL43	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	18-35								
PUL43 HSVIEB	GENE 17	MEMBRANE PROTEIN	UL43	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	15-31								
PUL43 VZVD	GENE 15	MEMBRANE PROTEIN	UL43	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	41-63								
PUL43 HSVI1	PROTEIN UL43			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	34-60								
PUL43 HSVIEB	PROTEIN UL43			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	88-114								
PUL43 HSVSA	PROTEIN UL43			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	25-46								
PUL43 VZVD	PROTEIN UL43			HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	35-46								
PUL47 HCMVA	UL47	MEMBRANE PROTEIN	UL47	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	191-218								
PUL47 HSVI1	UL47	MEMBRANE PROTEIN	UL47	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	404-425								
PUL47 HSVIEB	UL47	MEMBRANE PROTEIN	UL47	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	404-425								
PUL47 HSVSA	UL47	MEMBRANE PROTEIN	UL47	BOVINE HERPESVIRUS TYPE 1 (STRAIN PB-2)	681-702								
PUL47 VZVD	UL47	MEMBRANE PROTEIN	UL47	EQUINE HERPESVIRUS TYPE 4	580-601								

FCGENE	PL12CL2IP	All Viruses (No Bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	YRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PUL41 HSVB	97 KD ALPHA TRANS-INDUCING PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD16)	597-608								
PUL47 VZVD	ALPHA TRANS-INDUCING FACTOR 91 & 8 KD PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	42-58	608-627							
PUL49 EBV	HYPOTHETICAL BFR2 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	336-358								
PUL49 HCMVA	HYPOTHETICAL PROTEIN UL49	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	248-264	328-343							
PUL49 HSV11	TEGUMENT PROTEIN UL49	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	226-232								
PUL49 HSVSA	HYPOTHETICAL GENE 66 PROTEIN	HERPESVIRUS SAMIRI (STRAIN 11)	232-233								
PUL50 HCMVA	PROTEIN UL50	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	96-119								
PUL51 HSV11	PROTEIN UL51	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	49-66								
PUL51 HSVB4	GENE 8 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN 1942)	109-190								
PUL51 HSV11B	GENE 8 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN 1942)	164-180								
PUL51 VZVD	GENE 7 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	30-49								
PUL52 EBV	PROBABLE DNA REPLICATION PROTEIN BSLF1	EPSTEIN-BARR VIRUS (STRAIN B95-8)	44-59								
PUL52 HSV11	DNA REPLICATION PROTEIN UL52	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	17-37	65-91							
PUL52 HSVB4	DNA REPLICATION PROTEIN UL52	EQUINE HERPESVIRUS TYPE 1 (STRAIN 1942)	8-27								
PUL52 HSVB	DNA REPLICATION PROTEIN UL52	EQUINE HERPESVIRUS TYPE 1 (STRAIN 1942)	8-27	116-117							
PUL53 HSVSA	PROBABLE DNA REPLICATION GENE 56 PROTEIN	HERPESVIRUS SAMIRI (STRAIN 11)	489-508								
PUL53 VZVD	PROBABLE DNA REPLICATION GENE 6 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	446-466	645-670							
PUL53 HCMVA	PROTEIN UL53	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	173-188								
PUL53 HSV6U	UL53 PROTEIN HOMOLOG	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	64-80								
PUL60 HCMVA	HYPOTHETICAL PROTEIN UL60	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	120-141								
PUL63 HCMVA	HYPOTHETICAL PROTEIN UL63	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	63-84	176-205							
PUL68 HCMVA	HYPOTHETICAL PROTEIN UL68	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	87-107								
PUL70 HCMVA	PROBABLE DNA REPLICATION PROTEIN UL70	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	225-232	409-430	626-645	770-793					
PUL71 HCMVA	HYPOTHETICAL PROTEIN UL71	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	234-250								
PUL71 EBV	HYPOTHETICAL BLNF1 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	62-87								
PUL73 HSVSA	HYPOTHETICAL GENE 53 PROTEIN	HERPESVIRUS SAMIRI (STRAIN 11)	51-73								
PUL74 HCMVA	HYPOTHETICAL PROTEIN UL74	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	12-32								
PUL78 HCMVA	HYPOTHETICAL PROTEIN UL78	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	268-291	607-628							
PUL79 HCMVA	HYPOTHETICAL PROTEIN UL79	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	71-90	190-205							
PUL84 HCMVA	63 KD EARLY NONSTRUCTURAL PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	40-58								
PUL84 HCMVT	63 KD EARLY NONSTRUCTURAL PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	100-116								
PUL87 EBV	HYPOTHETICAL PROTEIN BICB1	EPSTEIN-BARR VIRUS (STRAIN B95-8)	100-116								
PUL87 HCMVA	HYPOTHETICAL PROTEIN UL87	HERPESVIRUS SAMIRI (STRAIN 11)	406-422	510-537							
PUL87 HSV6U	HYPOTHETICAL PROTEIN 3R	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	205-231	109-335	606-628	633-653	737-781				
PUL87 HSVSA	HYPOTHETICAL GENE 24 PROTEIN	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	301-322	507-529							
PUL88 HCMVA	HYPOTHETICAL PROTEIN UL88	HERPESVIRUS SAMIRI (STRAIN 11)	365-387	402-422	579-595						
PUL88 HSV6U	HYPOTHETICAL PROTEIN 6R	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	150-173	232-279							
PUL89 HCMVA	HYPOTHETICAL PROTEIN UL89	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	173-191								
PUL91 HSV6U	HYPOTHETICAL PROTEIN UL90	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	35-50								
PUL91 HCMVA	HYPOTHETICAL PROTEIN 8R	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	43-65								
PUL92 HCMVA	HYPOTHETICAL PROTEIN UL92	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	76-99								
PUL94 HCMVA	PROTEIN UL94	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	36-55	100-119							
PUL95 EBV	HYPOTHETICAL PROTEIN BGLF3	EPSTEIN-BARR VIRUS (STRAIN B95-8)	49-70								
PUL95 HCMVA	HYPOTHETICAL PROTEIN UL95	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	201-223								
PUL95 HSV6U	HYPOTHETICAL PROTEIN 13R	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	300-326								
PUL95 HSVSA	HYPOTHETICAL GENE 34 PROTEIN	HERPESVIRUS SAMIRI (STRAIN 11)	6-30	328-346							
PUL97 HCMVA	GANCICLOVIR KINASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	187-209								
PUL97 HCMVA	PROTEIN UL103	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	208-228	341-367							
PUL97 HCMVA	PROTEIN UL103	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	168-183								
PUL97 HCMVA	PROTEIN UL104	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	26-47								
PUL98 HCMVA	HYPOTHETICAL PROTEIN UL108	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	215-235	423-450							
PUL98 HCMVA	HYPOTHETICAL PROTEIN UL111	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	91-118								
PUL98 HCMVA	HYPOTHETICAL PROTEIN UL113	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	60-81								
PUL98 HCMVA	HYPOTHETICAL PROTEIN UL117	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	298-319								
PUL98 HCMVA	HYPOTHETICAL PROTEIN UL118	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	178-195								
PUL98 HCMVA	HYPOTHETICAL PROTEIN UL121	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	101-130								
PUL98 HCMVA	HYPOTHETICAL PROTEIN UL121	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	179-153								

GENE	FUNCTION	ALL Viruses (No. in parentheses)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10
FILE NABIC	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10
PUS01 HCMVA	HYPOTHETICAL PROTEIN UL112	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	4-22									
PUS02 HCMVA	URACIL-DNA GLYCOSYLASE	FOWLPOX VIRUS (STRAIN FP-1)	12-37									
PUS03 HCMVA	URACIL-DNA GLYCOSYLASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	224-230									
PUS04 HCMVA	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	82-103									
PUS05 HCMVA	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN WR)	82-103									
PUS06 HCMVA	URACIL-DNA GLYCOSYLASE	VARIOLA VIRUS	82-103									
PUS07 HCMVA	URACIL-DNA GLYCOSYLASE	VARIOLA-ZOSTER VIRUS (STRAIN DUMAS)	217-243									
PUS08 HCMVA	URACIL-DNA GLYCOSYLASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	48-63									
PUS09 HCMVA	URACIL-DNA GLYCOSYLASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN KENTUCKY A)	48-63									
PUS10 HCMVA	URACIL-DNA GLYCOSYLASE	PSEUDORABIES VIRUS (STRAIN NIA-3)	120-136									
PUS11 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	24-39									
PUS12 HCMVA	URACIL-DNA GLYCOSYLASE	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	53-70									
PUS13 HCMVA	URACIL-DNA GLYCOSYLASE	HERPES SIMPLEX VIRUS (TYPE 2)	53-70									
PUS14 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	179-206									
PUS15 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	98-113									
PUS16 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	29-50									
PUS17 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	11-33									
PUS18 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	236-260									
PUS19 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	378-402									
PUS20 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	151-174									
PUS21 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	110-126									
PUS22 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	120-142									
PUS23 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	41-67									
PUS24 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	220-292									
PUS25 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	292-310									
PUS26 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	352-373									
PUS27 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	34-49									
PUS28 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	140-160									
PUS29 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	34-49									
PUS30 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	246-269									
PUS31 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	102-128									
PUS32 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	41-59									
PUS33 HCMVA	URACIL-DNA GLYCOSYLASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	27-46									
PUS34 HCMVA	URACIL-DNA GLYCOSYLASE	POTATO VIRUS S (STRAIN PERUVIAN)	28-49									
PUS35 HCMVA	URACIL-DNA GLYCOSYLASE	POTATO VIRUS X (PVS)	31-48									
PUS36 HCMVA	URACIL-DNA GLYCOSYLASE	POTATO VIRUS X (STRAIN X3)	31-48									
PUS37 HCMVA	URACIL-DNA GLYCOSYLASE	POTATO VIRUS X (STRAIN X2)	31-48									
PUS38 HCMVA	URACIL-DNA GLYCOSYLASE	AFRICAN SWINE FEVER VIRUS (STRAIN LIS57)	73-94									
PUS39 HCMVA	URACIL-DNA GLYCOSYLASE	ALFALFA MOSAIC VIRUS (STRAIN 423 / ISOLATE LEIDEN)	59-79									
PUS40 HCMVA	URACIL-DNA GLYCOSYLASE	POTATO VIRUS M (STRAIN RUSSIAN)	70-96									
PUS41 HCMVA	URACIL-DNA GLYCOSYLASE	TORACCO RATTLE VIRUS (STRAIN PLB)	24-51									
PUS42 HCMVA	URACIL-DNA GLYCOSYLASE	AUTOGRAPIA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	79-102									
PUS43 HCMVA	URACIL-DNA GLYCOSYLASE	BARLEY STRIPE MOSAIC VIRUS (BSMV)	14-29									
PUS44 HCMVA	URACIL-DNA GLYCOSYLASE	ABELSON MURINE LEUKEMIA VIRUS	26-44									
PUS45 HCMVA	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN WR)	114-132									
PUS46 HCMVA	URACIL-DNA GLYCOSYLASE	BROAD BEAN MOTTLE VIRUS	198-220									
PUS47 HCMVA	URACIL-DNA GLYCOSYLASE	BROME MOSAIC VIRUS	747-767									
PUS48 HCMVA	URACIL-DNA GLYCOSYLASE	COWPEA CHLOROTIC MOTTLE VIRUS	744-763									
PUS49 HCMVA	URACIL-DNA GLYCOSYLASE	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	775-800									
PUS50 HCMVA	URACIL-DNA GLYCOSYLASE	CUCUMBER MOSAIC VIRUS (STRAIN O)	775-800									
PUS51 HCMVA	URACIL-DNA GLYCOSYLASE	CUCUMBER MOSAIC VIRUS (STRAIN Q)	774-799									
PUS52 HCMVA	URACIL-DNA GLYCOSYLASE	PEANUT STUNT VIRUS (STRAIN J)	472-493									
PUS53 HCMVA	URACIL-DNA GLYCOSYLASE	TURKEY HERPES VIRUS (STRAIN H2)	176-191									
PUS54 HCMVA	URACIL-DNA GLYCOSYLASE	POTATO LEAFROLL VIRUS (STRAIN I)	60-76									
PUS55 HCMVA	URACIL-DNA GLYCOSYLASE	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	60-76									
PUS56 HCMVA	URACIL-DNA GLYCOSYLASE	BEST WESTERN YELLOW VIRUS (ISOLATE FL-1)	136-157									
PUS57 HCMVA	URACIL-DNA GLYCOSYLASE	PEA EARLY BROWNING VIRUS	114-132									
PUS58 HCMVA	URACIL-DNA GLYCOSYLASE	BROME MOSAIC VIRUS	759-777									

PCGENE	PICTZIP	ALL Viruses (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PV2A CCMV	2A PROTEIN	COWPEA CHLOROTIC MOTTLE VIRUS	206-314							
PV2A TAV	2A PROTEIN	TOMATO ASPERMATOPHYTES VIRUS	214-235							
PV2K TAVTC	20-1 KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN TCM)	62-82							
PV2K TORSV	31-7 KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN WC)	226-230							
PV2S ASFB7	K762 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN B471V)	145-164							
PV2S ASFL3	LIS 373 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS57)	114-135							
PV2S ASFL3	LIS 383 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS57)	160-187							
PV2A CCMV	COWPEA CHLOROTIC MOTTLE VIRUS									
PV2A CCMV	2A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN ENY)	214-235							
PV2A CCMV	2A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN M)	214-235							
PV2A CCMV	2A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN O)	214-235							
PV2A CCMV	2A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN Q)	214-235							
PV2A CCMV	2A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN Y)	214-235							
PV2A IBVB	2A PROTEIN	AVIAN INFLUENZA VIRUS (STRAIN DEAUDETTE)	5-28							
PV2A IBVM	2A PROTEIN	AVIAN INFLUENZA VIRUS (STRAIN H41)	5-28							
PV2A IBVP3	2A PROTEIN	AVIAN INFLUENZA VIRUS (STRAIN PORTUGAL J12/83)	5-28							
PV2A IBVUS	2A PROTEIN	AVIAN INFLUENZA VIRUS (STRAIN UK/18/66)	5-28							
PV2A TAV	2A PROTEIN	TOMATO ASPERMATOPHYTES VIRUS	147-168							
PV2K BSMV	38 KD PROTEIN	BARLEY STRIPE MOSAIC VIRUS	320-340							
PV2K BSMV	PROTEIN 6B	CANINE ENTERIC CORONAVIRUS (STRAIN K378)	97-116							
PV2K TYMYA	59 KD PROTEIN	TURNIP YELLOW MOSAIC VIRUS (AUSTRALIAN ISOLATE)	12-35							
PV2K AMVLE	50 KD PROTEIN	ALFALFA MOSAIC VIRUS (STRAIN 03-1/ISOLA TE LEIDEN)	44-59							
PV2A VACC	PROTEIN A4	VACCINIA VIRUS (STRAIN COPENHAGEN)	217-244							
PV2A VACC	PROTEIN A4	VACCINIA VIRUS (STRAIN WR)	217-244							
PV2A VACC	PROTEIN A4	VARIOLA VIRUS	207-214							
PV2A VACC	PROTEIN A9	VACCINIA VIRUS (STRAIN COPENHAGEN)	41-66							
PV2A VACC	PROTEIN A9	VARIOLA VIRUS	41-66							
PV2A VACC	PROTEIN A11	VACCINIA VIRUS (STRAIN COPENHAGEN)	21-44							
PV2A VACC	PROTEIN A11	VARIOLA VIRUS	21-44							
PV2A VACC	PROTEIN A14	VACCINIA VIRUS (STRAIN COPENHAGEN)	19-62							
PV2A VACC	PROTEIN A14	VARIOLA VIRUS	19-62							
PV2A VACC	PROTEIN A16	VACCINIA VIRUS (STRAIN COPENHAGEN)	141-162							
PV2A VACC	PROTEIN A16	VARIOLA VIRUS	141-162							
PV2A VACC	56 KD ABORTIVE LATE PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	429-447							
PV2A VACC	56 KD ABORTIVE LATE PROTEIN	VACCINIA VIRUS (STRAIN WR)	429-447							
PV2A VACC	56 KD ABORTIVE LATE PROTEIN	VARIOLA VIRUS	429-447							
PV2A VACC	PROTEIN A20	VACCINIA VIRUS (STRAIN COPENHAGEN)	107-131							
PV2A VACC	PROTEIN A20	VARIOLA VIRUS	107-131							
PV2A VACC	PROTEIN A23	VACCINIA VIRUS (STRAIN WR) AND (STRAIN COPENHAGEN)	53-76							
PV2A VACC	PROTEIN A23	VARIOLA VIRUS	53-76							
PV2A VACC	PROTEIN A31	VACCINIA VIRUS (STRAIN WR) AND (STRAIN COPENHAGEN)	205-220							
PV2A VACC	PROTEIN A31	VARIOLA VIRUS	175-190							
PV2A VACC	PROTEIN A32	VACCINIA VIRUS (STRAIN COPENHAGEN)	33-49							
PV2A VACC	PROTEIN A32	VARIOLA VIRUS	33-49							
PV2A VACC	PROTEIN A33 PRECURSOR	VACCINIA VIRUS (STRAIN WR)	66-90							
PV2A VACC	PROTEIN A33 PRECURSOR	VACCINIA VIRUS (STRAIN WR)	66-90							
PV2A VACC	PROTEIN A37	VACCINIA VIRUS (STRAIN COPENHAGEN)	47-71							
PV2A VACC	PROTEIN A37	VARIOLA VIRUS	47-71							
PV2A VACC	PROTEIN A40	VACCINIA VIRUS (STRAIN COPENHAGEN)	59-79							
PV2A VACC	PROTEIN A40	VARIOLA VIRUS	59-79							
PV2A VACC	PROTEIN A41 PRECURSOR	VACCINIA VIRUS (STRAIN WR)	201-226							
PV2A VACC	PROTEIN A41 PRECURSOR	VARIOLA VIRUS	201-226							
PV2A VACC	PROTEIN A47	VACCINIA VIRUS (STRAIN COPENHAGEN)	247-266							
PV2A VACC	PROTEIN A47	VARIOLA VIRUS	247-266							
PV2A VACC	PROTEIN A53	VACCINIA VIRUS (STRAIN COPENHAGEN)	384-404							
PV2A VACC	PROTEIN A53	VARIOLA VIRUS	384-404							
PV2A VACC	PROTEIN A55	VACCINIA VIRUS (STRAIN WR)	56-75							
PV2A VACC	PROTEIN A55	BEEF CURLY TOP VIRUS	56-75							
PV2A BCTV	ALI PROTEIN									



PGENE	PROTEIN	PICTLZIP	All Viruses (No bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
TMENAS	PROTEIN											AREA2
PVCAP TGMVA	MAJOR CAPSID PROTEIN		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	668-684								AREA1
PVCAP HSV1	MAJOR CAPSID PROTEIN		HERPES SIMPLEX VIRUS (TYPE 1 STRAIN 17)	282-302	356-384	1137-1152						
PVCAP HSV2	MAJOR CAPSID PROTEIN		EQUINE HERPESVIRUS TYPE 1 (STRAIN AH41)	352-383	472-498							
PVCAP HSV3	MAJOR CAPSID PROTEIN		HERPESVIRUS SAIMIRI (STRAIN 11)	144-168	269-287	357-372	1062-1080					
PVCAP PRV1	MAJOR CAPSID PROTEIN		PSEUDORABIES VIRUS (STRAIN INDIANA S)	315-362								
PVCAP VZV1	MAJOR CAPSID PROTEIN		VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	181-401								
PVC31 NPVAC	DNA-BINDING PROTEIN		AUTOGRAPIA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS	60-81	891-910	1156-1176						
PVD01 VACCC	PROTEIN D3		VACCINIA VIRUS (STRAIN COPENHAGEN)	12-39								
PVD01 VACCV	PROTEIN D3		VACCINIA VIRUS (STRAIN WR)	12-39								
PVD01 VARV	PROTEIN D3		VARIOLA VIRUS	12-39								
PVD01 FOWP1	92 K D PROTEIN		FOWLPOX VIRUS (STRAIN FP-1)	246-265	315-337							
PVD01 SFYKA	PROTEIN D3		SHOPE FIBROMA VIRUS (STRAIN KASZA)	34-78	171-198							
PVD01 VACCC	PROTEIN D3		VACCINIA VIRUS (STRAIN COPENHAGEN)	320-340	694-714	715-734						
PVD01 VACCV	PROTEIN D3		VACCINIA VIRUS (STRAIN WR)	320-340	694-714	715-734						
PVD01 VARV	PROTEIN D3		VARIOLA VIRUS	320-340	694-714	715-734						
PVD01 CAMVC	DNA-BINDING PROTEIN		CAULIFLOWER MOSAIC VIRUS (STRAIN CN-1841)	37-56								
PVD01 CAMVD	DNA-BINDING PROTEIN		CAULIFLOWER MOSAIC VIRUS (STRAIN DRI)	37-56								
PVD01 CAMVB	DNA-BINDING PROTEIN		CAULIFLOWER MOSAIC VIRUS (STRAIN BRC)	37-56								
PVD01 CAMVN	DNA-BINDING PROTEIN		CAULIFLOWER MOSAIC VIRUS (STRAIN NY813)	37-56								
PVD01 CAMVS	DNA-BINDING PROTEIN		CAULIFLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	37-56								
PVE02 VACCC	PROTEIN E2		VACCINIA VIRUS (STRAIN COPENHAGEN)	70-97	355-380	340-558						
PVE02 VACCV	PROTEIN E2		VACCINIA VIRUS (STRAIN WR)	70-97	355-380	340-558						
PVE02 VARV	PROTEIN E2		VARIOLA VIRUS	70-97	355-380	340-558						
PVE03 VACCC	PROTEIN E3		VACCINIA VIRUS (STRAIN COPENHAGEN)	314-329								
PVE03 VACCV	PROTEIN E3		VACCINIA VIRUS (STRAIN WR)	324-339								
PVE03 VARV	PROTEIN E3		VARIOLA VIRUS	324-339								
PVE04 VACCC	PROTEIN E4		VACCINIA VIRUS (STRAIN COPENHAGEN)	410-431								
PVE04 VACCV	PROTEIN E4		VACCINIA VIRUS (STRAIN WR)	410-431								
PVE04 VARV	PROTEIN E4		VARIOLA VIRUS	410-431								
PVE05 VACCC	PROTEIN E5		VACCINIA VIRUS (STRAIN COPENHAGEN)	251-267	430-451							
PVE05 VACCV	PROTEIN E5		VACCINIA VIRUS (STRAIN WR)	254-270								
PVE05 VARV	PROTEIN E5		VARIOLA VIRUS	254-270								
PVE11 NPV16	PROBABLE E1 PROTEIN 2		HUMAN PAPILLOMAVIRUS TYPE 16	167-183								
PVE11 NPVAC	EARLY 18 3 KD PROTEIN		AUTOGRAPIA CALIFORNICA NUCLEAR POLYIHDROSIS VIRUS	106-133								
PVE1 BPV1	E1 PROTEIN		BOVINE PAPILLOMAVIRUS TYPE 1	265-282	517-531							
PVE1 BPV2	E1 PROTEIN		BOVINE PAPILLOMAVIRUS TYPE 2	265-281	516-532							
PVE1 CAPVK	E1 PROTEIN		COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN KANSAS)	7-22								
PVE1 HPV11	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 11	258-275	311-334							
PVE1 HPV12	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 12	308-324								
PVE1 HPV13	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 13	264-281	317-333	344-364						
PVE1 HPV14	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 14	237-254								
PVE1 HPV15	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 15	278-280								
PVE1 HPV16	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 16	314-354								
PVE1 HPV17	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 17	304-320								
PVE1 HPV18	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 18	238-260								
PVE1 HPV19	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 19	258-275	311-334							
PVE1 HPV20	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 20	310-326								
PVE1 HPV21	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 21	286-309								
PVE1 HPV22	E1 PROTEIN		COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN KANSAS)	308-333								
PVE1 HPV23	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 23	285-310								
PVE1 HPV24	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 24	291-320								
PVE1 HPV25	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 25	288-306								
PVE1 HPV26	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 26	284-300								
PVE1 HPV27	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 27	311-336								
PVE1 HPV28	E1 PROTEIN		HUMAN PAPILLOMAVIRUS TYPE 28	294-312								



PCGENE	PICTLZIP	All Viruses (No Bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
FILENAME	PROTEIN	VIRUS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
PVE1 HPV01	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 31	275-291							
PVE2 HPV02	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 33	289-307							
PVE3 HPV03	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 35	292-310							
PVE4 HPV04	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 39	311-328							
PVE5 HPV05	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 42	303-328							
PVE6 HPV06	E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 57	286-311							
PVE7 HPV07	PROBABLE E3 PROTEIN	DEER PAPILLOMAVIRUS	313-331							
PVE8 HPV08	E3 PROTEIN	PRIMATE PAPILLOMAVIRUS TYPE 1	295-320							
PVE9 HPV09	E3 PROTEIN	PIG PAPILLOMAVIRUS TYPE 1	295-320							
PVE10 HPV10	PROBABLE E3 PROTEIN	PIG PAPILLOMAVIRUS TYPE 1	295-320							
PVE11 HPV11	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 18	195-59							
PVE12 HPV12	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	56-76							
PVE13 HPV13	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 51	59-83							
PVE14 HPV14	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 1	61-87							
PVE15 HPV15	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 11	19-47							
PVE16 HPV16	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 14	19-47							
PVE17 HPV17	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 1, AND TYPE 2	2-26							
PVE18 HPV18	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 13	16-42							
PVE19 HPV19	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 31	31-52							
PVE20 HPV20	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 42	45-65							
PVE21 HPV21	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 51	31-52							
PVE22 HPV22	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 58	86-113							
PVE23 HPV23	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 1	109-132							
PVE24 HPV24	PROBABLE E3 PROTEIN	BOVINE PAPILLOMAVIRUS TYPE 1	21-41							
PVE25 HPV25	PROBABLE E3 PROTEIN	COTTONTAIL RABBIT (SHORE) PAPILLOMAVIRUS (STRAIN KANSAS)	6-23							
PVE26 HPV26	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 8	133-151							
PVE27 HPV27	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 2A	8-37							
PVE28 HPV28	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 31	9-26							
PVE29 HPV29	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 35	9-26							
PVE30 HPV30	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 51	8-37							
PVE31 HPV31	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 57	9-26							
PVE32 HPV32	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 58	9-26							
PVE33 HPV33	PROBABLE E3 PROTEIN	MICROMYS MINUTUS PAPILLOMAVIRUS	7-33							
PVE34 HPV34	PROBABLE E3 PROTEIN	COTTONTAIL RABBIT (SHORE) PAPILLOMAVIRUS (STRAIN KANSAS)	71-88							
PVE35 HPV35	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 13	77-93							
PVE36 HPV36	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 51	61-87							
PVE37 HPV37	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 68	20-37							
PVE38 HPV38	PROBABLE E3 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 1	79-105							
PVE39 HPV39	PROBABLE E3 PROTEIN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	78-99							
PVE40 HPV40	PROBABLE E3 PROTEIN	TRICHOPUS NUCLEOLUS VIRUS	154-175							
PVE41 HPV41	PROBABLE E3 PROTEIN	BERNE VIRUS	237-260							
PVE42 HPV42	PROBABLE E3 PROTEIN	DIORIN VIRUS (STRAIN INDIAN/13161)	63-86							
PVE43 HPV43	PROBABLE E3 PROTEIN	EQUINE ARTERITIS VIRUS	42-57							
PVE44 HPV44	PROBABLE E3 PROTEIN	LEISTAD VIRUS	25-41							
PVE45 HPV45	PROBABLE E3 PROTEIN	MOLLUSCUM CONTAGIOSUM VIRUS SUBTYPE 1	27-47							
PVE46 HPV46	PROBABLE E3 PROTEIN	MOLLUSCUM CONTAGIOSUM VIRUS SUBTYPE 2	61-80							
PVE47 HPV47	PROBABLE E3 PROTEIN	THOGOTO VIRUS	196-221							
PVE48 HPV48	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE49 HPV49	PROBABLE E3 PROTEIN	THOGOTO VIRUS	471-491							
PVE50 HPV50	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE51 HPV51	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE52 HPV52	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE53 HPV53	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE54 HPV54	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE55 HPV55	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE56 HPV56	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE57 HPV57	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE58 HPV58	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE59 HPV59	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE60 HPV60	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE61 HPV61	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE62 HPV62	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE63 HPV63	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE64 HPV64	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE65 HPV65	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE66 HPV66	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE67 HPV67	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE68 HPV68	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE69 HPV69	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE70 HPV70	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE71 HPV71	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE72 HPV72	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE73 HPV73	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE74 HPV74	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE75 HPV75	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE76 HPV76	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE77 HPV77	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE78 HPV78	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE79 HPV79	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE80 HPV80	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE81 HPV81	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE82 HPV82	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE83 HPV83	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE84 HPV84	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE85 HPV85	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE86 HPV86	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE87 HPV87	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE88 HPV88	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE89 HPV89	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE90 HPV90	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE91 HPV91	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE92 HPV92	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE93 HPV93	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE94 HPV94	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE95 HPV95	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE96 HPV96	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE97 HPV97	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE98 HPV98	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE99 HPV99	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							
PVE100 HPV100	PROBABLE E3 PROTEIN	THOGOTO VIRUS	356-383							

PCGENE	PICTURE	FILE NAME	ALL Viruses (No Bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
PF01	PROTEIN	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	3-26								
PF02	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	28-31								
PF03	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	297-323								
PF04	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	88-104								
PF05	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	89-111								
PF06	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	65-90								
PF07	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	51-76								
PF08	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	29-48								
PF09	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	72-94								
PF10	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	169-195								
PF11	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	210-225								
PF12	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	298-318								
PF13	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	237-257								
PF14	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	208-318								
PF15	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	58-82								
PF16	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	50-72								
PF17	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	11-33								
PF18	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	11-33								
PF19	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	31-51								
PF20	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	31-51								
PF21	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	134-149								
PF22	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	35-54								
PF23	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	109-124								
PF24	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	103-122								
PF25	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	131-178								
PF26	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	68-92								
PF27	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	88-112								
PF28	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	173-197								
PF29	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	14-40								
PF30	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	20-42								
PF31	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	166-191								
PF32	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	90-109								
PF33	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	108-123								
PF34	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	284-299								
PF35	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	648-673								
PF36	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	14-32								
PF37	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	11-38								
PF38	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	109-133								
PF39	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	134-156								
PF40	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	71-97								
PF41	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	5-30								
PF42	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	29-49								
PF43	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	84-102								
PF44	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	229-252								
PF45	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	22-37								
PF46	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	85-106								
PF47	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	1155-1176								
PF48	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	130-146								
PF49	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	142-161								
PF50	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	42-64								
PF51	PROTEIN F13	PROTEIN F13	VACCINIA VIRUS (STRAIN L-1VP)	31-75								



PCGENE	PICTLZIP	ALL Virus (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PVGLB_HSV1E1	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (ISOLATE JIV52A) (HIV-1)	716-753								
PVGLB_HSV1E2	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN A01)	675-692								
PVGLB_HSV1E3	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN A01)	716-753								
PVGLB_HSV1E4	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN A04F)	716-753								
PVGLB_HSV1E5	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN KENTUCKY D)	716-753								
PVGLB_HSV1E6	GLYCOPROTEIN B PRECURSOR	MAKES'S DISEASE HERPESVIRUS (STRAIN RD-10)	589-613								
PVGLB_HSV1E7	GLYCOPROTEIN B PRECURSOR	HERPESVIRUS SAMIRI (STRAIN 11)	483-506								
PVGLB_HSV1E8	GLYCOPROTEIN B PRECURSOR	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN 632)	256-275								
PVGLB_HSV1E9	GLYCOPROTEIN B PRECURSOR	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN SA-2)	607-631								
PVGLB_HSV1E10	GLYCOPROTEIN B PRECURSOR	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE VR2)	266-285								
PVGLB_HSV1E11	GLYCOPROTEIN B PRECURSOR	MURINE CYTOMEGALOVIRUS (STRAIN SMITH)	135-156								
PVGLB_HSV1E12	GLYCOPROTEIN B PRECURSOR	PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSEN / HICKIR)	566-589								
PVGLB_HSV1E13	GLYCOPROTEIN B PRECURSOR	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	203-218								
PVGLB_HSV1E14	GLYCOPROTEIN B PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	522-538								
PVGLB_HSV1E15	GLYCOPROTEIN B PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 3)	1-22								
PVGLB_HSV1E16	GLYCOPROTEIN B PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 3)	435-458								
PVGLB_HSV1E17	GLYCOPROTEIN B PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 27 / STRAIN 331)	436-459								
PVGLB_HSV1E18	GLYCOPROTEIN B PRECURSOR	BOVINE HERPESVIRUS TYPE 1 (STRAIN COOPER)	475-494								
PVGLB_HSV1E19	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN 1942)	444-459								
PVGLB_HSV1E20	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN A04F) AND (STRAIN KENTUCKY D)	427-442								
PVGLB_HSV1E21	SECRETORY GLYCOPROTEIN GP37-45 PRECURSOR	MAKES'S DISEASE HERPESVIRUS (STRAIN RD-10)	399-421								
PVGLB_HSV1E22	SECRETORY GLYCOPROTEIN GP37-45 PRECURSOR	MAKES'S DISEASE HERPESVIRUS (STRAIN RD-10)	399-421								
PVGLB_HSV1E23	SECRETORY GLYCOPROTEIN GP37-45 PRECURSOR	MAKES'S DISEASE HERPESVIRUS (STRAIN RD-10)	399-421								
PVGLB_HSV1E24	SECRETORY GLYCOPROTEIN GP37-45 PRECURSOR	MAKES'S DISEASE HERPESVIRUS (STRAIN RD-10)	399-421								
PVGLB_HSV1E25	SECRETORY GLYCOPROTEIN GP37-45 PRECURSOR	MAKES'S DISEASE HERPESVIRUS (STRAIN RD-10)	399-421								
PVGLB_HSV1E26	GLYCOPROTEIN GII PRECURSOR	PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSEN / HICKIR)	180-197								
PVGLB_HSV1E27	GLYCOPROTEIN GII PRECURSOR	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	431-449								
PVGLB_HSV1E28	GLYCOPROTEIN GII PRECURSOR	VARICELLA-ZOSTER VIRUS (STRAIN SCOTT)	431-449								
PVGLB_HSV1E29	GLYCOPROTEIN GII PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	70-94								
PVGLB_HSV1E30	GLYCOPROTEIN GII PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	104-129								
PVGLB_HSV1E31	GLYCOPROTEIN GII PRECURSOR	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	469-493								
PVGLB_HSV1E32	GLYCOPROTEIN GII PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A31908)	205-221								
PVGLB_HSV1E33	GLYCOPROTEIN GII PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COPIENHAGEN)	205-221								
PVGLB_HSV1E34	GLYCOPROTEIN GII PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN BBA4)	205-221								
PVGLB_HSV1E35	GLYCOPROTEIN GII PRECURSOR	CANINE DISTEMPER VIRUS (STRAIN ONDERSTPOORT)	316-361								
PVGLB_HSV1E36	GLYCOPROTEIN GII PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN 183)	205-221								
PVGLB_HSV1E37	GLYCOPROTEIN GII PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	205-221								
PVGLB_HSV1E38	GLYCOPROTEIN GII PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP A / STRAIN LO)	205-221								
PVGLB_HSV1E39	GLYCOPROTEIN GII PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN R35-2)	205-221								
PVGLB_HSV1E40	GLYCOPROTEIN GII PRECURSOR	MEASLES VIRUS (STRAIN EDMONSTON/WH4 (STRAIN HALL))	274-245								
PVGLB_HSV1E41	GLYCOPROTEIN GII PRECURSOR	MEASLES VIRUS (STRAIN IP-3-CA)	227-248								
PVGLB_HSV1E42	GLYCOPROTEIN GII PRECURSOR	MEASLES VIRUS (STRAIN YAMAGATA-1)	274-245								
PVGLB_HSV1E43	GLYCOPROTEIN GII PRECURSOR	MUMPS VIRUS (STRAIN SBL-1)	5-20								
PVGLB_HSV1E44	GLYCOPROTEIN GII PRECURSOR	MUMPS VIRUS (STRAIN MIYAHARA VACCINE)	276-292								
PVGLB_HSV1E45	GLYCOPROTEIN GII PRECURSOR	MUMPS VIRUS (STRAIN RW)	276-292								
PVGLB_HSV1E46	GLYCOPROTEIN GII PRECURSOR	MUMPS VIRUS (STRAIN SBL)	276-292								
PVGLB_HSV1E47	GLYCOPROTEIN GII PRECURSOR	MUMPS VIRUS (STRAIN RW)	276-292								
PVGLB_HSV1E48	GLYCOPROTEIN GII PRECURSOR	MUMPS VIRUS (STRAIN SBL)	276-292								
PVGLB_HSV1E49	GLYCOPROTEIN GII PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA/2)	271-289								
PVGLB_HSV1E50	GLYCOPROTEIN GII PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE C/45)	271-289								
PVGLB_HSV1E51	GLYCOPROTEIN GII PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN HER33)	271-289								
PVGLB_HSV1E52	GLYCOPROTEIN GII PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN BI-HITCHNER/41)	271-289								
PVGLB_HSV1E53	GLYCOPROTEIN GII PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN LAS/46)	271-289								
PVGLB_HSV1E54	GLYCOPROTEIN GII PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN MIYADAKA/51)	271-289								
PVGLB_HSV1E55	GLYCOPROTEIN GII PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN QUEENSLAND/66)	271-289								
PVGLB_HSV1E56	GLYCOPROTEIN GII PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN TEXAS)	271-289								
PVGLB_HSV1E57	GLYCOPROTEIN GII PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN TEXAS G B / 48)	271-289								
PVGLB_HSV1E58	GLYCOPROTEIN GII PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN ULSTER/67)	271-289								
PVGLB_HSV1E59	GLYCOPROTEIN GII PRECURSOR	PHOCINE DISTEMPER VIRUS	269-285								
PVGLB_HSV1E60	GLYCOPROTEIN GII PRECURSOR	PHOCINE DISTEMPER VIRUS	305-326								
PVGLB_HSV1E61	GLYCOPROTEIN GII PRECURSOR	PHOCINE DISTEMPER VIRUS	367-383								
PVGLB_HSV1E62	GLYCOPROTEIN GII PRECURSOR	PHOCINE DISTEMPER VIRUS	511-558								

PCGENE	PROTEIN	FILE NAME	All Viruses (No Bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
PVGLF_P1HIC	PROTEIN	PROTEIN	VIRUS	456-477								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C9)		450-471								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN GRIER)		450-471								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TOSHIH)		450-471								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	BOVINE PARAINFLUENZA 3 VIRUS		405-476								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIII 47845)		2-20	453-474							
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RINDERPEST VIRUS (STRAIN KAHETE C)		220-241	402-241							
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RINDERPEST VIRUS (STRAIN L)		220-241	402-241							
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN 2, MOST MUTANTS)		400-481								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN FUSIHI)		400-481								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN HARRIS)		400-481								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN HW)		400-481								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN Z)		400-481								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SIMIAN VIRUS 41		453-474								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SIMIAN VIRUS 3 (STRAIN WJ)		401-425	446-467							
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	TURKEY RHINOTRACHEITIS VIRUS		175-191	452-474							
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	INFECTIOUS HEMATOPOIETIC NECROSIS VIRUS (STRAIN ROUND HUT)		77-99								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRAIN ERA)		454-474								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRAIN PV)		372-391	454-474							
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRAIN SAD B19)		454-474								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRAIN STREET)		454-474								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	TURKEY RHINOTRACHEITIS VIRUS		169-216								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	VIRAL HEMORRHAGIC SEPTICEMIA VIRUS (STRAIN 07-71)		406-428								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)		211-237	363-382	574-598	691-712					
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN TOWNE)		210-236	364-381	575-597	690-711					
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)		245-262	443-467	801-827						
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN IFEN)		245-262	443-467	801-827						
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN GS)		314-332								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 4 / STRAIN 1942)		304-323	814-839							
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD47)md (ISOLATE IVSSA)		297-318	807-832							
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HERPESVIRUS SAIMIRI (STRAIN 11)		454-479	558-576							
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	MURINE CYTOMEGALOVIRUS (STRAIN SMITII)		670-690								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)		158-180								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)		43-60								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 1		44-63								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)		278-297								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	BUNYAVIRUS GERMISTON		117-136								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	BUNYAVIRUS LA CROSSE (ISOLATE L74)		31-55	81-98	190-211	1325-1345	1387-1410				
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	BUNYAVIRUS SNOWSHOE HARE		31-55	81-98	190-211	1325-1345	1387-1410				
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	BUNYAVIRUS VIRUS		193-218	1379-1404							
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	DUGRE VIRUS		355-371	692-717	900-915	999-1019					
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN B-1)		499-515	694-719	1000-1020						
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN HO10)		499-515	694-719	1000-1020						
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN LEE)		499-515	694-719	1001-1021						
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN 76-118)		499-515	694-719	1001-1021						
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	IMPATIENS NECROTIC SPOT VIRUS (NSV)		18-44	269-293	346-367	531-551	815-841				
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	PROSPECT HILL VIRUS		152-171								
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	PUNTA TORO PHLEBOVIRUS		743-763	997-1016	1275-1302						
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	PUMALA VIRUS (STRAIN HALLAS B1)		155-174	509-525	712-739						
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	PUMALA VIRUS (STRAIN SOTKANO)		155-174	509-525	712-739	1092-1117					
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RIFT VALLEY FEVER VIRUS		53-80	344-368	510-536						
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	RIFT VALLEY FEVER VIRUS (STRAIN ZH-448 N12)		53-80	344-368	510-536	1156-1176					
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SEOL VIRUS (STRAIN 00-59)		355-371	692-717	900-915	999-1019					
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SEOL VIRUS (STRAIN R23)		355-371	692-717	900-915	999-1019					
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	SEOL VIRUS (STRAIN SR-11) (SAPPORO RAT VIRUS)		355-371	692-717	900-915	999-1019					
PVGLF_P1HIC	FUSION GLYCOPROTEIN PRECURSOR	LUKUNEMI VIRUS		361-385	655-674	826-842	925-951	966-989				













PCGENE	FILE NAME	PROTEIN	PICTURE	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
			ALL Viruses (No Bacteriophage)									
			VIRUS									
PVNS1 IAMAN	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN AMALLARD/NEW YORK/67/50/78)	31-50	167-192							AREA 2
PVNS1 IAMAO	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN AMALLARD/NEW YORK/67/50/78)	31-50	167-192							
PVNS1 IAMYN	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN AMY/AMY/INDIA/THA/76)	28-47	164-189							
PVNS1 IAPIV	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN APINT/AL/ALBERTA/119/79)	167-192								
PVNS1 IAPII	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN APINT/AL/ALBERTA/121/79)	31-50	167-192							
PVNS1 IAPIJ	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN APINT/AL/ALBERTA/138/79)	31-50	167-192							
PVNS1 IAPIK	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN APINT/AL/ALBERTA/138/79)	31-50	167-192							
PVNS1 IAPIB	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN APINT/AL/ALBERTA/138/79)	31-50	167-192							
PVNS1 IATKC	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN ATURKEY/CANADA/63)	31-50	114-137	167-192						
PVNS1 IATKR	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN ATURKEY/YOCONG/71)	31-50	167-192							
PVNS1 IATRI	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN ATERN/SOUTH AFRICA/61)	28-47	164-189							
PVNS1 IATRO	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN ATERN/TURK/MENIA/18/72)	31-50	114-137	167-192						
PVNS1 IAUSJ	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN AUDON/10/72)	31-50	167-192							
PVNS1 IAZJI	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN AUSS/90/77)	222-248								
PVNS1 INCAA	NONSTRUCTURAL PROTEIN NS1		INFLUENZA A VIRUS (STRAIN AUSWINE/TOWA/15/00)	31-50	114-137	167-192						
PVNS1 INCCA	NONSTRUCTURAL PROTEIN NS1		INFLUENZA C VIRUS (STRAIN C/ANN ARBOR/15/0)	31-50	167-192							
PVNS2 BTY10	NONSTRUCTURAL PROTEIN NS2		INFLUENZA C VIRUS (STRAIN C/CALIFORNIA/78)	222-248								
PVNS2 BTY17	NONSTRUCTURAL PROTEIN NS2		BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	145-161	201-223							
PVNS2 BTY18	NONSTRUCTURAL PROTEIN NS2		BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	145-161	201-223							
PVNS2 BTY19	NONSTRUCTURAL PROTEIN NS2		BLUETONGUE VIRUS (SEROTYPE 1 / ISOLATE SOUTH AFRICA)	145-161								
PVNS2 EHDV2	NONSTRUCTURAL PROTEIN NS2		BLUETONGUE VIRUS (SEROTYPE 10)	145-161								
PVNS2 LAPES	NONSTRUCTURAL PROTEIN NS2		EPIZOOTIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 2 / STRAIN AL)	145-161								
PVNS2 LAPES	NONSTRUCTURAL PROTEIN NS2		INFLUENZA A VIRUS (STRAIN APUBERTO RICO/04)	3-28								
PVNS2 PVM	NONSTRUCTURAL PROTEIN 2		PNEUMONIA VIRUS OF MICE	36-80								
PVNS3 CVPF5	NONSTRUCTURAL PROTEIN 3-1		PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAI)	177-201								
PVNS3 CVPF6	NONSTRUCTURAL PROTEIN 3-1		PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAI)	98-122								
PVNS3 CVPF7	NONSTRUCTURAL PROTEIN 3-1		PORCINE RESPIRATORY CORONAVIRUS (STRAIN RM4)	177-201								
PVNS3 RSV	NONSTRUCTURAL PROTEIN NS3		RICE STRUPE VIRUS	16-40								
PVNS4 CVM23	NONSTRUCTURAL PROTEIN 4		HUMAN CORONAVIRUS (STRAIN 229E)	84-100								
PVNS4 CVM24	NONSTRUCTURAL PROTEIN 4		MURINE CORONAVIRUS MHV (STRAIN 5)	17-38								
PVNS4 CVPF3	NONSTRUCTURAL PROTEIN 4		PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAI)	4-31								
PVNS4 CVPF4	NONSTRUCTURAL PROTEIN 4		PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAI)	4-31								
PVNS4 CVPF5	NONSTRUCTURAL PROTEIN 4		PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAI)	4-31								
PVNS4 MSTV	NONSTRUCTURAL PROTEIN NS4		MAIZE STRUPE VIRUS	41-56								
PVNS4 RSV	NONSTRUCTURAL PROTEIN NS4		RICE STRUPE VIRUS	41-56	60-82	151-167						
PVNS7 CVPF3	NONSTRUCTURAL PROTEIN 7		FELINE ENTERIC CORONAVIRUS (STRAIN 79-1683)	59-84								
PVNS7 FIV	NONSTRUCTURAL PROTEIN 7		FELINE INFECTIOUS PERITONITIS VIRUS (STRAIN 79-1146)	59-84								
PVNSC PIH1B	NONSTRUCTURAL PROTEIN C		HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C13)	76-92								
PVNSC PIH1C	NONSTRUCTURAL PROTEIN C		HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C19)	76-92								
PVNSC PIH1D	NONSTRUCTURAL PROTEIN C		HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C13/73)	76-92								
PVNSC PIH1E	NONSTRUCTURAL PROTEIN C		HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C14/83)	76-92								
PVNS1 CVBQ	12 KD NONSTRUCTURAL PROTEIN		BOVINE CORONAVIRUS (STRAIN QUEBEC)	88-109								
PVNS1 INCG1	NONSTRUCTURAL PROTEINS NS1-NS2		INFLUENZA C VIRUS (STRAIN C/GREAT LAKES/16/74)	222-248								
PVNS1 INCG2	NONSTRUCTURAL PROTEINS NS1-NS2		INFLUENZA C VIRUS (STRAIN C/HANNESBURG/166)	222-248								
PVNS1 INCG3	NONSTRUCTURAL PROTEINS NS1-NS2		INFLUENZA C VIRUS (STRAIN C/MISSISSIPPI/80)	222-248								
PVNS1 INCG4	NONSTRUCTURAL PROTEINS NS1-NS2		INFLUENZA C VIRUS (STRAIN C/MISSISSIPPI/80)	222-248								
PVNS1 INCG5	NONSTRUCTURAL PROTEINS NS1-NS2		INFLUENZA C VIRUS (STRAIN C/MISSISSIPPI/80)	222-248								
PVNS1 PTV	NONSTRUCTURAL PROTEIN NS-5		PUNTA TORO PHLEBOVIRUS	48-63								
PVNS1 SF5V	NONSTRUCTURAL PROTEIN NS-5		SANDFLY FEVER SICILIAN VIRUS	16-34								
PVNS1 UUK	NONSTRUCTURAL PROTEIN NS-5		ULIKUNEMAI VIRUS	52-73	89-104							
PVNUA PRVKA	PROBABLE NUCLEAR ANTIGEN		PSEUDORABIES VIRUS (STRAIN KAPLAN)	736-777	1561-1583							
PVNUC DHV1	NUCLEOPROTEIN		DHOIR VIRUS (STRAIN INDIAN/131/61)	132-139	297-324							
PVNUC EBOV	NUCLEOPROTEIN		EBOLA VIRUS	132-139	297-324							
PVNUC IAAV	NUCLEOPROTEIN		INFLUENZA A VIRUS (STRAIN A/ANAS ACUTIPRIMORIE/69/76)	173-197	266-287							
PVNUC IAAV	NUCLEOPROTEIN		INFLUENZA A VIRUS (STRAIN A/ANAN ARBOR/6/66)	173-197								
PVNUC IABRA	NUCLEOPROTEIN		INFLUENZA A VIRUS (STRAIN A/BRAZIL/11/78)	173-197								













GENE	FUNCTION	ALL Viruses (No. Bacteriophages)	AREA 1 428-430	AREA 2 431-473	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
FILE NAME	PROTEIN	VIRUS									
PSV03 ROTHI	NONSTRUCTURAL PROTEIN NCVP2	HUMAN ROTAVIRUS (STRAIN IGV-80-3)									
PSV03 ROTPC	NONSTRUCTURAL PROTEIN NS3	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	140-157								
PSV03 ROTSI	NONSTRUCTURAL PROTEIN NCVP2	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	140-157								
PSV06 ROTBR	VP6 PROTEIN	BOVINE ROTAVIRUS (STRAIN R7)	399-414								
PSV06 ROTBS	VP6 PROTEIN	BOVINE ROTAVIRUS (GROUP C / STRAIN SHINTOKU)	202-225								
PSV06 ROTBU	VP6 PROTEIN	BOVINE ROTAVIRUS (STRAIN UK)	64-85								
PSV06 ROTF	VP6 PROTEIN	EQUINE ROTAVIRUS (STRAIN FL14)	202-225								
PSV06 ROTEL	VP6 PROTEIN	EQUINE ROTAVIRUS (STRAIN IL-2)	202-225								
PSV06 ROTGA	VP6 PROTEIN	ROTAVIRUS (GROUP B / STRAIN ADPV) (ADULT DIARRHEA ROTAVIRUS)	202-225								
PSV06 ROTGI	VP6 PROTEIN	ROTAVIRUS (GROUP B / STRAIN IDIR)	22-40								
PSV06 ROTHC	VP6 PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 076)	202-225								
PSV06 ROTHI	VP6 PROTEIN	HUMAN ROTAVIRUS (GROUP C / STRAIN BRISTOL)	64-85								
PSV06 ROTHS	VP6 PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN S3)	202-225								
PSV06 ROTHW	VP6 PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	202-225								
PSV06 ROTPC	VP6 PROTEIN	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	202-225								
PSV06 ROTPG	VP6 PROTEIN	PORCINE ROTAVIRUS (STRAIN GOTTFRIED)	64-85								
PSV07 ROTBI	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN KN-4)	202-225								
PSV07 ROTC	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	131-155								
PSV07 ROTD	GLYCOPROTEIN VP7	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	117-136								
PSV09 ROTB6	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (SEROTYPE 6 / STRAIN 61A)	274-295								
PSV09 ROTBB	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN A44)	131-155								
PSV09 ROTBT	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (SEROTYPE 10 / STRAIN B223)	131-155								
PSV09 ROTC	GLYCOPROTEIN VP7	BOVINE ROTAVIRUS (STRAIN KK)	131-155								
PSV09 ROTEL	GLYCOPROTEIN VP7	CHICKEN ROTAVIRUS (SEROTYPE 1 / STRAIN T449)	131-155								
PSV09 ROTG	GLYCOPROTEIN VP7	EQUINE ROTAVIRUS (SEROTYPE 2 / STRAIN C12)	134-158								
PSV09 ROTHA	GLYCOPROTEIN VP7	ROTAVIRUS (GROUP B / STRAIN IDIR)	205-232								
PSV09 ROTB	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN RV-4)	131-155								
PSV09 ROTD	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN IUS)	192-212								
PSV09 ROTHH	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN DS1)	192-212								
PSV09 ROTIL	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN IRI26)	192-212								
PSV09 ROTHM	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (STRAIN L26)	131-155								
PSV09 ROTHP	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN M37)	192-212								
PSV09 ROTHO	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN NO AND STRAIN D)	131-155								
PSV09 ROTIR	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN P)	131-155								
PSV09 ROTIS	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN RV)	131-155								
PSV09 ROTJS	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN S3)	192-212								
PSV09 ROTK	GLYCOPROTEIN VP7	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN VA10)	192-212								
PSV09 ROTL	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	131-155								
PSV09 ROTM	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN OSU)	131-155								
PSV09 ROTN	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN TFR-41)	192-212								
PSV09 ROTP	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 4 / STRAIN DEN-144)	192-212								
PSV09 ROTQ	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 4 / STRAIN BHI-1)	192-212								
PSV09 ROTR	GLYCOPROTEIN VP7	RUESUS ROTAVIRUS	131-155								
PSV09 ROTSI	GLYCOPROTEIN VP7	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	131-155								
PSV11 ROTGA	NONSTRUCTURAL PROTEIN	ROTAVIRUS (GROUP B / STRAIN ADPV) (ADULT DIARRHEA ROTAVIRUS)	136-153								
PSV11 ROTVA	SMALL HYDROPHOBIC PROTEIN	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	16-41								
PSV11 ROTW	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN SBL-1) AND MUMPS VIRUS (STRAIN SBL)	7-29								
PSV11 ROTX	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN EDINBURGH 2 & 6)	7-29								
PSV11 ROTY	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN EDINBURGH 4)	7-29								
PSV11 ROTZ	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN MATSUJAMA)	10-29								
PSV11 ROTAA	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN BELFAST)	7-29								
PSV11 ROTAB	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN ENDERS)	7-29								
PSV11 ROTAC	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN JERYL-LYN)	7-29								
PSV11 ROTAD	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN KILHAM)	7-29								
PSV11 ROTAE	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN BRISTOL 1)	6-29								
PSV11 ROTAF	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN MIYAHARA VACCINE)	10-29								





PGENE	PICTLZIP	All Viruses (No Bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PYL1 NAME	PROTEIN	VIRUS	10-27								
PYL2 SOCMV	HYPOTHETICAL PROTEIN 1	SOYBEAN CHLOROTIC MOTTLE VIRUS									
PYL3 ADE07	HYPOTHETICAL 9.2 KD EARLY PROTEIN	HUMAN ADENOVIRUS TYPE 7	54-77								
PYL4 SSV1	HYPOTHETICAL 9.2 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	16-41	62-77							
PYL5 EBV	HYPOTHETICAL BALF1 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	205-220								
PYL6 FOWPM	HYPOTHETICAL BANGH-ORF1 PROTEIN	FOWLPOX VIRUS (ISOLATE HP-418)(MUNICHII)	354-374								
PYL7 FOWPM	HYPOTHETICAL BANGH-ORF7 PROTEIN	FOWLPOX VIRUS (ISOLATE HP-418)(MUNICHII)	104-121								
PYL8 FOWPM	HYPOTHETICAL BANGH-ORF9 PROTEIN	FOWLPOX VIRUS (ISOLATE HP-418)(MUNICHII)	49-67								
PYL9 FOWPM	HYPOTHETICAL BANGH-ORF10 PROTEIN	FOWLPOX VIRUS (ISOLATE HP-418)(MUNICHII)	84-100								
PYL10 FOWPM	HYPOTHETICAL BANGH-ORF11 PROTEIN	FOWLPOX VIRUS (ISOLATE HP-418)(MUNICHII)	114-134	134-169							
PYL11 SFV1	BEL-2 PROTEIN	SRIAN FOAMY VIRUS (TYPE 37 STRAIN LK3)	113-128								
PYL12 FOAMV	BEL-2 PROTEIN	HUMAN SPONARETROVIRUS	52-78								
PYL13 HSV5C	HYP 28.7 KD PROTEIN IN DHFR 3 REGION	HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 488)	206-210								
PYL14 HSV5C	HYP 9.3 KD PROTEIN IN DHFR 3 REGION	HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 488)	69-90								
PYL15 EBV	HYPOTHETICAL ECRF4 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	200-222								
PYL16 HSVAB	HYPOTHETICAL 21.6 KD PROTEIN	MAREK'S DISEASE HERPESVIRUS (STRAIN BC-1)	175-190								
PYL17 HSVAB	HYPOTHETICAL 21.6 KD PROTEIN	MAREK'S DISEASE HERPESVIRUS (STRAIN AD5)	175-190								
PYL18 HCMVA	HYPOTHETICAL PROTEIN HRLF4	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	101-121								
PYL19 VACCV	HYP HOST RANGE 27.4 KD PROTEIN	VACCINIA VIRUS (STRAIN WR)	86-102								
PYL20 CVMA3	HYP PROTEIN IN NUCLEOCAPSID ORF	MURINE CORONA VIRUS MHV	141-156								
PYL21 CVMA3	HYP PROTEIN IN NUCLEOCAPSID ORF	MURINE CORONA VIRUS MHV	141-156								
PYL22 EBV	HYP PROTEIN IN NUCLEOCAPSID ORF	EPSTEIN-BARR VIRUS (STRAIN B95-8)	7-33								
PYL23 ADE41	HYPOTHETICAL BKRF2 PROTEIN	HUMAN ADENOVIRUS TYPE 41	67-90								
PYL24 EBV	BKRF2 PROTEIN	HUMAN ADENOVIRUS (STRAIN B95-8)	53-73								
PYL25 IRV22	HYPOTHETICAL 13.9 KD PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	76-100	128-135	215-241	310-330					
PYL26 ADEG1	HYPOTHETICAL PROTEIN	SIMULIUM IRIDESCENT VIRUS (INSECT IRIDESCENT VIRUS TYPE 22)	23-46								
PYL27 COYMY	HYPOTHETICAL 31 KD PROTEIN	AVIAN ADENOVIRUS GALI (STRAIN PHELPS) (FOWL ADENOVIRUS 1)	59-80								
PYL28 TTV1	HYPOTHETICAL 19 KD PROTEIN	COMELINA YELLOW MOTTLE VIRUS	56-83								
PYL29 COYMY	HYPOTHETICAL 13 KD PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	13-40								
PYL30 EAV	HYPOTHETICAL 13 KD PROTEIN	COMELINA YELLOW MOTTLE VIRUS	21-49								
PYL31 LELV	HYPOTHETICAL 14 KD PROTEIN	LELYSTAD VIRUS	165-192								
PYL32 LELV	HYPOTHETICAL 14 KD PROTEIN	LELYSTAD VIRUS	196-212								
PYL33 NMV	HYPOTHETICAL 11.8 KD PROTEIN	LILY VIRUS X	71-92								
PYL34 PVX	HYPOTHETICAL 13 KD PROTEIN	NARCISUS MOSAIC VIRUS	7-30								
PYL35 PVXCP	HYPOTHETICAL 12 KD PROTEIN	POTATO VIRUS X	11-34								
PYL36 WCMYM	HYPOTHETICAL 13 KD PROTEIN	WHITE CLOVER MOSAIC VIRUS (STRAIN CP)	11-34								
PYL37 WCMYO	HYPOTHETICAL 13 KD PROTEIN	WHITE CLOVER MOSAIC VIRUS (STRAIN M)	9-29								
PYL38 ADEG1	HYPOTHETICAL 11.5 KD PROTEIN	WHITE CLOVER MOSAIC VIRUS (STRAIN O)	9-31								
PYL39 EAV	HYPOTHETICAL 28.7 KD PROTEIN	AVIAN ADENOVIRUS GALI (STRAIN PHELPS) (FOWL ADENOVIRUS 1)	69-86								
PYL40 NMV	HYPOTHETICAL 10 KD PROTEIN	EQUINE ARTERITIS VIRUS	139-158								
PYL41 TTV1	HYPOTHETICAL 16.6 KD PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	10-26								
PYL42 TTV1	HYPOTHETICAL 16.6 KD PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	13-32								
PYL43 TTV1	HYPOTHETICAL 16.6 KD PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	16-39								
PYL44 TTV1	HYPOTHETICAL 38.6 KD PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	82-102								
PYL45 TTV1	HYPOTHETICAL 38.6 KD PROTEIN	THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	231-256								
PYL46 RTBV	HYPOTHETICAL P24 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS	91-113								
PYL47 RTBV	HYPOTHETICAL P24 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS	2-23	104-126							
PYL48 NPVAC	HYPOTHETICAL 41.3 KD PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES)	2-23	104-126							
PYL49 NPVOP	HYPOTHETICAL 12.2 KD PROTEIN	AUTOGRAFIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	21-34								
PYL50 NPVOP	HYPOTHETICAL 40.0 KD PROTEIN	ORGANIA PSEUDOTUGATA MULTICAPSID POLYHEDROSIS VIRUS (OP)	82-108								
PYL51 TNYD	HYPOTHETICAL P7B PROTEIN	ORGANIA PSEUDOTUGATA MULTICAPSID POLYHEDROSIS VIRUS (OP)	27-34	215-230							
PYL52 NPVLD	HYPOTHETICAL 8.3 KD PROTEIN	TOBACCO NECROSIS VIRUS (STRAIN D) (TNV)	13-31								
PYL53 NPV60	HYPOTHETICAL PROTEIN RF1	LYMANTRIA DISPAR MULTICAPSID NUCLEAR POLYHEDROSIS VIRUS	16-35								
PYL54 NPV60	HYPOTHETICAL PROTEIN RF2	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN G5)	42-66								
PYL55 NPV60	HYPOTHETICAL PROTEIN RF3	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN G5)	55-74								
PYL56 IRV6	REPETITIVE PROTEIN ORF1	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN G5)	32-36								
PYL57 IRV6	REPETITIVE PROTEIN ORF2	CHILLO IRIDESCENT VIRUS (CIV) (INSECT IRIDESCENT VIRUS TYPE 6)	20-43								
PYL58 IRV6	REPETITIVE PROTEIN ORF3	CHILLO IRIDESCENT VIRUS (CIV) (INSECT IRIDESCENT VIRUS TYPE 6)	44-69								
PYL59 IRV6	REPETITIVE PROTEIN ORF4	CHILLO IRIDESCENT VIRUS (CIV) (INSECT IRIDESCENT VIRUS TYPE 6)	179-204	260-285							

PGCENE	PICTLZIP	PROTEIN	ALL Viruses (No Bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
SILVADIA	PROTEIN		VIRUS									
PYR1 ERV	HYPOTHETICAL BARR1 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	199-123								
PYR2 ERV	HYPOTHETICAL BARR2 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	164-182								
PYR3 ERV	HYPOTHETICAL BARR3 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	92-113								
PYR4 ERV	HYPOTHETICAL BARR4 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	181-401								
PYR5 ERV	HYPOTHETICAL BARR5 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	131-152								
PYR6 ERV	HYPOTHETICAL BARR6 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	82-99								
PYR7 ERV	HYPOTHETICAL BARR7 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	17-40								
PYR8 ERV	HYPOTHETICAL BARR8 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	31-43								
PYR9 ERV	HYPOTHETICAL BARR9 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	18-46								
PYR10 ERV	HYPOTHETICAL BARR10 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	9-28								
PYR11 ERV	HYPOTHETICAL BARR11 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	37-34								
PYR12 ERV	HYPOTHETICAL BARR12 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	18-35								
PYR13 ERV	HYPOTHETICAL BARR13 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	16-52								
PYR14 ERV	HYPOTHETICAL BARR14 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	22-38								
PYR15 ERV	HYPOTHETICAL BARR15 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	44-64								
PYR16 ERV	HYPOTHETICAL BARR16 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	31-18								
PYR17 ERV	HYPOTHETICAL BARR17 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	48-67								
PYR18 ERV	HYPOTHETICAL BARR18 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	23-42								
PYR19 ERV	HYPOTHETICAL BARR19 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	105-127								
PYR20 ERV	HYPOTHETICAL BARR20 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	54-70								
PYR21 ERV	HYPOTHETICAL BARR21 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	150-166								
PYR22 ERV	HYPOTHETICAL BARR22 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	54-80								
PYR23 ERV	HYPOTHETICAL BARR23 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	100-125								
PYR24 ERV	HYPOTHETICAL BARR24 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	50-73								
PYR25 ERV	HYPOTHETICAL BARR25 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	163-188								
PYR26 ERV	HYPOTHETICAL BARR26 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	90-106								
PYR27 ERV	HYPOTHETICAL BARR27 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	65-90								
PYR28 ERV	HYPOTHETICAL BARR28 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	122-142								
PYR29 ERV	HYPOTHETICAL BARR29 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	23-44								
PYR30 ERV	HYPOTHETICAL BARR30 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	21-36								
PYR31 ERV	HYPOTHETICAL BARR31 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	3-25								
PYR32 ERV	HYPOTHETICAL BARR32 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	96-120								
PYR33 ERV	HYPOTHETICAL BARR33 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	80-105								
PYR34 ERV	HYPOTHETICAL BARR34 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	10-37								
PYR35 ERV	HYPOTHETICAL BARR35 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	54-77								
PYR36 ERV	HYPOTHETICAL BARR36 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	16-41								
PYR37 ERV	HYPOTHETICAL BARR37 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	205-220								
PYR38 ERV	HYPOTHETICAL BARR38 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	334-374								
PYR39 ERV	HYPOTHETICAL BARR39 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	104-121								
PYR40 ERV	HYPOTHETICAL BARR40 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	49-67								
PYR41 ERV	HYPOTHETICAL BARR41 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	84-100								
PYR42 ERV	HYPOTHETICAL BARR42 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	114-134								
PYR43 ERV	HYPOTHETICAL BARR43 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	113-128								
PYR44 ERV	HYPOTHETICAL BARR44 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	52-78								
PYR45 ERV	HYPOTHETICAL BARR45 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	206-230								
PYR46 ERV	HYPOTHETICAL BARR46 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	69-90								
PYR47 ERV	HYPOTHETICAL BARR47 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	200-222								
PYR48 ERV	HYPOTHETICAL BARR48 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	173-190								
PYR49 ERV	HYPOTHETICAL BARR49 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	173-190								
PYR50 ERV	HYPOTHETICAL BARR50 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	101-121								
PYR51 ERV	HYPOTHETICAL BARR51 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	86-102								
PYR52 ERV	HYPOTHETICAL BARR52 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	141-156								
PYR53 ERV	HYPOTHETICAL BARR53 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	141-156								
PYR54 ERV	HYPOTHETICAL BARR54 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	7-33								
PYR55 ERV	HYPOTHETICAL BARR55 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	67-90								
PYR56 ERV	HYPOTHETICAL BARR56 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	15-73								
PYR57 ERV	HYPOTHETICAL BARR57 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	76-100								
PYR58 ERV	HYPOTHETICAL BARR58 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	128-155								
PYR59 ERV	HYPOTHETICAL BARR59 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	215-241								
PYR60 ERV	HYPOTHETICAL BARR60 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	330-350								
PYR61 ERV	HYPOTHETICAL BARR61 PROTEIN		EPSTEIN-BARR VIRUS (STRAIN D95-4)	23-46								



**TABLE XIV**

**SEARCH RESULTS SUMMARY**

**FOR P23TLZIPC MOTIF**









PCGENE	FUNCTION	PROTEIN	ALL VIRUSES (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
PRP1	PROTEIN	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
PRP2	REPEAT CSV	REPEAT ELEMENT PROTEIN	CANIPOLIS SONORENSIS VIRUS (CSV)	131-149					
PRP3	REV PROTEIN	REV PROTEIN	BOVINE IMMUNODEFICIENCY VIRUS (ISOLATE 127) (BIV)	74-109					
PRP4	REV PROTEIN	REV PROTEIN	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE 1369) (EIAV)	41-79					
PRP5	REV PROTEIN	REV PROTEIN	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE CL23) (EIAV)	44-79					
PRP6	REV PROTEIN	REV PROTEIN	EQUINE INFECTIOUS ANEMIA VIRUS (ISOLATE WYONING) (EIAV)	74-109					
PRP7	REV PROTEIN	REV PROTEIN	SINIAN IMMUNODEFICIENCY VIRUS (TYO-1 ISOLATE) (SIV-AGN)	75-62					
PRP8	REPEAT CSV	REPEAT ELEMENT PROTEIN	AFRICAN SWINE FEVER VIRUS (ISOLATE MALAWI LIL 20/1) (ASFV)	630-666					
PRP9	REPEAT CSV	REPEAT ELEMENT PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	279-311					
PRP10	REPEAT CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AIMP) (EHV-1)	60-92					
PRP11	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	201-235					
PRP12	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	201-235					
PRP13	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	201-235					
PRP14	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS (STRAIN DUNAS) (V2V)	34-72					
PRP15	REPEAT CSV	REPEAT ELEMENT PROTEIN	AVIAN ROUS-ASSOCIATED VIRUS TYPE 1	131-161					
PRP16	REPEAT CSV	REPEAT ELEMENT PROTEIN	AVIAN RETROVIRUS IC10	131-161					
PRP17	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	199-427					
PRP18	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	199-427					
PRP19	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	1005-1033					
PRP20	REPEAT CSV	REPEAT ELEMENT PROTEIN	CAPRIPOX VIRUS (STRAIN KS-1)	297-333					
PRP21	REPEAT CSV	REPEAT ELEMENT PROTEIN	COWPOX VIRUS (CPV)	202-216					
PRP22	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP23	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP24	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP25	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP26	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP27	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP28	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP29	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP30	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP31	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP32	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP33	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP34	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP35	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP36	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP37	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP38	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP39	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP40	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP41	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP42	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP43	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP44	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP45	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP46	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP47	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP48	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP49	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP50	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP51	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP52	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP53	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP54	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP55	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP56	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP57	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP58	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP59	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP60	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP61	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP62	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP63	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP64	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP65	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP66	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP67	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP68	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP69	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP70	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP71	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP72	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP73	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP74	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP75	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP76	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP77	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP78	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP79	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP80	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP81	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP82	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP83	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP84	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP85	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP86	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP87	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP88	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP89	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP90	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP91	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP92	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP93	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP94	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP95	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP96	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP97	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP98	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					
PRP99	REPEAT CSV	REPEAT ELEMENT PROTEIN	VARIOLA VIRUS	202-216					
PRP100	REPEAT CSV	REPEAT ELEMENT PROTEIN	VACCINIA VIRUS (STRAIN WR)	202-216					











PCGENE	FUNCTION	ALL Viruses (no bacteriophage g2)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA7
ELKNAME	PROTEIN	VIRUS	82-115					
PVAL3 BCTV	AL3 PROTEIN	BEBE CURLY TOP VIRUS (ICTV)	77-113					
PVAL3 CLVK	AL3 PROTEIN	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 844)	77-113					
PVAL3 CLVN	AL3 PROTEIN	CASSAVA LATENT VIRUS (STRAIN NIGERIAN)	77-113					
PVAL3 TYLCM	AL3 PROTEIN	TOMATO YELLOW LEAF CURL VIRUS (STRAIN MABMANDE)(TYLCV)	77-113					
PVAL3 TYLCV	AL3 PROTEIN	TOMATO YELLOW LEAF CURL VIRUS (TYLCV)	77-113					
PVAL3 CAMVC	APHID TRANSMISSION PROTEIN	CADUFLLOWER MOSAIC VIRUS (STRAIN CM-1841)(CAMV)	81-116					
PVAL3 CAMVD	APHID TRANSMISSION PROTEIN	CADUFLLOWER MOSAIC VIRUS (STRAIN D71)(CAMV)	20-53					
PVAL3 CAMVE	APHID TRANSMISSION PROTEIN	CADUFLLOWER MOSAIC VIRUS (STRAIN BRC)(CAMV)	20-53					
PVAL3 CAMVN	APHID TRANSMISSION PROTEIN	CADUFLLOWER MOSAIC VIRUS (STRAIN NY1433)(CAMV)	81-116					
PVAL3 CAMVP	APHID TRANSMISSION PROTEIN	CADUFLLOWER MOSAIC VIRUS (STRAIN PV147)(CAMV)	20-53					
PVAL3 CAMVS	APHID TRANSMISSION PROTEIN	CADUFLLOWER MOSAIC VIRUS (STRAIN STRASBOURG)(CAMV)	81-116					
PVAL3 CAMVCC	PROTEIN B4	VACCINIA VIRUS (STRAIN COPENHAGEN)	20-53					
PVAL3 CAMVCCV	PROTEIN B4	VACCINIA VIRUS (STRAIN WR)	124-156					
PVAL3 VARV	PROTEIN B4	VACCINIA VIRUS (STRAIN WR)	124-156					
PVAL3 COMPX	INTERLEUKIN-1 BINDING PROTEIN PRECURSOR	COMPOX VIRUS (CPV)	489-523					
PVAL3 VACCC	INTERLEUKIN-1 BINDING PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN WR)	89-126					
PVAL3 VACCCV	SURFACE ANTIGEN S PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	89-126					
PVAL3 VACCCD	SURFACE ANTIGEN S PRECURSOR	VACCINIA VIRUS (STRAIN DAIREN I)	213-244					
PVAL3 VACCCV	SURFACE ANTIGEN S PRECURSOR	VACCINIA VIRUS (STRAIN WR)	211-242					
PVAL3 VARV	SURFACE ANTIGEN S PRECURSOR	VACCINIA VIRUS (STRAIN WR)	211-242					
PVAL3 BGMV	BRI PROTEIN	BEAN GOLDEN MOSAIC VIRUS	166-198					
PVAL3 SFVKA	G-PROTEIN COUPLED RECEPTOR HOMOLOG C1	SHOPE FIBROMA VIRUS (STRAIN KASZA)(SFV)	94-110					
PVAL3 VACCC	PROTEIN C4	VACCINIA VIRUS (STRAIN COPENHAGEN)	109-139					
PVAL3 VACCCV	PROTEIN C4	VACCINIA VIRUS (STRAIN WR)	109-139					
PVAL3 VACCC	PROTEIN C6	VACCINIA VIRUS (STRAIN COPENHAGEN)	109-139					
PVAL3 VACCCV	PROTEIN C6	VACCINIA VIRUS (STRAIN WR)	109-139					
PVAL3 VARV	PROTEIN C6	VACCINIA VIRUS (STRAIN WR)	109-139					
PVAL3 SFVKA	HYPOTHETICAL PROTEIN C7	SHOPE FIBROMA VIRUS (STRAIN KASZA)(SFV)	36-67					
PVAL3 VACCC	PROTEIN C9	VACCINIA VIRUS (STRAIN COPENHAGEN)	36-67					
PVAL3 VACCCV	PROTEIN C9	VACCINIA VIRUS (STRAIN WR)	60-97					
PVAL3 SFVKA	HYPOTHETICAL PROTEIN C10	SHOPE FIBROMA VIRUS (STRAIN KASZA)(SFV)	531-610					
PVAL3 VACCC	PROTEIN C10	VACCINIA VIRUS (STRAIN COPENHAGEN)	571-610					
PVAL3 VACCCV	PROTEIN C10	VACCINIA VIRUS (STRAIN WR)	85-121					
PVAL3 VARV	PROTEIN C10	VACCINIA VIRUS (STRAIN WR)	121-158					
PVAL3 VACCC	PROTEIN C11/12	VACCINIA VIRUS (STRAIN COPENHAGEN)	121-158					
PVAL3 VACCCV	PROTEIN C11/12	VACCINIA VIRUS (STRAIN WR)	121-158					
PVAL3 EHV	MAJOR CAPSID PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)(HUMAN HERPESVIRUS 4)	3-34					
PVAL3 HCMVA	MAJOR CAPSID PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	148-183					
PVAL3 ISVTI	MAJOR CAPSID PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1)(STRAIN 17)	43-78					
PVAL3 HSV6U	MAJOR CAPSID PROTEIN	HERPES SIMPLEX VIRUS (TYPE 6)(STRAIN UGANDA-1102)	238-286					
PVAL3 HSV4	MAJOR CAPSID PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN ARUP)(EIV-1)	10-49					
PVAL3 PRVS	MAJOR CAPSID PROTEIN	HERPESVIRUS SAKIBIRI (STRAIN 11)	124-161					
PVAL3 VZV	MAJOR CAPSID PROTEIN	PSEUDORABIES VIRUS (STRAIN INDIANA S)(PRV)	17-54					
PVAL3 ADFH2	MINOR CORE PROTEIN	VARIICELLA-ZOSTER VIRUS (STRAIN DUNAS)(VZV)	144-179					
PVAL3 ADEB1	MINOR CORE PROTEIN	HUMAN ADENOVIRUS TYPE 2	189-221					
PVAL3 VACCC	PROTEIN D3	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-68					
PVAL3 VACCCV	PROTEIN D3	VACCINIA VIRUS (STRAIN WR)	85-114					
PVAL3 VARV	PROTEIN D3	VACCINIA VIRUS (STRAIN WR)	12-50					
PVAL3 FOWP1	92 S KD PROTEIN	VARIOLA VIRUS	140-182					
PVAL3 VACCC	PROTEIN D5	FOWLPOX VIRUS (STRAIN FP-1)	12-50					
PVAL3 VACCCV	PROTEIN D5	VACCINIA VIRUS (STRAIN COPENHAGEN)	315-332					
PVAL3 VARV	PROTEIN D5	VACCINIA VIRUS (STRAIN WR)	370-348					
PVAL3 FOWP1	PROTEIN D10	VARIOLA VIRUS	370-348					
PVAL3 VACCC	PROTEIN E3	FOWLPOX VIRUS (STRAIN FP-1)	114-143					
PVAL3 VACCCV	PROTEIN E3	VACCINIA VIRUS (STRAIN DAIREN I)	31-60					
PVAL3 VACCC	PROTEIN E6	VACCINIA VIRUS (STRAIN COPENHAGEN)	226-260					
PVAL3 VACCCV	PROTEIN E6	VACCINIA VIRUS (STRAIN WR)	430-438					





PCGENE	FUNCTION	PROTEIN	ALL Viruses (no bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7
PV01 VACCC	PROTEIN F3	PROTEIN F3	VIRUS	2-40	61-93					
PV02 VACCC	PROTEIN F3	PROTEIN F3	VACCINIA VIRUS (STRAIN COPENHAGEN)	2-40	61-93					
PV03 VACCC	PROTEIN F3	PROTEIN F3	VACCINIA VIRUS (STRAIN WR)	2-40	61-93					
PV04 FOWPV	PROTEIN F4	PROTEIN F4	FOWL POX VIRUS	292-370						
PV05 FOWPV	PROTEIN F4	PROTEIN F4	FOWL POX VIRUS	292-370						
PV06 FOWPV	PROTEIN F4	PROTEIN F4	FOWL POX VIRUS	292-370						
PV07 CAPVK	PROTEIN F7	PROTEIN F7	CATRIPOX VIRUS (STRAIN KS-1)	217-267						
PV08 VACCC	14 KD FUSION PROTEIN	14 KD FUSION PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	89-118						
PV09 VACCC	14 KD FUSION PROTEIN	14 KD FUSION PROTEIN	VACCINIA VIRUS (STRAIN WR)	28-61						
PV10 VACCC	14 KD FUSION PROTEIN	14 KD FUSION PROTEIN	VACCINIA VIRUS	28-61						
PV11 HSYV	HYPOTHETICAL GENE 1 PROTEIN	HYPOTHETICAL GENE 1 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	317-346						
PV12 HSYV	HYPOTHETICAL GENE 2 PROTEIN	HYPOTHETICAL GENE 2 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1)	163-196						
PV13 VACCC	ISATIN-BETA-THIOSEMICARBAZONE DEPENDENT PROTEIN	ISATIN-BETA-THIOSEMICARBAZONE DEPENDENT PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	92-120						
PV14 VACCC	ISATIN-BETA-THIOSEMICARBAZONE DEPENDENT PROTEIN	ISATIN-BETA-THIOSEMICARBAZONE DEPENDENT PROTEIN	VACCINIA VIRUS	92-120						
PV15 HSYV	HYPOTHETICAL GENE 3 PROTEIN	HYPOTHETICAL GENE 3 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	108-136						
PV16 HSYV	HYPOTHETICAL GENE 3 PROTEIN	HYPOTHETICAL GENE 3 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	54-83						
PV17 VACCC	HYPOTHETICAL GENE 6 MEMBRANE PROTEIN	HYPOTHETICAL GENE 6 MEMBRANE PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	99-136						
PV18 VACCC	HYPOTHETICAL GENE 6 MEMBRANE PROTEIN	HYPOTHETICAL GENE 6 MEMBRANE PROTEIN	VACCINIA VIRUS	99-136						
PV19 VACCC	PROTEIN G6	PROTEIN G6	VACCINIA VIRUS (STRAIN COPENHAGEN)	113-145						
PV20 VACCC	PROTEIN G7	PROTEIN G7	VACCINIA VIRUS	113-145						
PV21 VACCC	PROTEIN F1	PROTEIN F1	VACCINIA VIRUS (STRAIN COPENHAGEN)	303-338						
PV22 VACCC	PROTEIN F1	PROTEIN F1	VACCINIA VIRUS (STRAIN WR)	303-338						
PV23 VACCC	PROTEIN F1	PROTEIN F1	VACCINIA VIRUS	303-338						
PV24 VACCC	PROTEIN F1	PROTEIN F1	VACCINIA VIRUS	303-338						
PV25 HSYV	HYPOTHETICAL GENE 11 ZINC-BINDING PROTEIN	HYPOTHETICAL GENE 11 ZINC-BINDING PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	150-183						
PV26 HSYV	HYPOTHETICAL GENE 12 ZINC-BINDING PROTEIN	HYPOTHETICAL GENE 12 ZINC-BINDING PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	206-243						
PV27 HSYV	HYPOTHETICAL GENE 12 ZINC-BINDING PROTEIN	HYPOTHETICAL GENE 12 ZINC-BINDING PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	68-106						
PV28 HSYV	HYPOTHETICAL GENE 12 ZINC-BINDING PROTEIN	HYPOTHETICAL GENE 12 ZINC-BINDING PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	354-292	303-337	414-432				
PV29 HSYV	HYPOTHETICAL GENE 22 PROTEIN	HYPOTHETICAL GENE 22 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	300-337	167-678					
PV30 HSYV	HYPOTHETICAL GENE 23 PROTEIN	HYPOTHETICAL GENE 23 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	70-108						
PV31 HSYV	HYPOTHETICAL GENE 26 PROTEIN	HYPOTHETICAL GENE 26 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	94-125						
PV32 HSYV	HYPOTHETICAL GENE 27 PROTEIN	HYPOTHETICAL GENE 27 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 1)	36-74						
PV33 HSYV	HYPOTHETICAL GENE 28 PROTEIN	HYPOTHETICAL GENE 28 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	491-521						
PV34 HSYV	HYPOTHETICAL GENE 28 PROTEIN	HYPOTHETICAL GENE 28 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	180-217						
PV35 HSYV	HYPOTHETICAL GENE 28 PROTEIN	HYPOTHETICAL GENE 28 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	209-244						
PV36 HSYV	HYPOTHETICAL GENE 33 PROTEIN	HYPOTHETICAL GENE 33 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	15-46	190-226					
PV37 HSYV	POSSIBLE TYROSINE-PROTEIN KINASE	POSSIBLE TYROSINE-PROTEIN KINASE	HERPESVIRUS SAIMIRI (STRAIN 1)	131-185						
PV38 HSYV	HYPOTHETICAL GENE 39 PROTEIN	HYPOTHETICAL GENE 39 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	543-577	648-682					
PV39 HSYV	HYPOTHETICAL GENE 40 PROTEIN	HYPOTHETICAL GENE 40 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 1)	187-216						
PV40 HSYV	HYPOTHETICAL GENE 41 PROTEIN	HYPOTHETICAL GENE 41 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	11-45	202-233					
PV41 HSYV	HYPOTHETICAL GENE 42 PROTEIN	HYPOTHETICAL GENE 42 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	91-123						
PV42 HSYV	HYPOTHETICAL GENE 43 PROTEIN	HYPOTHETICAL GENE 43 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	109-140	157-183					
PV43 HSYV	HYPOTHETICAL GENE 43 PROTEIN	HYPOTHETICAL GENE 43 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	888-925						
PV44 HSYV	PROBABLE MAJOR GLYCOPROTEIN	PROBABLE MAJOR GLYCOPROTEIN	HERPESVIRUS SAIMIRI (STRAIN 1)	379-337						
PV45 HSYV	PROBABLE TRANSCRIPTION ACTIVATOR-EDRF	PROBABLE TRANSCRIPTION ACTIVATOR-EDRF	HERPESVIRUS SAIMIRI (STRAIN 1)	113-141						
PV46 HSYV	HYPOTHETICAL GENE 51 MEMBRANE PROTEIN	HYPOTHETICAL GENE 51 MEMBRANE PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	29-64	14-120					
PV47 HSYV	HYPOTHETICAL GENE 52 PROTEIN	HYPOTHETICAL GENE 52 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	98-134						
PV48 HSYV	HYPOTHETICAL GENE 53 PROTEIN	HYPOTHETICAL GENE 53 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	100-129						
PV49 HSYV	HYPOTHETICAL GENE 55 PROTEIN	HYPOTHETICAL GENE 55 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	364-396	611-667	1091-1126				
PV50 HSYV	HYPOTHETICAL GENE 58 PROTEIN	HYPOTHETICAL GENE 58 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	342-375	480-508					
PV51 HSYV	HYPOTHETICAL GENE 58 PROTEIN	HYPOTHETICAL GENE 58 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 1)	25-60	195-233					
PV52 HSYV	HYPOTHETICAL GENE 59 MEMBRANE PROTEIN	HYPOTHETICAL GENE 59 MEMBRANE PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	82-118						
PV53 HSYV	HYPOTHETICAL GENE 61 PROTEIN	HYPOTHETICAL GENE 61 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	76-109						
PV54 HSYV	HYPOTHETICAL GENE 64 PROTEIN	HYPOTHETICAL GENE 64 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	55-89	163-401	420-452				
PV55 HSYV	HYPOTHETICAL GENE 65 PROTEIN	HYPOTHETICAL GENE 65 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	801-836	1146-1174	1290-1326				
PV56 HSYV	HYPOTHETICAL GENE 67 PROTEIN	HYPOTHETICAL GENE 67 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	1150-1185						
PV57 HSYV	GENE 6 PROTEIN	GENE 6 PROTEIN	SPROPLASMA VIRUS SPV1-RAA2 B	60-89						
PV58 HSYV	HYPOTHETICAL GENE 71 PROTEIN	HYPOTHETICAL GENE 71 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 1)	128-158						
PV59 HSYV	HYPOTHETICAL GENE 72 PROTEIN	HYPOTHETICAL GENE 72 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	445-478	720-751	1158-1189	1352-1285			
PV60 HSYV	HYPOTHETICAL GENE 75 PROTEIN	HYPOTHETICAL GENE 75 PROTEIN	ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV)	263-291	387-422					









[illegible]











TABLE XV  
RESPIRATORY SYNCYTIAL VIRUS DP107 F2 REGION ANALOG  
CARBOXY TRUNCATIONS

	X-YTS-Z
	X-YTSV-Z
5	X-YTSVI-Z
	X-YTSVIT-Z
	X-YTSVITI-Z
	X-YTSVITIE-Z
	X-YTSVITIEL-Z
	X-YTSVITIELS-Z
	X-YTSVITIELSN-Z
10	X-YTSVITIELSNI-Z
	X-YTSVITIELSNIK-Z
	X-YTSVITIELSNIKE-Z
	X-YTSVITIELSNIKEN-Z
	X-YTSVITIELSNIKENK-Z
	X-YTSVITIELSNIKENKC-Z
	X-YTSVITIELSNIKENKCN-Z
	X-YTSVITIELSNIKENKCNG-Z
15	X-YTSVITIELSNIKENKCNGT-Z
	X-YTSVITIELSNIKENKCNGTD-Z
	X-YTSVITIELSNIKENKCNGTDA-Z
	X-YTSVITIELSNIKENKCNGTDAK-Z
	X-YTSVITIELSNIKENKCNGTDAKV-Z
	X-YTSVITIELSNIKENKCNGTDAKVK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKL-Z
20	X-YTSVITIELSNIKENKCNGTDAKVKLI-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQE-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEEL-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKY-Z
25	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKN-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNA-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAV-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTE-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTEL-Z
30	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTELQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTELQL-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTELQLL-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTELQLLM-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTELQLLMQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTELQLLMQS-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIQEELDKYKNAVTELQLLMQST-Z

35     The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxycarbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVI  
RESPIRATORY SYNCYTIAL VIRUS F2 DP178/DP107 REGION ANALOG  
AMINO TRUNCATIONS

	X-QST-Z
	X-MQST-Z
5	X-LMQST-Z
	X-LLMQST-Z
	X-QLLMQST-Z
	X-LQLLMQST-Z
	X-ELQLLMQST-Z
	X-TELQLLMQST-Z
	X-VTELQLLMQST-Z
10	X-AVTELQLLMQST-Z
	X-NAVTELQLLMQST-Z
	X-KNAVTELQLLMQST-Z
	X-YKNAVTELQLLMQST-Z
	X-KYKNAVTELQLLMQST-Z
	X-DKYKNAVTELQLLMQST-Z
	X-LDKYKNAVTELQLLMQST-Z
	X-ELDKYKNAVTELQLLMQST-Z
15	X-QELDKYKNAVTELQLLMQST-Z
	X-KQELDKYKNAVTELQLLMQST-Z
	X-IKQELDKYKNAVTELQLLMQST-Z
	X-LIKQELDKYKNAVTELQLLMQST-Z
	X-KLIKQELDKYKNAVTELQLLMQST-Z
	X-VKLIKQELDKYKNAVTELQLLMQST-Z
	X-KVKLIKQELDKYKNAVTELQLLMQST-Z
20	X-AKVLIKQELDKYKNAVTELQLLMQST-Z
	X-DAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-TDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-GTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-CNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-KCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
25	X-KENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-IKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-SNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-LSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-ELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-IELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
30	X-TIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-ITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-VITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-SVITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-TSVITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z

The one letter amino acid code is used.

35 Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVII  
RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG  
CARBOXY TRUNCATIONS

	X-FYD-Z
	X-FYDP-Z
	X-FYDPL-Z
5	X-FYDPLV-Z
	X-FYDPLVF-Z
	X-FYDPLVFP-Z
	X-FYDPLVFPS-Z
	X-FYDPLVFPSD-Z
	X-FYDPLVFPSDE-Z
	X-FYDPLVFPSDEF-Z
10	X-FYDPLVFPSDEFD-Z
	X-FYDPLVFPSDEFDA-Z
	X-FYDPLVFPSDEFDAS-Z
	X-FYDPLVFPSDEFDASI-Z
	X-FYDPLVFPSDEFDASIS-Z
	X-FYDPLVFPSDEFDASISQ-Z
	X-FYDPLVFPSDEFDASISQV-Z
	X-FYDPLVFPSDEFDASISQVN-Z
15	X-FYDPLVFPSDEFDASISQVNE-Z
	X-FYDPLVFPSDEFDASISQVNEK-Z
	X-FYDPLVFPSDEFDASISQVNEKI-Z
	X-FYDPLVFPSDEFDASISQVNEKIN-Z
	X-FYDPLVFPSDEFDASISQVNEKINQ-Z
	X-FYDPLVFPSDEFDASISQVNEKINQS-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSL-Z
20	X-FYDPLVFPSDEFDASISQVNEKINQSLA-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAF-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFI-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIR-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRK-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKS-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSD-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDE-Z
25	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDEL-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,  
 30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier

group including but not limited to lipid-fatty acid  
conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVIII  
RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG  
AMINO TRUNCATIONS

	X-DELL-Z
	X-SDELL-Z
5	X-KSDELL-Z
	X-RKSDELL-Z
	X-IRKSDELL-Z
	X-FIRKSDELL-Z
	X-AFIRKSDELL-Z
	X-LAFIRKSDELL-Z
	X-SLAFIRKSDELL-Z
10	X-QSLAFIRKSDELL-Z
	X-NQSLAFIRKSDELL-Z
	X-INQSLAFIRKSDELL-Z
	X-KINQSLAFIRKSDELL-Z
	X-EKINQSLAFIRKSDELL-Z
	X-NEKINQSLAFIRKSDELL-Z
	X-VNEKINQSLAFIRKSDELL-Z
	X-QVNEKINQSLAFIRKSDELL-Z
15	X-SQVNEKINQSLAFIRKSDELL-Z
	X-ISQVNEKINQSLAFIRKSDELL-Z
	X-SISQVNEKINQSLAFIRKSDELL-Z
	X-ASISQVNEKINQSLAFIRKSDELL-Z
	X-DASISQVNEKINQSLAFIRKSDELL-Z
	X-FDASISQVNEKINQSLAFIRKSDELL-Z
	X-EFDASISQVNEKINQSLAFIRKSDELL-Z
20	X-DEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-SDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-PSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-FPSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-VFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-LVFPSEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-PLVFPSEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-DPLVFPSEFDASISQVNEKINQSLAFIRKSDELL-Z
25	X-YDPLVFPSEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,  
 "X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxy, dansyl, or  
 30 T-butyloxycarbonyl; an acetyl group; a 9-  
 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a  
 T-butyloxycarbonyl group; a macromolecular carrier  
 35 group including but not limited to lipid-fatty acid  
 conjugates, polyethylene glycol, or carbohydrates.

TABLE XIX  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG  
CARBOXY TRUNCATIONS

X-ITL-Z  
 X-ITLN-Z  
 X-ITLNN-Z  
 5 X-ITLNNS-Z  
 X-ITLNNSV-Z  
 X-ITLNNSVA-Z  
 X-ITLNNSVAL-Z  
 X-ITLNNSVALD-Z  
 X-ITLNNSVALDP-Z  
 X-ITLNNSVALDPI-Z  
 10 X-ITLNNSVALDPID-Z  
 X-ITLNNSVALDPIDI-Z  
 X-ITLNNSVALDPIDIS-Z  
 X-ITLNNSVALDPIDISI-Z  
 X-ITLNNSVALDPIDISIE-Z  
 X-ITLNNSVALDPIDISIEL-Z  
 X-ITLNNSVALDPIDISIELN-Z  
 X-ITLNNSVALDPIDISIELNK-Z  
 15 X-ITLNNSVALDPIDISIELNKA-Z  
 X-ITLNNSVALDPIDISIELNKAK-Z  
 X-ITLNNSVALDPIDISIELNKAKS-Z  
 X-ITLNNSVALDPIDISIELNKAKSD-Z  
 X-ITLNNSVALDPIDISIELNKAKSDL-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLE-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLEE-Z  
 20 X-ITLNNSVALDPIDISIELNKAKSDLEES-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLEESK-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLEESKE-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLEESKEW-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLEESKEWI-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIR-Z  
 X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIRR-Z  
 25 X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxy, dansyl, or  
 T-butyloxycarbonyl; an acetyl group; a 9-  
 30 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a  
 T-butyloxycarbonyl group; a macromolecular carrier  
 group including but not limited to lipid-fatty acid  
 35 conjugates, polyethylene glycol, or carbohydrates.

TABLE XX  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG  
AMINO TRUNCATIONS

	X-RRS-Z
	X-IRRS-Z
5	X-WIRRS-Z
	X-EWIRRS-Z
	X-KEWIRRS-Z
	X-SKEWIRRS-Z
	X-ESKEWIRRS-Z
	X-EESKEWIRRS-Z
	X-LEESKEWIRRS-Z
10	X-DLEESKEWIRRS-Z
	X-SDLEESKEWIRRS-Z
	X-KSDLEESKEWIRRS-Z
	X-AKSDLEESKEWIRRS-Z
	X-KAKSDLEESKEWIRRS-Z
	X-NKAKSDLEESKEWIRRS-Z
	X-LNKAKSDLEESKEWIRRS-Z
	X-ELNKAKSDLEESKEWIRRS-Z
15	X-IELNKAKSDLEESKEWIRRS-Z
	X-SIELNKAKSDLEESKEWIRRS-Z
	X-ISIELNKAKSDLEESKEWIRRS-Z
	X-DISIELNKAKSDLEESKEWIRRS-Z
	X-IDISIELNKAKSDLEESKEWIRRS-Z
	X-PIDISIELNKAKSDLEESKEWIRRS-Z
	X-DPIDISIELNKAKSDLEESKEWIRRS-Z
20	X-LDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-ALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-VALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-SVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-NSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-NNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-LNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
25	X-TLNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XXI  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG  
CARBOXY TRUNCATIONS

X-ALG-Z  
 X-ALGV-Z  
 X-ALGVA-Z  
 5 X-ALGVAT-Z  
 X-ALGVATS-Z  
 X-ALGVATSA-Z  
 X-ALGVATSAQ-Z  
 X-ALGVATSAQI-Z  
 X-ALGVATSAQIT-Z  
 X-ALGVATSAQITA-Z  
 10 X-ALGVATSAQITAA-Z  
 X-ALGVATSAQITA-AV-Z  
 X-ALGVATSAQITA-AVA-Z  
 X-ALGVATSAQITA-AVAL-Z  
 X-ALGVATSAQITA-AVALV-Z  
 X-ALGVATSAQITA-AVALVE-Z  
 X-ALGVATSAQITA-AVALVEA-Z  
 X-ALGVATSAQITA-AVALVEAK-Z  
 15 X-ALGVATSAQITA-AVALVEAKQ-Z  
 X-ALGVATSAQITA-AVALVEAKQA-Z  
 X-ALGVATSAQITA-AVALVEAKQAR-Z  
 X-ALGVATSAQITA-AVALVEAKQARS-Z  
 X-ALGVATSAQITA-AVALVEAKQARSD-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDI-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIE-Z  
 20 X-ALGVATSAQITA-AVALVEAKQARSDIEK-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEK-LK-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEK-LKE-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEK-LKEA-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEK-LKEAI-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEK-LKEAIR-Z

25 The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxy, dansyl, or  
 T-butyloxycarbonyl; an acetyl group; a 9-  
 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 30 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a  
 T-butyloxycarbonyl group; a macromolecular carrier  
 group including but not limited to lipid-fatty acid  
 conjugates, polyethylene glycol, or carbohydrates.

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TABLE XXII  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG  
AMINO TRUNCATIONS

	X-IRD-Z
	X-AIRD-Z
5	X-EAIRD-Z
	X-KEAIRD-Z
	X-LKEAIRD-Z
	X-KLKEAIRD-Z
	X-EKLKEAIRD-Z
	X-IEKLKEAIRD-Z
	X-DIEKLKEAIRD-Z
10	X-SDIEKLKEAIRD-Z
	X-RSDIEKLKEAIRD-Z
	X-ARSDIEKLKEAIRD-Z
	X-QARSDIEKLKEAIRD-Z
	X-KQARSDIEKLKEAIRD-Z
	X-AKQARSDIEKLKEAIRD-Z
	X-EAKQARSDIEKLKEAIRD-Z
	X-VEAKQARSDIEKLKEAIRD-Z
15	X-LVEAKQARSDIEKLKEAIRD-Z
	X-ALVEAKQARSDIEKLKEAIRD-Z
	X-VALVEAKQARSDIEKLKEAIRD-Z
	X-AVALVEAKQARSDIEKLKEAIRD-Z
	X-AAVALVEAKQARSDIEKLKEAIRD-Z
	X-TAAVALVEAKQARSDIEKLKEAIRD-Z
	X-ITAAVALVEAKQARSDIEKLKEAIRD-Z
20	X-QITAAVALVEAKQARSDIEKLKEAIRD-Z
	X-AQITAAVALVEAKQARSDIEKLKEAIRD-Z
	X-SAQITAAVALVEAKQARSDIEKLKEAIRD-Z
	X-TSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
	X-ATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
	X-VATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
	X-GVATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
25	X-LGVATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a  
30 macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier  
35 group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XXIII  
REPRESENTATIVE DP107/DP178 ANALOG ANTIVIRAL PEPTIDES

Anti-Respiratory syncytial virus peptides

X-TSVITIELSNIKENKCNCTDAKVKLIKQELDKYKN-Z  
X-SVITIELSNIKENKCNCTDAKVKLIKQELDKYKNA-Z  
5 X-VITIELSNIKENKCNCTDAKVKLIKQELDKYKNAV-Z  
X-AVASKVLHLEGEVNKIALLLSTNKAVVSLSNQVSV-Z  
X-AVSKVLHLEGEVNKIALLLSTNKAVVSLSNQVSV-Z  
X-VSKVLHLEGEVNKIALLLSTNKAVVSLSNQVSVL-Z  
X-SKVLHLEGEVNKIALLLSTNKAVVSLSNQVSVLT-Z  
X-KVLHLEGEVNKIALLLSTNKAVVSLSNQVSVLTS-Z  
X-LEGEVNKIALLLSTNKAVVSLSNQVSVLTSKVLD-Z  
10 X-GEVNKIALLLSTNKAVVSLSNQVSVLTSKVLDLK-Z  
X-EVNKIALLLSTNKAVVSLSNQVSVLTSKVLDLKN-Z  
X-VNKIALLLSTNKAVVSLSNQVSVLTSKVLDLKNY-Z  
X-NKIALLLSTNKAVVSLSNQVSVLTSKVLDLKNYI-Z  
X-KIALLLSTNKAVVSLSNQVSVLTSKVLDLKNYID-Z  
X-IALLSTNKAVVSLSNQVSVLTSKVLDLKNYIDK-Z  
X-ALLSTNKAVVSLSNQVSVLTSKVLDLKNYIDKQ-Z  
X-AVASKVLHLEGEVNKIALLLSTNKAVVSLSNQVSV-Z  
15 X-AVSKVLHLEGEVNKIALLLSTNKAVVSLSNQVSV-Z  
X-VSKVLHLEGEVNKIALLLSTNKAVVSLSNQVSVL-Z  
X-SKVLHLEGEVNKIALLLSTNKAVVSLSNQVSVLT-Z  
X-KVLHLEGEVNKIALLLSTNKAVVSLSNQVSVLTS-Z  
X-LEGEVNKIALLLSTNKAVVSLSNQVSVLTSKVLD-Z  
X-GEVNKIALLLSTNKAVVSLSNQVSVLTSKVLDLK-Z  
X-EVNKIALLLSTNKAVVSLSNQVSVLTSKVLDLKN-Z  
20 X-VNKIALLLSTNKAVVSLSNQVSVLTSKVLDLKNY-Z  
X-NKIALLLSTNKAVVSLSNQVSVLTSKVLDLKNYI-Z  
X-KIALLLSTNKAVVSLSNQVSVLTSKVLDLKNYID-Z  
X-IALLSTNKAVVSLSNQVSVLTSKVLDLKNYIDK-Z  
X-ALLSTNKAVVSLSNQVSVLTSKVLDLKNYIDKQ-Z

Anti-human parainfluenza virus 3 peptides

25 X-TLNNVALDPIDISIELNKAQSDLEESKEWIRRSN-Z  
X-LNNVALDPIDISIELNKAQSDLEESKEWIRRSNQ-Z  
X-NNNVALDPIDISIELNKAQSDLEESKEWIRRSNQK-Z  
X-NSVALDPIDISIELNKAQSDLEESKEWIRRSNQKL-Z  
X-SVALDPIDISIELNKAQSDLEESKEWIRRSNQKLD-Z  
X-VALDPIDISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-ALDPIDISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
30 X-LDPIDISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-DPIDISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-PIDISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-IDISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-DISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-ISIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-SIELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-IELNKAQSDLEESKEWIRRSNQKLDL-Z  
35 X-ELNKAQSDLEESKEWIRRSNQKLDL-Z  
X-TAAVALVEAKQARSDIEKLKEAIRDTNKAVQSVQSS-Z

X-AVALVEAKQARSDIEKLKEAIRD TNKAVQSVQSSI-Z  
 X-LVEAKQARSDIEKLKEAIRD TNKAVQSVQSSIGNL-Z  
 X-VEAKQARSDIEKLKEAIRD TNKAVQSVQSSIGNLI-Z  
 X-EAKQARSDIEKLKEAIRD TNKAVQSVQSSIGNLIV-Z  
 X-AKQARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVA-Z  
 X-KQARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAI-Z  
 X-QARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIAIK-Z  
 5 X-ARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIAIKS-Z  
 X-RSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIAIKSV-Z  
 X-SDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIAIKSVQ-Z  
 X-KLKEAIRD TNKAVQSVQSSIGNLIVAIAIKSVQDYVN-Z  
 X-LKEAIRD TNKAVQSVQSSIGNLIVAIAIKSVQDYVVK-Z  
 X-AIRD TNKAVQSVQSSIGNLIVAIAIKSVQDYVNKEIV-Z

10 Anti-simian immunodeficiency virus peptides

X-WQEWERKVD FLEENITALLEEAQIQQEK NMYELQK-Z  
 X-QEWERKVD FLEENITALLEEAQIQQEK NMYELQKL-Z  
 X-EWERKVD FLEENITALLEEAQIQQEK NMYELQKLN-Z  
 X-WERKVD FLEENITALLEEAQIQQEK NMYELQKLNS-Z  
 X-ERKVD FLEENITALLEEAQIQQEK NMYELQKLNSW-Z  
 X-RKVD FLEENITALLEEAQIQQEK NMYELQKLNSWD-Z  
 15 X-KVD FLEENITALLEEAQIQQEK NMYELQKLNSWDV-Z  
 X-VDFLEENITALLEEAQIQQEK NMYELQKLNSWDVF-Z  
 X-DFLEENITALLEEAQIQQEK NMYELQKLNSWDVFG-Z  
 X-FLEENITALLEEAQIQQEK NMYELQKLNSWDVFGN-Z

Anti-measles virus peptides

20 X-LHRIDLGPPI SLERLDVGTNLGN AIAKLEAKELL-Z  
 X-HRIDLGPPISLERLDVGTNLGN AIAKLEAKELLE-Z  
 X-RIDLGPPI SLERLDVGTNLGN AIAKLEAKELLES-Z  
 X-IDLGPPISLERLDVGTNLGN AIAKLEAKELLESS-Z  
 X-DLGPPISLERLDVGTNLGN AIAKLEAKELLESSD-Z  
 X-LGPPISLERLDVGTNLGN AIAKLEAKELLESSDQ-Z  
 X-GPPISLERLDVGTNLGN AIAKLEAKELLESSDQI-Z  
 25 X-PPISLERLDVGTNLGN AIAKLEAKELLESSDQIL-Z  
 X-PISLERLDVGTNLGN AIAKLEAKELLESSDQILR-Z  
 X-SLERLDVGTNLGN AIAKLEAKELLESSDQILRSM-Z  
 X-LERLDVGTNLGN AIAKLEAKELLESSDQILRSMK-Z

The one letter amino acid code is used.

30 Additionally,  
 "X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxy, dansyl, or  
 T-butyloxycarbonyl; an acetyl group; a 9-  
 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.  
 35

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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#### 5.4. SYNTHESIS OF PEPTIDES

The peptides of the invention may be synthesized or prepared by techniques well known in the art. See, for example, Creighton, 1983, Proteins: Structures  
5 and Molecular Principles, W.H. Freeman and Co., NY, which is incorporated herein by reference in its entirety. Short peptides, for example, can be synthesized on a solid support or in solution. Longer  
10 peptides may be made using recombinant DNA techniques. Here, the nucleotide sequences encoding the peptides of the invention may be synthesized, and/or cloned, and expressed according to techniques well known to those of ordinary skill in the art. See, for example,  
15 Sambrook, et al., 1989, Molecular Cloning, A Laboratory Manual, Vols. 1-3, Cold Spring Harbor Press, NY.

The peptides of the invention may alternatively be synthesized such that one or more of the bonds which link the amino acid residues of the peptides are  
20 non-peptide bonds. These alternative non-peptide bonds may be formed by utilizing reactions well known to those in the art, and may include, but are not limited to imino, ester, hydrazide, semicarbazide, and azo bonds, to name but a few. In yet another  
25 embodiment of the invention, peptides comprising the sequences described above may be synthesized with additional chemical groups present at their amino and/or carboxy termini, such that, for example, the stability, bioavailability, and/or inhibitory activity  
30 of the peptides is enhanced. For example, hydrophobic groups such as carbobenzoxyl, dansyl, or t-butylloxycarbonyl groups, may be added to the peptides' amino termini. Likewise, an acetyl group or a 9-fluorenylmethoxy-carbonyl group may be placed at the  
35 peptides' amino termini. (See "X" in Tables I to IV,

above.) Additionally, the hydrophobic group, t-butyloxycarbonyl, or an amido group may be added to the peptides' carboxy termini. (See "Z" in Tables I to IV, above.)

5 Further, the peptides of the invention may be synthesized such that their steric configuration is altered. For example, the D-isomer of one or more of the amino acid residues of the peptide may be used, rather than the usual L-isomer.

10 Still further, at least one of the amino acid residues of the peptides of the invention may be substituted by one of the well known non-naturally occurring amino acid residues. Alterations such as these may serve to increase the stability, bioavailability and/or inhibitory action of the  
15 peptides of the invention.

Any of the peptides described above may, additionally, have a macromolecular carrier group covalently attached to their amino and/or carboxy termini. Such macromolecular carrier groups may  
20 include, for example, lipid-fatty acid conjugates, polyethylene glycol, carbohydrates or additional peptides. "X", in Tables I to IV, above, may therefore additionally represent any of the above macromolecular carrier groups covalently attached to  
25 the amino terminus of a peptide, with an additional peptide group being preferred. Likewise, "Z", in Tables I to IV, may additionally represent any of the macromolecular carrier groups described above.

30 5.5. ASSAYS FOR ANTI-MEMBRANE FUSION ACTIVITY

Described herein, are methods for ability of a compound, such as the peptides of the invention, to inhibit membrane fusion events. Specifically, assays for cell fusion events are described in Section 5.5.1,  
35

below, and assays for antiviral activity are described in Section 5.5.2, below.

#### 5.5.1 ASSAYS FOR CELL FUSION EVENTS

5 Assays for cell fusion events are well known to those of skill in the art, and may be used in conjunction, for example, with the peptides of the invention to test the peptides' antifusogenic capabilities.

10 Cell fusion assays are generally performed in vitro. Such an assay may comprise culturing cells which, in the absence of any treatment would undergo an observable level of syncytial formation. For example, uninfected cells may be incubated in the presence of cells chronically infected with a virus  
15 that induces cell fusion. Such viruses may include, but are not limited to, HIV, SIV, or respiratory syncytial virus.

For the assay, cells are incubated in the presence of a peptide to be assayed. For each  
20 peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added.

Standard conditions for culturing cells, well known to those of ordinary skill in the art, are used.  
25 After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytial formation. Well known stains, such as  
30 crystal violet stain, may be used to facilitate the visualization of syncytial formation.

#### 5.5.2 ASSAYS FOR ANTIVIRAL ACTIVITY

35 The antiviral activity exhibited by the peptides of the invention may be measured, for example, by

easily performed in vitro assays, such as those described below, which can test the peptides' ability to inhibit syncytia formation, or their ability to inhibit infection by cell-free virus. Using these assays, such parameters as the relative antiviral activity of the peptides, exhibit against a given strain of virus and/or the strain specific inhibitory activity of the peptide can be determined.

A cell fusion assay may be utilized to test the peptides' ability to inhibit viral-induced, such as HIV-induced, syncytia formation in vitro. Such an assay may comprise culturing uninfected cells in the presence of cells chronically infected with a syncytial-inducing virus and a peptide to be assayed. For each peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added. Standard conditions for culturing, well known to those of ordinary skill in the art, are used. After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytia formation. Well known stains, such as crystal violet stain, may be used to facilitate syncytial visualization. Taking HIV as an example, such an assay would comprise CD-4<sup>+</sup> cells (such as Molt or CEM cells, for example) cultured in the presence of chronically HIV-infected cells and a peptide to be assayed.

Other well known characteristics of viral infection may also be assayed to test a peptide's antiviral capabilities. Once again taking HIV as an example, a reverse transcriptase (RT) assay may be utilized to test the peptides' ability to inhibit infection of CD-4<sup>+</sup> cells by cell-free HIV. Such an assay may comprise culturing an appropriate

concentration (i.e., TCID<sub>50</sub>) of virus and CD-4<sup>+</sup> cells in the presence of the peptide to be tested. Culture conditions well known to those in the art are used. As above, a range of peptide concentrations may be used, in addition to a control culture wherein no peptide has been added. After incubation for an appropriate period (e.g., 7 days) of culturing, a cell-free supernatant is prepared, using standard procedures, and tested for the presence of RT activity as a measure of successful infection. The RT activity may be tested using standard techniques such as those described by, for example, Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and/or Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). These references are incorporated herein by reference in their entirety.

Standard methods which are well-known to those of skill in the art may be utilized for assaying non-retroviral activity. See, for example, Pringle et al. (Pringle, C.R. et al., 1985, J. Medical Virology 17:377-386) for a discussion of respiratory syncytial virus and parainfluenza virus activity assay techniques. Further, see, for example, "Zinsser Microbiology", 1988, Joklik, W.K. et al., eds., Appleton & Lange, Norwalk, CT, 19th ed., for a general review of such techniques. These references are incorporated by reference herein in their entirety. In addition, the Examples presented below, in Sections 17, 18, 26 and 27 each provide additional assays for the testing of a compound's antiviral capability.

In vivo assays may also be utilized to test, for example, the antiviral activity of the peptides of the invention. To test for anti-HIV activity, for example, the in vivo model described in Barnett et al. (Barnett, S.W. et al., 1994, Science 266:642-646) may be used.

Additionally, anti-RSV activity can be assayed in vivo via well known mouse models. For example, RSV can be administered intranasally to mice of various inbred strains. Virus replicates in lungs of all strains, but the highest titers are obtained in P/N, C57L/N and DBA/2N mice. Infection of BALB/c mice produces an asymptomatic bronchiolitis characterized by lymphocytic infiltrates and pulmonary virus titers of  $10^4$  to  $10^5$  pfu/g of lung tissue (Taylor, G. et al., 1984, Infect. Immun. 43:649-655).

Cotton rat models of RSV are also well known. Virus replicates to high titer in the nose and lungs of the cotton rat but produces few if any signs of inflammation.

#### 5.6. USES OF THE PEPTIDES OF THE INVENTION

The peptides of the invention may be utilized as antifusogenic or antiviral compounds, or as compounds which modulate intracellular processes involving coiled coil peptide structures. Further, such peptides may be used to identify agents which exhibit antifusogenic, antiviral or intracellular modulatory activity. Still further, the peptides of the invention may be utilized as organism or viral type/subtype-specific diagnostic tools.

The antifusogenic capability of the peptides of the invention may additionally be utilized to inhibit or treat/ameliorate symptoms caused by processes involving membrane fusion events. Such events may include, for example, virus transmission via cell-cell fusion, abnormal neurotransmitter exchange via cell-fusion, and sperm-egg fusion. Further, the peptides of the invention may be used to inhibit free viral, such as retroviral, particularly HIV, transmission to uninfected cells wherein such viral infection involves membrane fusion events or involves fusion of a viral

structure with a cell membrane. Among the intracellular disorders involving coiled coil peptides structures which may be ameliorated by the peptides of the invention are disorders involving, for example, bacterial toxins.

5       With respect to antiviral activity, the viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to all strains of the viruses listed above, in Tables V through VII, and IX through XIV.

10       These viruses include, for example, human retroviruses, particularly HIV-1 and HIV-2 and the human T-lymphocyte viruses (HTLV-I and II). The non-human retroviruses whose transmission may be inhibited by the peptides of the invention include, but are not  
15       limited to bovine leukosis virus, feline sarcoma and leukemia viruses, simian immunodeficiency, sarcoma and leukemia viruses, and sheep progress pneumonia viruses.

20       /       Non retroviral viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to human respiratory syncytial virus, canine distemper virus, newcastle disease virus, human parainfluenza virus, influenza viruses, measles viruses, Epstein-Barr viruses, hepatitis B  
25       viruses, and simian Mason-Pfizer viruses.

      Non enveloped viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to picornaviruses such as polio viruses, hepatitis A virus, enterovirus, echoviruses  
30       and coxsackie viruses, papovaviruses such as papilloma virus, parvoviruses, adenoviruses and reoviruses.

      As discussed more fully, below, in Section 5.5.1 and in the Example presented, below, in Section 8, DP107, DP178, DP107 analog and DP178 analog peptides  
35       form non-covalent protein-protein interactions which

are required for normal activity of the virus. Thus, the peptides of the invention may also be utilized as components in assays for the identification of compounds that interfere with such protein-protein interactions and may, therefore, act as antiviral agents. These assays are discussed, below, in Section 5.5.1.

As demonstrated in the Example presented below in Section 6, the antiviral activity of the peptides of the invention may show a pronounced type and subtype specificity, i.e., specific peptides may be effective in inhibiting the activity of only specific viruses. This feature of the invention presents many advantages. One such advantage, for example, lies in the field of diagnostics, wherein one can use the antiviral specificity of the peptide of the invention to ascertain the identity of a viral isolate. With respect to HIV, one may easily determine whether a viral isolate consists of an HIV-1 or HIV-2 strain. For example, uninfected CD-4<sup>+</sup> cells may be co-infected with an isolate which has been identified as containing HIV the DP178 (SEQ ID:1) peptide, after which the retroviral activity of cell supernatants may be assayed, using, for example, the techniques described above in Section 5.2. Those isolates whose retroviral activity is completely or nearly completely inhibited contain HIV-1. Those isolates whose viral activity is unchanged or only reduced by a small amount, may be considered to not contain HIV-1. Such an isolate may then be treated with one or more of the other DP178 peptides of the invention, and subsequently be tested for its viral activity in order to determine the identify of the viral isolate. The DP107 and DP178 analogs of the invention may also be utilized in a diagnostic capacity specific to the type and subtype of virus or organism in which the specific



peptide sequence is found. A diagnostic procedure as described, above, for DP178, may be used in conjunction with the DP107/DP178 analog of interest.

#### 5.5.1. SCREENING ASSAYS

5 As demonstrated in the Example presented in Section 8, below, DP107 and DP178 portions of the TM protein gp41 form non-covalent protein-protein interactions. As is also demonstrated, the maintenance of such interactions is necessary for  
10 normal viral infectivity. Thus, compounds which bind DP107, bind DP178, and/or act to disrupt normal DP107/DP178 protein-protein interactions may act as antifusogenic, antiviral or cellular modulatory agents. Described below are assays for the  
15 identification of such compounds. Note that, while, for ease and clarity of discussion, DP107 and DP178 peptides will be used as components of the assays described, but it is to be understood that any of the DP107 analog or DP178 analog peptides described,  
20 above, in Sections 5.1 through 5.3 may also be utilized as part of these screens for compounds.

Compounds which may be tested for an ability to bind DP107, DP178, and/or disrupt DP107/DP178 interactions, and which therefore, potentially  
25 represent antifusogenic, antiviral or intracellular modulatory compounds, include, but are not limited to, peptides made of D- and/or L-configuration amino acids (in, for example, the form of random peptide libraries; see Lam, K.S. et al., 1991, Nature 354:82-  
30 84), phosphopeptides (in, for example, the form of random or partially degenerate, directed phosphopeptide libraries; see, for example, Songyang, Z. et al., 1993, Cell 72:767-778), antibodies, and small organic or inorganic molecules. Synthetic  
35 compounds, natural products, and other sources of

potentially effective materials may be screened in a variety of ways, as described in this Section.

The compounds, antibodies, or other molecules identified may be tested, for example, for an ability to inhibit cell fusion or viral activity, utilizing,  
5 for example, assays such as those described, above, in Section 5.5.

Among the peptides which may be tested are soluble peptides comprising DP107 and/or DP178 domains, and peptides comprising DP107 and/or DP178  
10 domains having one or more mutations within one or both of the domains, such as the M41-P peptide described, below, in the Example presented in Section 8, which contains a isoleucine to proline mutation within the DP178 sequence.

15 In one embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

(a) exposing at least one compound to a peptide comprising a DP107 peptide for a time  
20 sufficient to allow binding of the compound to the DP107 peptide;

(b) removing non-bound compounds; and

(c) determining the presence of the compound bound to the DP107 peptide,  
25 thereby identifying an agent to be tested for antiviral ability.

In a second embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

30 (a) exposing at least one compound to a peptide comprising a DP178 peptide for a time sufficient to allow binding of the compound to the DP178 peptide;

(b) removing non-bound compounds; and

(c) determining the presence of the compound bound to the DP178 peptide, thereby identifying an agent to be tested for antiviral ability.

5 One method utilizing these types of approaches that may be pursued in the isolation of such DP107-binding or DP178-binding compounds is an assay which would include the attachment of either the DP107 or the DP178 peptide to a solid matrix, such as, for example, agarose or plastic beads, microtiter plate  
10 wells, petri dishes, or membranes composed of, for example, nylon or nitrocellulose. In such an assay system, either the DP107 or DP178 protein may be anchored onto a solid surface, and the compound, or test substance, which is not anchored, is labeled,  
15 either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored component may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface  
20 with a solution of the protein and drying.

Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and  
25 stored.

In order to conduct the assay, the labeled compound is added to the coated surface containing the anchored DP107 or DP178 peptide. After the reaction is complete, unreacted components are removed (e.g.,  
30 by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the compound is pre-labeled, the detection of  
35 label immobilized on the surface indicates that

complexes were formed. Where the labeled component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the compound (the antibody, in turn, may be directly labeled or  
5 indirectly labeled with a labeled anti-Ig antibody).

Alternatively, such an assay can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for DP107 or  
10 DP178, whichever is appropriate for the given assay, or an antibody specific for the compound, i.e., the test substance, in order to anchor any complexes formed in solution, and a labeled antibody specific for the other member of the complex to detect anchored  
15 complexes.

By utilizing procedures such as this, large numbers of types of molecules may be simultaneously screened for DP107 or DP178-binding capability, and thus potential antiviral activity.

Further, compounds may be screened for an ability to inhibit the formation of or, alternatively, disrupt DP107/DP178 complexes. Such compounds may then be tested for antifusogenic, antiviral or intercellular modulatory capability. For ease of description, DP107  
25 and DP178 will be referred to as "binding partners." Compounds that disrupt such interactions may exhibit antiviral activity. Such compounds may include, but are not limited to molecules such as antibodies, peptides, and the like described above.

30 The basic principle of the assay systems used to identify compounds that interfere with the interaction between the DP107 and DP178 peptides involves preparing a reaction mixture containing peptides under conditions and for a time sufficient to allow the two  
35 peptides to interact and bind, thus forming a complex.

In order to test a compound for disruptive activity, the reaction is conducted in the presence and absence of the test compound, i.e., the test compound may be initially included in the reaction mixture, or added at a time subsequent to the addition of one of the  
5 binding partners; controls are incubated without the test compound or with a placebo. The formation of any complexes between the binding partners is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing  
10 the test compound indicates that the compound interferes with the interaction of the DP107 and DP178 peptides.

The assay for compounds that interfere with the interaction of the binding partners can be conducted  
15 in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring one of the binding partners onto a solid phase and detecting complexes anchored on the solid phase at the end of the reaction. In homogeneous assays, the entire  
20 reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the  
25 binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test substance; i.e., by adding the test substance to the reaction mixture prior to or simultaneously with the binding partners. On the  
30 other hand, test compounds that disrupt preformed complexes, e.g. compounds with higher binding constants that displace one of the binding partners from the complex, can be tested by adding the test compound to the reaction mixture after complexes have  
35

been formed. The various formats are described briefly below.

5 In a heterogeneous assay system, one binding partner, e.g., either the DP107 or DP178 peptide, is anchored onto a solid surface, and its binding partner, which is not anchored, is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored species may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be  
10 accomplished simply by coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

15 In order to conduct the assay, the binding partner of the immobilized species is added to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes  
20 formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the binding partner was pre-labeled, the detection of label immobilized on the surface  
25 indicates that complexes were formed. Where the binding partner is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the binding partner (the antibody, in turn, may be  
30 directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.

35

Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for one binding partner to anchor any complexes formed in solution, and a labeled antibody specific for the other binding partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds which inhibit complex or which disrupt preformed complexes can be identified.

In an alternate embodiment of the invention, a homogeneous assay can be used. In this approach, a preformed complex of the DP107 and DP178 peptides is prepared in which one of the binding partners is labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the binding partners from the preformed complex will result in the generation of a signal above background. In this way, test substances which disrupt DP-107/DP-178 protein-protein interaction can be identified.

In an alternative screening assay, test compounds may be assayed for the their ability to disrupt a DP178/DP107 interaction, as measured immunometrically using an antibody specifically reactive to a DP107/DP178 complex (i.e., an antibody that recognizes neither DP107 nor DP178 individually). Such an assay acts as a competition assay, and is based on techniques well known to those of skill in the art.

The above competition assay may be described, by way of example, and not by way of limitation, by using the DP178 and M41Δ178 peptides and by assaying test

compounds for the disruption of the complexes formed by these two peptides by immunometrically visualizing DP178/M41Δ178 complexes via the human recombinant Fab, Fab-d, as described, below, in the Example presented in Section 8. M41Δ178 is a maltose binding fusion  
5 protein containing a gp41 region having its DP178 domain deleted, and is described, below, in the Example presented in Section 8.

Utilizing such an assay, M41Δ178 may be immobilized onto solid supports such as microtiter  
10 wells. A series of dilutions of a test compound may then be added to each M41Δ178-containing well in the presence of a constant concentration of DP-178 peptide. After incubation, at, for example, room temperature for one hour, unbound DP-178 and test  
15 compound are removed from the wells and wells are then incubated with the DP178/M41Δ178-specific Fab-d antibody. After incubation and washing, unbound Fab-d is removed from the plates and bound Fab-d is quantitated. A no-inhibitor control should also be  
20 conducted. Test compounds showing an ability to disrupt DP178/M41Δ178 complex formation are identified by their concentration-dependent decrease in the level of Fab-d binding.

A variation of such an assay may be utilized to  
25 perform a rapid, high-throughput binding assay which is capable of directly measuring DP178 binding to M41Δ178 for the determination of binding constants of the ligand or inhibitory constants for competitors of DP178 binding.

30 Such an assay takes advantage of accepted radioligand and receptor binding principles. (See, for example, Yamamura, H.I. et al., 1985, "Neurotransmitter Receptor Binding", 2nd ed., Raven Press, NY.) As above, M41Δ178 is immobilized onto a  
35 solid support such as a microtiter well. DP178



binding to M41Δ178 is then quantitated by measuring the fraction of DP178 that is bound as <sup>125</sup>I-DP178 and calculating the total amount bound using a value for specific activity (dpm/μg peptide) determined for each labeled DP178 preparation. Specific binding to  
5 M41Δ178 is defined as the difference of the binding of the labeled DP178 preparation in the microtiter wells (totals) and the binding in identical wells containing, in addition, excess unlabeled DP178 (nonspecifics).  
10

#### 5.5 PHARMACEUTICAL FORMULATIONS, DOSAGES AND MODES OF ADMINISTRATION

The peptides of the invention may be administered using techniques well known to those in the art.  
15 Preferably, agents are formulated and administered systemically. Techniques for formulation and administration may be found in "Remington's Pharmaceutical Sciences", 18th ed., 1990, Mack Publishing Co., Easton, PA. Suitable routes may  
20 include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as, intrathecal, direct intraventricular, intravenous, intraperitoneal,  
25 intranasal, or intraocular injections, just to name a few. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiological saline  
30 buffer. For such transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

In instances wherein intracellular administration  
35 of the peptides of the invention or other inhibitory

agents is preferred, techniques well known to those of ordinary skill in the art may be utilized. For example, such agents may be encapsulated into liposomes, then administered as described above. Liposomes are spherical lipid bilayers with aqueous interiors. All molecules present in an aqueous solution at the time of liposome formation are incorporated into the aqueous interior. The liposomal contents are both protected from the external microenvironment and, because liposomes fuse with cell membranes, are effectively delivered into the cell cytoplasm. Additionally, due to their hydrophobicity, when small molecules are to be administered, direct intracellular administration may be achieved.

Nucleotide sequences encoding the peptides of the invention which are to be intracellularly administered may be expressed in cells of interest, using techniques well known to those of skill in the art. For example, expression vectors derived from viruses such as retroviruses, vaccinia viruses, adeno-associated viruses, herpes viruses, or bovine papilloma viruses, may be used for delivery and expression of such nucleotide sequences into the targeted cell population. Methods for the construction of such vectors and expression constructs are well known. See, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor NY, and Ausubel et al., 1989, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, NY.

With respect to HIV, peptides of the invention, particularly DP107 and DP178, may be used as therapeutics in the treatment of AIDS. In addition, the peptides may be used as prophylactic measures in previously uninfected individuals after acute exposure

to an HIV virus. Examples of such prophylactic use of the peptides may include, but are not limited to, prevention of virus transmission from mother to infant and other settings where the likelihood of HIV transmission exists, such as, for example, accidents  
5 in health care settings wherein workers are exposed to HIV-containing blood products. The successful use of such treatments do not rely upon the generation of a host immune response directed against such peptides.

Effective dosages of the peptides of the  
10 invention to be administered may be determined through procedures well known to those in the art which address such parameters as biological half-life, bioavailability, and toxicity. Given the data presented below in Section 6, DP178, for example, may  
15 prove efficacious in vivo at doses required to achieve circulating levels of about 1 to about 10 ng per ml of peptide.

A therapeutically effective dose refers to that amount of the compound sufficient to result in  
20 amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD<sub>50</sub>  
25 (the dose lethal to 50% of the population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD<sub>50</sub>/ED<sub>50</sub>. Compounds  
30 which exhibit large therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of  
35 circulating concentrations that include the ED<sub>50</sub> with

little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated  
5 initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the  $IC_{50}$  (e.g., the concentration of the test compound which achieves a half-maximal inhibition of the fusogenic  
10 event, such as a half-maximal inhibition of viral infection relative to the amount of the event in the absence of the test compound) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels  
15 in plasma may be measured, for example, by high performance liquid chromatography (HPLC).

The peptides of the invention may, further, serve the role of a prophylactic vaccine, wherein the host raises antibodies against the peptides of the  
20 invention, which then serve to neutralize HIV viruses by, for example, inhibiting further HIV infection.

Administration of the peptides of the invention as a prophylactic vaccine, therefore, would comprise administering to a host a concentration of peptides  
25 effective in raising an immune response which is sufficient to neutralize HIV, by, for example, inhibiting HIV ability to infect cells. The exact concentration will depend upon the specific peptide to be administered, but may be determined by using  
30 standard techniques for assaying the development of an immune response which are well known to those of ordinary skill in the art. The peptides to be used as vaccines are usually administered intramuscularly.

The peptides may be formulated with a suitable  
35 adjuvant in order to enhance the immunological

response. Such adjuvants may include, but are not limited to mineral gels such as aluminum hydroxide; surface active substances such as lysolecithin, pluronic polyols, polyanions; other peptides; oil emulsions; and potentially useful human adjuvants such as BCG and Corynebacterium parvum. Many methods may be used to introduce the vaccine formulations described here. These methods include but are not limited to oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, and intranasal routes.

Alternatively, an effective concentration of polyclonal or monoclonal antibodies raised against the peptides of the invention may be administered to a host so that no uninfected cells become infected by HIV. The exact concentration of such antibodies will vary according to each specific antibody preparation, but may be determined using standard techniques well known to those of ordinary skill in the art. Administration of the antibodies may be accomplished using a variety of techniques, including, but not limited to those described in this section.

For all such treatments described above, the exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g. Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p1).

It should be noted that the attending physician would know how to and when to terminate, interrupt, or adjust administration due to toxicity, or to organ dysfunctions. Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding toxicity). The magnitude of an administered dose in the management of the oncogenic disorder of interest

will vary with the severity of the condition to be treated and the route of administration. The dose and perhaps dose frequency, will also vary according to the age, body weight, and response of the individual patient. A program comparable to that discussed above  
5 may be used in veterinary medicine.

Use of pharmaceutically acceptable carriers to formulate the compounds herein disclosed for the practice of the invention into dosages suitable for systemic administration is within the scope of the  
10 invention. With proper choice of carrier and suitable manufacturing practice, the compositions of the present invention, in particular, those formulated as solutions, may be administered parenterally, such as by intravenous injection. The compounds can be  
15 formulated readily using pharmaceutically acceptable carriers well known in the art into dosages suitable for oral administration. Such carriers enable the compounds of the invention to be formulated as tablets, pills, capsules, liquids, gels, syrups,  
20 slurries, suspensions and the like, for oral ingestion by a patient to be treated.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective  
25 amount to achieve its intended purpose. Determination of the effective amounts is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

In addition to the active ingredients, these  
30 pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. The preparations formulated  
35

for oral administration may be in the form of tablets, dragees, capsules, or solutions.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

Pharmaceutical preparations for oral use can be obtained by combining the active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be

added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be  
5 used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or  
10 dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a  
15 plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In  
20 soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added.

25 6. EXAMPLE: DP178 (SEQ ID:1) IS A POTENT INHIBITOR OF HIV-1 INFECTION

In this example, DP178 (SEQ ID:1) is shown to be a potent inhibitor of HIV-1 mediated CD-4<sup>+</sup> cell-cell fusion and infection by cell free virus. In the  
30 fusion assay, this peptide completely blocks virus induced syncytia formation at concentrations of from 1-10 ng/ml. In the infectivity assay the inhibitory concentration is somewhat higher, blocking infection at 90ng/ml. It is further shown that DP178 (SEQ ID:1)  
35 shows that the antiviral activity of DP178 (SEQ ID:1)



is highly specific for HIV-1. Additionally, a synthetic peptide, DP-185 (SEQ ID:3), representing a HIV-1-derived DP178 homolog is also found to block HIV-1-mediated syncytia formation.

5

#### 6.1. MATERIALS AND METHODS

##### 6.1.1. PEPTIDE SYNTHESIS

Peptides were synthesized using Fast Moc chemistry on an Applied Biosystems Model 431A peptide synthesizer. Generally, unless otherwise noted, the peptides contained amidated carboxy termini and acetylated amino termini. Amidated peptides were prepared using Rink resin (Advanced Chemtech) while peptides containing free carboxy termini were synthesized on Wang (p-alkoxy-benzyl-alcohol) resin (Bachem). First residues were double coupled to the appropriate resin and subsequent residues were single coupled. Each coupling step was followed by acetic anhydride capping. Peptides were cleaved from the resin by treatment with trifluoroacetic acid (TFA) (10ml), H<sub>2</sub>O (0.5ml), thioanisole (0.5ml), ethanedithiol (0.25ml), and crystalline phenol (0.75g). Purification was carried out by reverse phase HPLC. Approximately 50mg samples of crude peptide were chromatographed on a Waters Delta Pak C18 column (19mm x 30cm, 15μ spherical) with a linear gradient; H<sub>2</sub>O/acetonitrile 0.1% TFA. Lyophilized peptides were stored desiccated and peptide solutions were made in water at about 1mg/ml. Electrospray mass spectrometry yielded the following results: DP178 (SEQ ID:1):4491.87 (calculated 4491.94); DP-180 (SEQ ID:2):4491.45 (calculated 4491.94); DP-185 (SEQ ID:3):not done (calculated 4546.97).

35

#### 6.1.2. VIRUS

The HIV-1<sub>LAI</sub> virus was obtained from R. Gallo (Popovic, M. et al., 1984, Science 224:497-508) and propagated in CEM cells cultured in RPMI 1640  
5 containing 10% fetal calf serum. Supernatant from the infected CEM cells was passed through a 0.2 $\mu$ m filter and the infectious titer estimated in a microinfectivity assay using the AA5 cell line to support virus replication. For this purpose, 25 $\mu$ l of  
10 serial diluted virus was added to 75 $\mu$ l AA5 cells at a concentration of  $2 \times 10^5$ /ml in a 96-well microtitre plate. Each virus dilution was tested in triplicate. Cells were cultured for eight days by addition of  
15 fresh medium every other day. On day 8 post infection, supernatant samples were tested for virus replication as evidenced by reverse transcriptase activity released to the supernatant. The TCID<sub>50</sub> was calculated according to the Reed and Muench formula (Reed, L.J. et al., 1938, Am. J. Hyg. 27:493-497).  
20 The titer of the HIV-1<sub>LAI</sub> and HIV-1<sub>MN</sub> stocks used for these studies, as measured on the AA5 cell line, was approximately  $1.4 \times 10^6$  and  $3.8 \times 10^4$  TCID<sub>50</sub>/ml, respectively.

#### 6.1.3. CELL FUSION ASSAY

25 Approximately  $7 \times 10^4$  Molt cells were incubated with  $1 \times 10^4$  CEM cells chronically infected with the HIV-1<sub>LAI</sub> virus in 96-well plates (one-half area cluster plates; Costar, Cambridge, MA) in a final volume of  
30 100 $\mu$ l culture medium as previously described (Matthews, T.J. et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5428). Peptide inhibitors were added in a volume of 10 $\mu$ l and the cell mixtures were incubated for 24 hr. at 37°C. At that time, multinucleated  
35 giant cells were estimated by microscopic examination

at a 40x magnification which allowed visualization of the entire well in a single field.

#### 6.1.4. CELL FREE VIRUS INFECTION ASSAY

5 Synthetic peptides were incubated at 37°C with either 247 TCID<sub>50</sub> (for experiment depicted in FIG. 2), or 62 TCID<sub>50</sub> (for experiment depicted in FIG.3) units of HIV-1<sub>LAI</sub> virus or 25 TCID<sub>50</sub> units of HIV-2<sub>NIH</sub> and CEM CD4<sup>+</sup> cells at peptide concentrations of 0, 0.04, 0.4, 4.0, and 40µg/ml for 7 days. The resulting reverse  
10 transcriptase (RT) activity in counts per minute was determined using the assay described, below, in Section 6.1.5. See, Reed, L.J. et al., 1938, Am. J. Hyg. 27: 493-497 for an explanation of TCID<sub>50</sub> calculations.

15

#### 6.1.5. REVERSE TRANSCRIPTASE ASSAY

The micro-reverse transcriptase (RT) assay was adapted from Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). Supernatants from  
20 virus/cell cultures are adjusted to 1% Triton-X100. A 10µl sample of supernatant was added to 50µl of RT cocktail in a 96-well U-bottom microtitre plate and the samples incubated at 37°C for 90 min. The RT  
25 cocktail contained 75mM KCl, 2mM dithiothreitol, 5mM MgCl<sub>2</sub>, 5µg/ml poly A (Pharmacia, cat. No. 27-4110-01), 0.25 units/ml oligo dT (Pharmacia, cat. No. 27-7858-01), 0.05% NP40, 50mM Tris-HCl, pH 7.8, 0.5µM non-radioactive dTTP, and 10µCi/ml <sup>32</sup>P-dTTP (Amersham, cat.  
30 No. PB.10167).

After the incubation period, 40µl of reaction mixture was applied to a Schleicher and Schuell (S+S) NA45 membrane (or DE81 paper) saturated in 2 x SSC buffer (0.3M NaCl and 0.003M sodium citrate) held in a  
35 S+S Minifold over one sheet of GB003 (S+S) filter

paper, with partial vacuum applied. Each well of the minifold was washed four times with 200 $\mu$ l 2xSSC, under full vacuum. The membrane was removed from the minifold and washed 2 more times in a pyrex dish with an excess of 2xSSC. Finally, the membrane was drained  
5 on absorbent paper, placed on Whatman #3 paper, covered with Saran wrap, and exposed to film overnight at -70°C.

## 6.2. RESULTS

### 10 6.2.1. PEPTIDE INHIBITION OF INFECTED CELL-INDUCED SYNCYTIA FORMATION

The initial screen for antiviral activity assayed peptides' ability to block syncytium formation induced by overnight co-cultivation of uninfected Molt4 cells  
15 with chronically HIV-1 infected CEM cells. The results of several such experiments are presented herein. In the first of these experiments, serial DP178 (SEQ ID:1) peptide concentrations between 10 $\mu$ g/ml and 12.5ng/ml were tested for blockade of the  
20 cell fusion process. For these experiments, CEM cells chronically infected with either HIV-1<sub>LAI</sub>, HIV-1<sub>MN</sub>, HIV-1<sub>RF</sub>, or HIV-1<sub>SF2</sub> virus were cocultivated overnight with uninfected Molt 4 cells. The results (FIG. 4) show that DP178 (SEQ ID:1) afforded complete protection  
25 against each of the HIV-1 isolates down to the lowest concentration of DP178 (SEQ ID:1) used. For HIV<sub>LAI</sub> inhibition, the lowest concentration tested was 12.5ng/ml; for all other HIV-1 viruses, the lowest concentration of DP178 (SEQ ID:1) used in this study  
30 was 100ng/ml. A second peptide, DP-180 (SEQ ID:2), containing the same amino acid residues as DP178 (SEQ ID:1) but arranged in a random order exhibited no evidence of anti-fusogenic activity even at the high concentration of 40 $\mu$ g/ml (FIG. 4). These observations  
35 indicate that the inhibitory effect of DP178 (SEQ

ID:1) is primary sequence-specific and not related to non-specific peptide/protein interactions. The actual endpoint (i.e., the lowest effective inhibitory concentration) of DP178 inhibitory action is within the range of 1-10 ng/ml.

5       The next series of experiments involved the preparation and testing of a DP178 (SEQ ID:1) homolog for its ability to inhibit HIV-1-induced syncytia formation. As shown in FIG. 1, the sequence of DP-185 (SEQ ID:3) is slightly different from DP178 (SEQ ID:1) in that its primary sequence is taken from the HIV-1<sub>SF2</sub> isolate and contains several amino acid differences relative to DP178 (SEQ ID:1) near the N terminus. As shown in FIG. 4, DP-185 (SEQ ID:3), exhibits inhibitory activity even at 312.5ng/ml, the lowest concentration tested.

10       The next series of experiments involved a comparison of DP178 (SEQ ID:1) HIV-1 and HIV-2 inhibitory activity. As shown in FIG. 5, DP178 (SEQ ID:1) blocked HIV-1-mediated syncytia formation at peptide concentrations below 1ng/ml. DP178 (SEQ ID:1) failed, however, to block HIV-2 mediated syncytia formation at concentrations as high as 10µg/ml. This striking 4 log selectivity of DP178 (SEQ ID:1) as an inhibitor of HIV-1-mediated cell fusion demonstrates an unexpected HIV-1 specificity in the action of DP178 (SEQ ID:1). DP178 (SEQ ID:1) inhibition of HIV-1-mediated cell fusion, but the peptide's inability to inhibit HIV-2 mediated cell fusion in the same cell type at the concentrations tested provides further evidence for the high degree of selectivity associated with the antiviral action of DP178 (SEQ ID:1).

35

6.2.2. PEPTIDE INHIBITION OF INFECTION BY  
CELL-FREE VIRUS

DP178 (SEQ ID:1) was next tested for its ability to block CD-4<sup>+</sup> CEM cell infection by cell free HIV-1 virus. The results, shown in FIG. 2, are from an experiment in which DP178 (SEQ ID:1) was assayed for its ability to block infection of CEM cells by an HIV-1<sub>LAI</sub> isolate. Included in the experiment were three control peptides, DP-116 (SEQ ID:9), DP-125 (SEQ ID:8), and DP-118 (SEQ ID:10). DP-116 (SEQ ID:9) represents a peptide previously shown to be inactive using this assay, and DP-125 (SEQ ID:8; Wild, C. et al., 1992, Proc. Natl. Acad. Sci. USA 89:10,537) and DP-118 (SEQ ID:10) are peptides which have previously been shown to be active in this assay. Each concentration (0, 0.04, 0.4, 4, and 40 µg/ml) of peptide was incubated with 247 TCID<sub>50</sub> units of HIV-1<sub>LAI</sub> virus and CEM cells. After 7 days of culture, cell-free supernatant was tested for the presence of RT activity as a measure of successful infection. The results, shown in FIG. 2, demonstrate that DP178 (SEQ ID:1) inhibited the de novo infection process mediated by the HIV-1 viral isolate at concentrations as low as 90ng/ml (IC<sub>50</sub>=90ng/ml). In contrast, the two positive control peptides, DP-125 (SEQ ID:8) and DP-118 (SEQ ID:10), had over 60-fold higher IC<sub>50</sub> concentrations of approximately 5 µg/ml.

In a separate experiment, the HIV-1 and HIV-2 inhibitory action of DP178 (SEQ ID:1) was tested with CEM cells and either HIV-1<sub>LAI</sub> or HIV-2<sub>NIHZ</sub>. 62 TCID<sub>50</sub> HIV-1<sub>LAI</sub> or 25 GCID<sub>50</sub> HIV-2<sub>NIHZ</sub> were used in these experiments, and were incubated for 7 days. As may be seen in FIG. 3, DP178 (SEQ ID:1) inhibited HIV-1 infection with an IC<sub>50</sub> of about 31ng/ml. In contrast, DP178 (SEQ ID:1) exhibited a much higher IC<sub>50</sub> for HIV-2<sub>NIHZ</sub>, thus making DP178 (SEQ ID:1) two logs more potent

as a HIV-1 inhibitor than a HIV-2 inhibitor. This finding is consistent with the results of the fusion inhibition assays described, above, in Section 6.2.1, and further supports a significant level of selectivity (i.e., for HIV-1 over HIV-2).

5

7. EXAMPLE: THE HIV-1 INHIBITOR, DP178 (SEQ ID:1) IS NON-CYTOTOXIC

In this Example, the 36 amino acid synthetic peptide inhibitor DP178 (SEQ ID:1) is shown to be non-cytotoxic to cells in culture, even at the highest peptide concentrations (40µg/ml) tested.

10

7.1. MATERIALS AND METHODS

Cell proliferation and toxicity assay:

Approximately  $3.8 \times 10^5$  CEM cells for each peptide concentration were incubated for 3 days at 37°C in T25 flasks. Peptides tested were DP178 (SEQ ID:1) and DP-116 (SEQ ID:9), as described in FIG. 1. Peptides were synthesized as described, above, in Section 6.1. The concentrations of each peptide used were 0, 2.5, 10, and 40µg/ml. Cell counts were taken at incubation times of 0, 24, 48, and 72 hours.

15

20

7.2. RESULTS

Whether the potent HIV-1 inhibitor DP178 (SEQ ID:1) exhibited any cytotoxic effects was assessed by assaying the peptide's effects on the proliferation and viability of cells in culture. CEM cells were incubated in the presence of varying concentrations of DP178 (SEQ ID:1), and DP-116 (SEQ ID:9), a peptide previously shown to be ineffective as a HIV inhibitor (Wild, C. et al., 1992, Proc. Natl. Acad. Sci. USA 89:10,537-10,541). Additionally, cells were incubated in the absence of either peptide.

30

35

The results of the cytotoxicity study demonstrate that DP178 (SEQ ID:1) exhibits no cytotoxic effects on cells in culture. As can be seen, below, in Table XXIV, even the proliferation and viability characteristics of cells cultured for 3 days in the presence of the highest concentration of DP178 (SEQ ID:1) tested (40µg/ml) do not significantly differ from the DP-116 (SEQ ID:9) or the no-peptide controls. The cell proliferation data is also represented in graphic form in FIG. 6. As was demonstrated in the Working Example presented above in Section 6, DP178 (SEQ ID:1) completely inhibits HIV-1 mediated syncytia formation at peptide concentrations between 1 and 10ng/ml, and completely inhibits cell-free viral infection at concentrations of at least 90ng/ml. Thus, this study demonstrates that even at peptide concentrations greater than 3 log higher than the HIV inhibitory dose, DP178 (SEQ ID:1) exhibits no cytotoxic effects.



TABLE XXIV

5	Peptide	Peptide Concentration $\mu\text{g/ml}$	% Viability at time (hours)			
			0	24	48	72
	DP178 (SEQ ID:1)	40	98	97	95	97
10		10	98	97	98	98
		2.5	98	93	96	96
	DP116 (SEQ ID:9)	40	98	95	98	97
15		10	98	95	93	98
		2.5	98	96	98	99
	No Peptide	0	98	97	99	98
20						

8. EXAMPLE: THE INTERACTION OF DP178 AND DP107

Soluble recombinant forms of gp41 used in the  
 25 example described below provide evidence that the  
 DP178 peptide associates with a distal site on gp41  
 whose interactive structure is influenced by the DP107  
 leucine zipper motif. A single mutation disrupting  
 the coiled-coil structure of the leucine zipper domain  
 30 transformed the soluble recombinant gp41 protein from  
 an inactive to an active inhibitor of HIV-1 fusion.  
 This transformation may result from liberation of the  
 potent DP178 domain from a molecular clasp with the  
 leucine zipper, DP107, determinant. The results also  
 35 indicate that the anti-HIV activity of various gp41  
 derivatives (peptides and recombinant proteins) may be



were checked by restriction enzyme analysis and confirmed by DNA sequencing.

#### 8.1.2. PURIFICATION AND CHARACTERIZATION OF FUSION PROTEINS

5        The fusion proteins were purified according to the protocol described in the manufacturer's brochure of protein fusion and purification systems from New England Biolabs (NEB). Fusion proteins (10 ng) were analyzed by electrophoresis on 8% SDS polyacrylamide  
10        gels. Western blotting analysis was performed as described by Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2d Ed, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, Ch. 18, pp. 64-75. An HIV-1 positive serum diluted 1000-fold,  
15        or a human Fab derived from repertoire cloning was used to react with the fusion proteins. The second antibody was HRP-conjugated goat antihuman Fab. An ECL Western blotting detection system (Amersham) was used to detect the bound antibody. A detailed  
20        protocol for this detection system was provided by the manufacturer. Rainbow molecular weight markers (Amersham) were used to estimate the size of fusion proteins.

#### 25        8.1.3. CELL FUSION ASSAYS FOR ANTI-HIV ACTIVITY

Cell fusion assays were performed as previously described (Matthews et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5481). CEM cells ( $7 \times 10^4$ ) were incubated with HIV-1<sub>IIIb</sub> chronically infected CEM cells  
30        ( $10^4$ ) in 96-well flat-bottomed half-area plates (Costar) in 100  $\mu$ l culture medium. Peptide and fusion proteins at various concentrations in 10  $\mu$ l culture medium were incubated with the cell mixtures at 37°C for 24 hours. Multinucleated syncytia were estimated  
35        with microscopic examination. Both M41 and M41-P did

not show cytotoxicity at the concentrations tested and shown in FIG. 8.

Inhibition of HIV-1 induced cell-cell fusion activity was carried out in the presence of 10 nM DP178 and various concentrations of M41Δ178 or M41-PA178 as indicated in FIG. 9. There was no observable syncytia in the presence of 10 nM DP178. No peptide or fusion protein was added in the control samples.

8.1.4. ELISA ANALYSIS OF DP178 BINDING TO THE LEUCINE ZIPPER MOTIF OF GP41

The amino acid sequence of DP178 used is: YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF. For enzyme linked immunoassay (ELISA), M41Δ178 or M41-PA178 (5 μg/ml) in 0.1M NaHCO<sub>3</sub>, pH 8.6, were coated on 96 wells Linbro ELISA plates (Flow Lab, Inc.) overnight. Each well was washed three times with distilled water then blocked with 3% bovine serum albumin (BSA) for 2 hours. After blocking, peptides with 0.5% BSA in TBST (40 mM Tris-HCl pH7.5, 150 mM NaCl, 0.05% Tween 20) were added to the ELISA plates and incubated at room temperature for 1 hour. After washing three times with TBST, Fab-d was added at a concentration of 10 ng/ml with 0.5% BSA in TBST. The plates were washed three times with TBST after incubation at room temperature for 1 hour. Horse radish peroxidase (HRP) conjugated goat antihuman Fab antiserum at a 2000 fold dilution in TBST with 0.5% BSA was added to each well and incubated at room temperature for 45 minutes. The plates were then washed four times with TBST. The peroxidase substrate o-phenylene diamine (2.5 mg/ml) and 0.15% H<sub>2</sub>O<sub>2</sub> were added to develop the color. The reaction was stopped with an equal volume of 4.5 N H<sub>2</sub>SO<sub>4</sub> after incubation at room temperature for 10 minutes. The optical density of the stopped reaction mixture was measured with a micro plate reader

(Molecular Design) at 490 nm. Results are shown in FIG. 10.

## 8.2. RESULTS

### 8.2.1. THE EXPRESSION AND CHARACTERIZATION OF THE ECTODOMAIN OF gp41

5 As a step toward understanding the roles of the two helical regions in gp41 structure and function, the ectodomain of gp41 was expressed as a maltose binding fusion protein (M41) (FIG. 7). The fusogenic  
10 peptide sequence at the N-terminal of gp41 was omitted from this recombinant protein and its derivatives to improve solubility. The maltose binding protein facilitated purification of the fusion proteins under relatively mild, non-denaturing conditions. Because  
15 the M41 soluble recombinant gp41 was not glycosylated, lacked several regions of the transmembrane protein (*i.e.*, the fusion peptide, the membrane spanning, and the cytoplasmic domains), and was expressed in the absence of gp120, it was not expected to precisely  
20 reflect the structure of native gp41 on HIV-1 virions. Nevertheless, purified M41 folded in a manner that preserved certain discontinuous epitopes as evidenced by reactivity with human monoclonal antibodies, 98-6, 126-6, and 50-69, previously shown to bind  
25 conformational epitopes on native gp41 expressed in eukaryotic cells (Xu et al., 1991, J. Virol. 65: 4832-4838; Chen, 1994, J. Virol. 68:2002-2010). Thus, at least certain regions of native gp41 defined by these antibodies appear to be reproduced in the recombinant  
30 fusion protein M41. Furthermore, M41 reacted with a human recombinant Fab (Fab-d) that recognizes a conformational epitope on gp41 and binds HIV-1 virions as well as HIV-1 infected cells but not uninfected cells as analyzed by FACS. Deletion of either helix  
35 motif, *i.e.*, DP107 or DP178, of the M41 fusion protein

eliminated reactivity with Fab-d. These results indicate that both helical regions, separated by 60 amino acids in the primary sequence, are required to maintain the Fab-d epitope.

5

#### 8.2.2. ANTI-HIV ACTIVITY OF THE RECOMBINANT ECTODOMAIN OF GP41

The wild type M41 fusion protein was tested for anti-HIV-1 activity. As explained, *supra*, synthetic  
10 peptides corresponding to the leucine zipper (DP107) and the C-terminal putative helix (DP178) show potent anti-HIV activity. Despite inclusion of both these regions, the recombinant M41 protein did not affect HIV-1 induced membrane fusion at concentrations as  
15 high as 50  $\mu$ M (Table XXV, below).

---

TABLE XXV  
DISRUPTION OF THE LEUCINE ZIPPER OF  
GP41 FREES THE ANTI-HIV MOTIF

20		<u>DP107</u>	<u>DP178</u>	<u>M41</u>	<u>M41-P</u>	<u>M41-PA178</u>
	Cell fusion (IC <sub>50</sub> )	1 $\mu$ M	1 nM	> 50 $\mu$ M	83 nM	> 50 $\mu$ M
25	Fab-D binding (k <sub>D</sub> )	-	-	3.5x10 <sup>-9</sup>	2.5x10 <sup>-8</sup>	-
	HIV infectiv- ity (IC <sub>50</sub> )	1 $\mu$ M	80 nM	> 16 $\mu$ M	66 nM	> 8 $\mu$ M

---

30 1 The affinity constants of Fab-d binding to the fusion proteins were determined using a protocol described by B. Friguet et al., 1985, J. Immunol. Method. 77:305-319.

- = No detectable binding of Fab-d to the fusion proteins.

35 *Antiviral Infectivity Assays.* 20  $\mu$ l of serially diluted virus stock was incubated for 60 minutes at ambient temperature with 20  $\mu$ l of the indicated

concentration of purified recombinant fusion protein in RPMI 1640 containing 10% fetal bovine serum and antibiotics in a 96-well microtiter plate. 20  $\mu$ l of CEM4 cells at  $6 \times 10^5$  cells/ml were added to each well, and cultures were incubated at 37°C in a humidified CO<sub>2</sub> incubator. Cells were cultured for 9 days by the addition of fresh medium every 2 to 3 days. On days 5, 7, and 9 postinfection, supernatant samples were assayed for reverse transcriptase (RT) activity, as described below, to monitor viral replication. The 50% tissue culture infectious dose (TCID<sub>50</sub>) was calculated for each condition according to the formula of Reed & Muench, 1937, Am. J. Hyg. 27:493-497. RT activity was determined by a modification of the published methods of Goff et al., 1981, J. Virol. 38:239-248 and Willey et al., 1988, J. Virol. 62:139-147 as described in Chen et al., 1993, AIDS Res. Human Retroviruses 9:1079-1086.

Surprisingly, a single amino acid substitution, proline in place of isoleucine in the middle of the leucine zipper motif, yielded a fusion protein (M41-P) which did exhibit antiviral activity (Table XXV and Fig. 8). As seen in Table XXV, M41-P blocked syncytia formation by 90% at approximately 85 nM and neutralized HIV-1<sub>IIIB</sub> infection by 90% at approximately 70 nM concentrations. The anti-HIV-1 activity of M41-P appeared to be mediated by the C-terminal helical sequence since deletion of that region from M41-P yielded an inactive fusion protein, M41-PA178 (Table XXV). This interpretation was reinforced by experiments demonstrating that a truncated fusion protein lacking the DP178 sequence, M41 $\Delta$ 178, abrogated the potent anti-fusion activity of the DP178 peptide in a concentration-dependent manner (FIG. 9). The same truncated fusion protein containing the proline mutation disrupting the leucine zipper, M41-PA178, was not active in similar competition experiments (FIG. 9). The results indicate that the DP178 peptide associates with a second site on gp41 whose interactive structure is dependent on a wild type leucine zipper sequence. A similar interaction may occur within the wild type fusion protein, M41, and act to form an intramolecular clasp which sequesters

the DP178 region, making it unavailable for anti-viral activity.

5 A specific association between these two domains is also indicated by other human monoclonal Fab-d studies. For example, Fab-d failed to bind either the DP178 peptide or the fusion protein M41Δ178, but its epitope was reconstituted by simply mixing these two reagents together (FIG. 10). Again, the proline mutation in the leucine zipper domain of the fusion protein, M41-PA178, failed to reconstitute the epitope  
10 in similar mixing experiments.

9. EXAMPLE: METHOD FOR COMPUTER-ASSISTED  
IDENTIFICATION OF DP107-LIKE  
AND DP178-LIKE SEQUENCES

15 A number of known coiled-coil sequences have been well described in the literature and contain heptad repeat positioning for each amino acid. Coiled-coil nomenclature labels each of seven amino acids of a heptad repeat A through G, with amino acids A and D  
20 tending to be hydrophobic positions. Amino acids E and G tend to be charged. These four positions (A, D, E, and G) form the amphipathic backbone structure of a monomeric alpha-helix. The backbones of two or more amphipathic helices interact with each other to form  
25 di-, tri-, tetrameric, etc., coiled-coil structures. In order to begin to design computer search motifs, a series of well characterized coiled coils were chosen including yeast transcription factor GCN4, Influenza Virus hemagglutinin loop 36, and human proto-oncogenes  
30 c-Myc, c-Fos, and c-Jun. For each peptide sequence, a strict homology for the A and D positions, and a list of the amino acids which could be excluded for the B, C, E, F, and G positions (because they are not observed in these positions) was determined. Motifs  
35 were tailored to the DP107 and DP178 sequences by



deducing the most likely possibilities for heptad positioning of the amino acids of HIV-1 Bru DP-107, which is known to have coiled-coil structure, and HIV-1 Bru DP178, which is still structurally undefined. The analysis of each of the sequences is contained in  
 5 FIG. 12. For example, the motif for GCN4 was designed as follows:

1. The only amino acids (using standard single letter amino acid codes) found in the A or D positions of GCN4 were [LMNV].
- 10 2. All amino acids were found at B, C, E, F, and G positions except {CFGIMPTW}.
3. The PESEARCH motif would, therefore, be written as follows:  
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-  
 15 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-  
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-  
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)

Translating or reading the motif: "at the first A  
 20 position either L, M, N, or V must occur; at positions B and C (the next two positions) accept everything except C, F, G, I, M, P, T, or W; at the D position either L, M, N, or V must occur; at positions E, F, and G (the next 3 positions) accept everything except  
 25 C, F, G, I, M, P, T, or W." This statement is contained four times in a 28-mer motif and five times in a 35-mer motif. The basic motif key then would be: [LMNV]-{CFGIMPTW}. The motif keys for the remaining well described coiled-coil sequences are summarized in  
 30 FIG. 12.

The motif design for DP107 and DP178 was slightly different than the 28-mer model sequences described above due to the fact that heptad repeat positions are not defined and the peptides are both longer than 28  
 35 residues. FIG. 13 illustrates several possible

sequence alignments for both DP107 and DP178 and also includes motif designs based on 28-mer, 35-mer, and full-length peptides. Notice that only slight differences occur in the motifs as the peptides are lengthened. Generally, lengthening the base peptide  
5 results in a less stringent motif. This is very useful in broadening the possibilities for identifying DP107-or DP-178-like primary amino acid sequences referred to in this document as "hits".

10 In addition to making highly specific motifs for each type peptide sequence to be searched, it is also possible to make "hybrid" motifs. These motifs are made by "crossing" two or more very stringent motifs to make a new search algorithm which will find not only both "parent" motif sequences but also any  
15 peptide sequences which have similarities to one, the other, or both "parents". For example, in FIG. 14 the "parent" sequence of GCN4 is crossed with each of the possible "parent" motifs of DP-107. Now the hybrid motif must contain all of the amino acids found in the  
20 A and D positions of both parents, and exclude all of the amino acids not found in either parent at the other positions. The resulting hybrid from crossing GCN4 or [LMNV]{CFGIMPTW} and DP107 (28-mer with the first L in the D position) or [ILQT]{CDFIMPST}, is  
25 [ILMNQTV]{CFIMPT}. Notice that now only two basic hybrid motifs exist which cover both framing possibilities, as well as all peptide lengths of the parent DP-107 molecule. FIG. 15 represents the "hybridizations" of GCN4 with DP-178. FIG. 16  
30 represents the "hybridizations" of DP107 and DP178. It is important to keep in mind that the represented motifs, both parent and hybrid, are motif keys and not the depiction of the full-length motif needed to actually do the computer search.

35

Hybridizations can be performed on any combination of two or more motifs. FIG. 17 summarizes several three-motif hybridizations including GCN4, DP107 (both frames), and DP178 (also both frames). Notice that the resulting motifs are now becoming much more similar to each other. In fact, the first and third hybrid motifs are actually subsets of the second and fourth hybrid motifs respectively. This means that the first and third hybrid motifs are slightly more stringent than the second and fourth. It should also be noted that with only minor changes in these four motifs, or by hybridizing them, a single motif could be obtained which would find all of the sequences. However, it should be remembered that stringency is also reduced. Finally, the most broad-spectrum and least-stringent hybrid motif is described in FIG. 18 which summarizes the hybridization of GCN4, DP107 (both frames), DP178 (both frames), c-Fos, c-Jun, c-Myc, and Flu loop 36.

A special set of motifs was designed based on the fact that DP-178 is located only approximately ten amino acids upstream of the transmembrane spanning region of gp41 and just C-terminal to a proline which separates DP107 and DP178. It has been postulated that DP178 may be an amphipathic helix when membrane associated, and that the proline might aid in the initiation of the helix formation. The same arrangement was observed in Respiratory Syncytial Virus; however, the DP178-like region in this virus also had a leucine zipper just C-terminal to the proline. Therefore, N-terminal proline-leucine zipper motifs were designed to analyze whether any other viruses might contain this same pattern. The motifs are summarized in FIG. 19.

The PC/Gene protein database contains 5879 viral amino acid sequences (library file PVIRUSES; CD-ROM

release 11.0). Of these, 1092 are viral enveloped or glycoprotein sequences (library file PVIRUSE1). Tables V through XIV contain lists of protein sequence names and motif hit locations for all the motifs searched.

5

10. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION  
OF DP107 AND DP178-LIKE SEQUENCES  
IN HUMAN IMMUNODEFICIENCY VIRUS

FIG. 20 represents search results for HIV-1 BRU isolate gp41 (PC/Gene protein sequence PENV\_HV1BR). Notice that the hybrid motif which crosses DP-107 and DP-178 (named 107x178x4; the same motif as found in FIG. 16 found three hits including amino acids 550-599, 636-688, and 796-823. These areas include DP-107 plus eight N-terminal and four C-terminal amino acids; DP178 plus seven N-terminal and ten C-terminal amino acids; and an area inside the transmembrane region (cytoplasmic). FIG. 20 also contains the results obtained from searching with the motif named ALLMOTI5, for which the key is found in FIG. 17 ({CDGHP}{CFP}x5). This motif also found three hits including DP107 (amino acids 510-599), DP178 (615-717), and a cytoplasmic region (772-841). These hits overlap the hits found by the motif 107x178x4 with considerable additional sequences on both the amino and carboxy termini. This is not surprising in that 107x178x4 is a subset of the ALLMOTI5 hybrid motif. Importantly, even though the stringency of ALLMOTI5 is considerably less than 107x178x4, it still selectively identifies the DP107 and DP178 regions of gp41 shown to contain sequences for inhibitory peptides of HIV-1. The results of these two motif searches are summarized in Table V under the PC/Gene protein sequence name PENV HV1BR. The proline-leucine zipper motifs also gave several hits in HIV-1 BRU including 503-525 which is

at the very C-terminus of gp120, just upstream of the cleavage site (P7LZIPC and P12LZIPC); and 735-768 in the cytoplasmic domain of gp41 (P23LZIPC). These results are found in Tables VIII, IX, and X under the same sequence name as mentioned above. Notice that  
5 the only area of HIV-1 BRU which is predicted by the Lupas algorithm to contain a coiled-coil region, is from amino acids 635-670. This begins eight amino acids N-terminal to the start and ends eight amino acids N-terminal to the end of DP178. DP107, despite  
10 the fact that it is a known coiled coil, is not predicted to contain a coiled-coil region using the Lupas method.

11. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION  
15 OF DP107-LIKE AND DP178-LIKE  
SEQUENCES IN HUMAN RESPIRATORY  
SYNCYTIAL VIRUS

FIG. 21 represents search results for Human Respiratory Syncytial Virus (RSV; Strain A2) fusion glycoprotein F1 (PC/Gene protein sequence name PVGLF\_ HRSVA). Motif 107x178x4 finds three hits including  
20 amino acids 152-202, 213-243, and 488-515. The arrangement of these hits is similar to what is found in HIV-1 except that the motif finds two regions with similarities to DP-178, one just downstream of what  
25 would be called the DP107 region or amino acids 213-243, and one just upstream of the transmembrane region (also similar to DP178) or amino acids 488-515. Motif ALLMOTI5 also finds three areas including amino acids  
30 116-202, 267-302, and 506-549. The proline-leucine zipper motifs also gave several hits including amino acids 205-221 and 265-287 (P1LZIPC 265-280, P12LZIPC), and 484-513 (P7LZIPC and P12LZIPC 484-506, P23LZIPC). Notice that the PLZIP motifs also identify regions  
35 which share location similarities with DP-178 of HIV-1.

12. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP107-LIKE AND DP178-LIKE SEQUENCES  
IN SIMIAN IMMUNODEFICIENCY VIRUS

Motif hits for Simian immunodeficiency Virus gp41 (AGM3 isolate; PC/Gene protein sequence name PENV\_SIVAG) are shown in FIG. 22. Motif 107x178x4 finds three hits including amino acids 566-593, 597-624, and 703-730. The first two hits only have three amino acids between them and could probably be combined into one hit from 566-624 which would represent a DP107-like hit. Amino acids 703 to 730 would then represent a DP178-like hit. ALLMOTI5 also finds three hits including amino acids 556-628 (DP107-like), 651-699 (DP178-like), and 808-852 which represents the transmembrane spanning region. SIV also has one region from 655-692 with a high propensity to form a coiled coil as predicted by the Lupas algorithm. Both 107x178x4 and ALLMOTI5 motifs find the same region. SIV does not have any PLZIP motif hits in gp41.

The identification of DP178/DP107 analogs for a second SIV isolate (MM251) is demonstrated in the Example presented, below, in Section 19.

13. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP107-LIKE AND DP178 LIKE SEQUENCES  
IN CANINE DISTEMPER VIRUS

Canine Distemper Virus (strain Onderstepoort) fusion glycoprotein F1 (PC/Gene Protein sequence name PVGLF\_CDVO) has regions similar to Human RSV which are predicted to be DP107-like and DP178-like (FIG. 23). Motif 107x178x4 highlights one area just C-terminal to the fusion peptide at amino acids 252-293. Amino acids 252-286 are also predicted to be coiled coil using the Lupas algorithm. Almost 100 amino acids C-terminal to the first region is a DP178-like area at residues 340-367. ALLMOTI5 highlights three areas of

interest including: amino acids 228-297, which completely overlaps both the Lupas prediction and the DP107-like 107x178x4 hit; residues 340-381, which overlaps the second 107x178x4 hit; and amino acids 568-602, which is DP178-like in that it is located just N-terminal to the transmembrane region. It also overlaps another region (residues 570-602) predicted by the Lupas method to have a high propensity to form a coiled coil. Several PLZIP motifs successfully identified areas of interest including P6 and P12LZIPC which highlight residues 336-357 and 336-361 respectively; P1 and P12LZIPC which find residues 398-414; and P12 and P23LZIPC which find residues 562-589 and 562-592 respectively.

14. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP107-LIKE AND DP178-LIKE SEQUENCES  
IN NEWCASTLE DISEASE VIRUS

FIG. 24 shows the motif hits found in Newcastle Disease Virus (strain Australia-Victoria/32; PC Gene protein sequence name PVGLF\_NDVA). Motif 107x178x4 finds two areas including a DP107-like hit at amino acids 151-178 and a DP178-like hit at residues 426-512. ALLMOTI5 finds three areas including residues 117-182, 231-272, and 426-512. The hits from 426-512 include a region which is predicted by the Lupas method to have a high coiled-coil propensity (460-503). The PLZIP motifs identify only one region of interest at amino acids 273-289 (P1 and 12LZIPC).

15. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION  
OF DP107-LIKE AND DP178-LIKE  
SEQUENCES IN HUMAN PARAINFLUENZA VIRUS

Both motifs 107x178x4 and ALLMOTI5 exhibit DP107-like hits in the same region, 115-182 and 117-182 respectively, of Human Parainfluenza Virus (strain NIH 47885; PC/Gene protein sequence name PVGLF\_p13H4;

(FIG. 25). In addition, the two motifs have a DP178-like hit just slightly C-terminal at amino acids 207-241. Both motifs also have DP178-like hits nearer the transmembrane region including amino acids 457-497 and 462-512 respectively. Several PLZIP motif hits are  
5 also observed including 283-303 (P5LZIPC), 283-310 (P12LZIPC), 453-474 (P6LZIPC), and 453-481 (P23LZIPC). The Lupas algorithm predicts that amino acids 122-176 may have a propensity to form a coiled-coil.

10 16. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP107-LIKE AND DP178-LIKE SEQUENCES OF  
INFLUENZA A VIRUS

FIG. 26 illustrates the Lupas prediction for a coiled coil in Influenza A Virus (strain A/Aichi/2/68)  
15 at residues 379-436, as well as the motif hits for 107x178x4 at amino acids 387-453, and for ALLMOTI5 at residues 380-456. Residues 383-471 (38-125 of HA2) were shown by Carr and Kim to be an extended coiled coil when under acidic pH (Carr and Kim, 1993, Cell  
20 73: 823-832). The Lupas algorithm predicts a coiled-coil at residues 379-436. All three methods successfully predicted the region shown to actually have coiled-coil structure; however, ALLMOTI5 predicted the greatest portion of the 88 residue  
25 stretch.

17. EXAMPLE: POTENTIAL RESPIRATORY SYNCYTIAL VIRUS  
DP178/DP107 ANALOGS: CD AND  
ANTIVIRAL CHARACTERIZATION

In the Example presented herein, respiratory  
30 syncytial virus (RSV) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 11, above, were tested for anti-RSV activity. Additionally, circular dichroism (CD) structural analyses were conducted on  
35 the peptides, as discussed below. It is demonstrated



that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of these peptides exhibit a substantial helical character.

5

#### 17.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a  
10 Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptides were synthesized according to the methods described, above, in Section 6.1. Peptide concentrations were determined from  $A_{280}$  using Edlehoch's method (1967, Biochemistry 6:1948).

15

Anti-RSV antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of HEp2 cells acutely infected with RSV (i.e., cells which are infected with a multiplicity of infection of greater than 2) to fuse  
20 and cause syncytial formation on a monolayer of uninfected an uninfected line of Hep-2 cells. The lower the observed level of fusion, the greater the antiviral activity of the peptide was determined to be.

25

Uninfected confluent monolayers of Hep-2 cells were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes  
30 at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 3%, antibiotics (penicillin/streptomycin; Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

35

To prepare Hep2 cells for addition to uninfected cells, cultures of acutely infected Hep2 cells were

washed with DPBS (Dulbecco's Phosphate Buffered Saline w/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected Hep-2 cells.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Hep-2 cells, then adding peptides (at the dilutions described below) in 3% EMEM, and 100 acutely RSV-infected Hep2 cells per well. Wells were then incubated at 37°C for 48 hours.

After incubation, cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of either Crystal Violet stain or XTT. With respect to Crystal Violet, approximately 50µl 0.25% Crystal Violet stain in methanol were added to each well. The wells were rinsed immediately, to remove excess stain, and were allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

With respect to XTT (2,3-bis[2-Methoxy-4-nitro-5-sulfophenyl]-2H-tetrazolium-5-carboxyanilide inner salt), 50µl XTT (1mg/ml in RPMI buffered with 100mM HEPES, pH 7.2-7.4, plus 5% DMSO) were added to each well. The OD<sub>450/690</sub> was measured (after blanking against growth medium without cells or reagents, and against reagents) according to standard procedures.

Peptides: The peptides characterized in the study presented herein were:

1) peptides T-142 to T-155 and T-575, as shown in FIG. 27A, and peptides T-22 to T-27, T-68, T-334 and T-371 to T-375 and T-575, as shown in FIG. 27B;

2) peptides T-120 to T-141 and T-576, as shown in FIG. 27B, and peptides T-12, T-13, T-15, T-19, T-28 to T-30, T-66, T-69, T-70 and T-576, as shown in FIG. 27D; and  
3) peptides T-67 and T-104 to T-119 and T-384, as shown in FIG. 28A, and peptides T-71, T-613 to T-617, T-662 to T-676 and T-730, as shown in FIG. 28B.

The peptides of group 1 represent portions of the RSV F2 protein DP178/107-like region. The peptides of group 2 represent portions of the RSV F1 protein DP107-like region. The peptides of groups 3 represent portions of the RSV F1 protein DP178-like region.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used. The IC<sub>50</sub> data for each peptide represents the average of several experiments conducted utilizing that peptide.

## 17.2 RESULTS

The data summarized in FIGS. 27A-B and 28A-B represent antiviral and structural information obtained from peptides derived from the RSV F2 DP178/DP107-like F2 region (FIG. 27A-B), the RSV F1 DP-107-like region (FIG. 27C-D) and the RSV DP178-like F2 region (FIG. 28A-B).

As shown in FIGS. 27A-D, a number of the RSV DP178/DP107-like peptides exhibited a detectable level of antiviral activity. Peptides from the RSV DP178/DP107-like F2 region (FIG. 27A-B), for example, T-142 to T-145 and T-334 purified peptides, exhibited detectable levels of antiviral activity, as evidenced by their IC<sub>50</sub> values. Further, a number of RSV F1 DP107-like peptides (FIG. 27C-D) exhibited a sizable level of antiviral activity as purified peptides, including, for example, peptides T-124 to T-127, T-

131, T-135 and T-137 to T-139, as demonstrated by their low IC<sub>50</sub> values. In addition, CD analysis FIG. 27A, 27C) reveals that many of the peptides exhibit some detectable level of helical structure.

5 The results summarized in FIG. 28A-B demonstrate that a number of DP178-like purified peptides exhibit a range of potent anti-viral activity. These peptides include, for example, T-67, T-104, T-105 and T-107 to T-119, as listed in FIG. 28A, and T-665 to T-669 and T-671 to T-673, as listed in FIG. 28B. In addition,  
10 some of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, successfully identified viral peptide domains that represent highly promising anti-RSV  
15 antiviral compounds.

18. EXAMPLE: POTENTIAL HUMAN PARAINFLUENZA VIRUS  
TYPE 3 DP178/DP107 ANALOGS: CD AND  
ANTIVIRAL CHARACTERIZATION

20 In the Example presented herein, human parainfluenza virus type 3 (HPIV3) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 15, above, were tested for anti-HPIV3 activity.  
25 Additionally, circular dichroism (CD) structural analyses were conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of  
30 these peptides exhibit a substantial helical character.

18.1 MATERIALS AND METHODS

Structural analyses: Structural analyses  
35 consisted of circular dichroism (CD) studies. The CD

spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were  
5 determined from  $A_{280}$  using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-HPIV3 antiviral activity assays: The assay utilized herein tested the ability of the peptides to  
10 disrupt the ability of Hep2 cells chronically infected with HPIV3 to fuse and cause syncytial formation on a monolayer of an uninfected line of CV-1W cells. The more potent the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of CV-1W cells  
15 were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented  
20 at 3%, antibiotics/antimycotics (Gibco BRL Life Technologies Cat. No. 15040-017) added at 1%, and glutamine added at 1%.

To prepare Hep2 cells for addition to uninfected cells, cultures of chronically infected Hep2 cells  
25 were washed with DPBS (Dulbecco's Phosphate Buffered Saline w/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and  
30 resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected CV-1W cells.

The antiviral assay was conducted by, first, removing all media from the wells containing  
35 uninfected CV-1W cells, then adding peptides (at the

dilutions described below) in 3% EMEM, and 500 chronically HPIV3-infected Hep2 cells per well. Wells were then incubated at 37°C for 24 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50 $\mu$ l 0.25% Crystal Violet stain in methanol. Wells were rinsed immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Alternatively, instead of Crystal Violet analysis, cells were assayed with XTT, as described, above, in Section 17.1.

Peptides: The peptides characterized in the study presented herein were:

- 1) Peptides 157 to 188, as shown in FIG. 29A, and peptides T-38 to T-40, T-42 to T-46 and T-582, as shown in FIG. 29B. These peptides are derived from the DP107 region of the HPIV3 F1 fusion protein (represented by HPF3 107, as shown in FIG. 29A); and
- 2) Peptides 189 to 210, as shown in FIG. 30A, and T-269, T-626, T-383 and T-577 to T-579, as shown in FIG. 30B. These peptides are primarily derived from the DP178 region of the HPIV3 F1 fusion protein (represented by HPF3 178, as shown in FIG. 30A). Peptide T-626 contains two mutated amino acid residues (represented by a shaded background). Additionally, peptide T-577 represents F1 amino acids 65-100, T-578 represents F1 amino acids 207-242 and T-579 represents F1 amino acids 273-309.

Each peptide was tested at 2-fold serial dilutions ranging from 500 $\mu$ g/ml to approximately

500ng/ml. For each of the assays, a well containing no peptide was also used.

## 18.2 RESULTS

5 The data summarized in FIGS. 29A-C and 30A-B represent antiviral and structural information obtained from peptides derived from the HPIV3 fusion protein DP107-like region (FIG. 29A-C) and the HPIV3 fusion protein DP178-like region (FIG. 30A-B).

10 As shown in FIG. 29A-B, a number of the HPIV3 DP107-like peptides exhibited potent levels of antiviral activity. These peptides include, for example, peptides T-40, T-172 to T-175, T-178, T-184 and T-185.

15 CD analysis reveals that a number of the peptides exhibit detectable to substantial level of helical structure. The CD spectra for one of the peptides, 184, which exhibits substantial helicity is summarized in FIG. 29C.

20 The results summarized in FIG. 30A-B demonstrate that a number of the DP178-like peptides tested exhibit a range of anti-viral activity. These peptides include, for example, peptides 194 to 211, as evidenced by their low  $IC_{50}$  values. In fact, peptides 201 to 205 exhibit  $IC_{50}$  values in the nanogram/ml  
25 range. In addition, many of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, have successfully identified viral  
30 peptide domains that represent highly promising anti-HPIV3 antiviral compounds.

### 19. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN IMMUNODEFICIENCY VIRUS

35 FIG. 31 represents search results for SIV isolate MM251 (PC/Gene® protein sequence PENV\_SIVM2). Both

107x178x4 and ALLMOTI5 search motifs identified two regions with similarities to DP107 and/or DP178.

The peptide regions found by 107x178x4 were located at amino acid residues 156-215 and 277-289. The peptide regions found by ALLMOTI5 were located at amino acid residues 156-219 and 245-286. Both motifs, therefore, identify similar regions.

Interestingly, the first SIV peptide region (i.e., from amino acid residue 156 to approximately amino acid residue 219) correlates with a DP107 region, while the second region identified (i.e., from approximately amino acid residue 245 to approximately amino acid residue 289) correlates with the DP178 region of HIV. In fact, an alignment of SIV isolate MM251 and HIV isolate BRU, followed by a selection of the best peptide matches for HIV DP107 and DP178, reveals that the best matches are found within the peptide regions identified by the 107x178x4 and ALLMOTI5 search motifs.

It should be noted that a potential coiled-coil region at amino acid residues 242-282 is predicted by the Lupas program. This is similar to the observation in HIV in which the coiled-coil is predicted by the Lupas program to be in the DP178 rather than in the DP107 region. It is possible, therefore, that SIV may be similar to HIV in that it may contain a coiled-coil structure in the DP107 region, despite such a structure being missed by the Lupas algorithm. Likewise, it may be that the region corresponding to a DP178 analog in SIV may exhibit an undefined structure, despite the Lupas program's prediction of a coiled-coil structure.

35



20.   EXAMPLE:   COMPUTER-ASSISTED IDENTIFICATION OF  
                  DP178/DP107 ANALOGS IN EPSTEIN-BARR  
                  VIRUS

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          The results presented herein describe the  
          identification of DP178/DP107 analogs within two  
5       different Epstein-Barr Virus proteins. Epstein-Barr  
          is a human herpes virus which is the causative agent  
          of, for example, infectious mononucleosis (IM), and is  
          also associated with nasopharyngeal carcinomas (NPC),  
          Burkitt's lymphoma and other diseases. The virus  
10       predominantly exists in the latent form and is  
          activated by a variety of stimuli.

          FIG. 32 depicts the search motif results for the  
          Epstein-Barr Virus (Strain B95-8; PC/Gene® protein  
          sequence PVGLB\_EBV) glycoprotein gp110 precursor  
15       (gp115). The 107x178x4 motif identified two regions  
          of interest, namely the regions covered by amino acid  
          residues 95-122 and 631-658. One PZIP region was  
          identified at amino acid residue 732-752 which is most  
          likely a cytoplasmic region of the protein. The Lupas  
20       algorithm predicts a coiled-coil structure for amino  
          acids 657-684. No ALLMOTI5 regions were identified.

          FIG. 33 depicts the search motif results for the  
          Zebra (or EB1) trans-activator protein (BZLF1) of the  
          above-identified Epstein-Barr virus. This protein is  
25       a transcription factor which represents the primary  
          mediator of viral reactivation. It is a member of the  
          b-ZIP family of transcription factors and shares  
          significant homology with the basic DNA-binding and  
          dimerization domains of the cellular oncogenes c-fos  
30       and C/EBP. The Zebra protein functions as a  
          homodimer.

          Search results demonstrate that the Zebra protein  
          exhibits a single region which is predicted to be  
          either of DP107 or DP178 similarity, and is found  
35       between the known DNA binding and dimerization regions  
          of the protein. Specifically, this region is located

at amino acid residues 193-220, as shown in FIG. 33.  
The Lupas program predicted no coiled-coil regions.

21. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS IN MEASLES VIRUS

5 FIG. 34 illustrates the motif search results for  
the fusion protein F1 of measles virus, strain  
Edmonston (PC Gene® protein sequence PVGLF\_MEASE),  
successfully identifying DP178/DP107 analogs.

The 107x178x4 motif identifies a single region at  
10 amino acid residues 228-262. The ALLMOTI5 search  
motif identifies three regions, including amino acid  
residues 116-184, 228-269 and 452-500. Three regions  
containing proline residues followed by a leucine  
zipper-like sequence were found beginning at proline  
15 residues 214, 286 and 451.

The Lupas program identified two regions it  
predicted had potential for coiled-coil structure,  
which include amino acid residues 141-172 and 444-483.

20 22. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS IN HEPATITIS B  
VIRUS

FIG. 35 depicts the results of a PZIP motif  
search conducted on the Hepatitis B virus subtype AYW.  
Two regions of interest within the major surface  
25 antigen precursor S protein were identified. The  
first lies just C-terminal to the proposed fusion  
peptide of the major surface antigen (Hbs) which is  
found at amino acid residues 174-191. The second  
region is located at amino acid residues 233-267. The  
30 Lupas program predicts no coiled-coil repeat regions.

In order to test the potential anti-HBV antiviral  
activity of these D178/DP107 analog regions, peptides  
derived from area around the analog regions are  
synthesized, as shown in FIG. 52A-B. These peptides  
35 represent one amino acid peptide "walks" through the

putative DP178/DP107 analog regions. The peptides are synthesized according to standard Fmoc chemistry on Rinkamide MBHA resins to provide for carboxy terminal blockade (Chang, C.D. and Meinhofer, J., 1978, Int. J. Pept. Protein Res. 11:246-249; Fields, G.B. and Noble, R.L., 1990, Int. J. Pept. Protein Res. 35:161-214). Following complete synthesis, the peptide amino-terminus is blocked through automated acetylation and the peptide is cleaved with trifluoroacetic acid (TFA) and the appropriate scavengers (King, D.S. et al., 1990, Int. J. Pept. Res. 36:255-266). After cleavage, the peptide is precipitated with ether and dried under vacuum for 24 hours.

The anti-HBV activity of the peptides is tested by utilizing standard assays to determine the test peptide concentration required to cause an acceptable (e.g., 90%) decrease in the amount of viral progeny formed by cells exposed to an HBV viral inoculum. Candidate antiviral peptides are further characterized in model systems such as wood chuck tissue culture and animal systems, prior to testing on humans.

23. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN MASON-PFIZER MONKEY VIRUS

The results depicted herein illustrate the results of search motifs conducted on the Simian Mason-Pfizer monkey virus. The motifs reveal DP178/DP107 analogs within the enveloped (TM) protein GP20, as shown in FIG. 36.

The 107x178x4 motifs identifies a region at amino acid residues 422-470. The ALLMOTI5 finds a region at amino acid residues 408-474. The Lupas program predicted a coiled-coil structure a amino acids 424-459.

35

24. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS IN BACTERIAL  
PROTEINS

The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to sequences present in proteins of a variety of bacterial species.

FIG. 37 depicts the search motif results for the *Pseudomonas aeruginosa* fimbrial protein (Pilin). Two regions were identified by motifs 107x178x4 and ALLMOTI5. The regions located at amino acid residues 30-67 and 80-144 were identified by the 107x178x4 motif. The regions at amino acid residues 30-68 and 80-125 were identified by the ALLMOTI5.

FIG. 38 depicts the search motif results for the *Pseudomonas gonorrhoeae* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 66-97 was identified by the 107x178x4 motif. The region located at amino acid residues 66-125 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 39 depicts the search motif results for the *Hemophilus Influenza* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 40 depicts the search motif results for the *Staphylococcus aureus* toxic shock syndrome *Hemophilus Influenza* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The

region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

5       FIG. 41 summarizes the motif search results conducted on the Staphylococcus aureus enterotoxin Type E protein. These results demonstrate the successful identification of DP178/DP107 analogs corresponding to peptide sequences within this protein, as described below.

10       The ALLMOTI5 motif identified a region at amino acid residues 22-27. The 107x178x4 motif identified two regions, with the first at amino acid residues 26-69 and the second at 88-115. A P12LZIPC motif search identified two regions, at amino acid residues 163-181 and 230-250.

15       The Lupas program predicted a region with a high propensity for coiling at amino acid residues 25-54. This sequence is completely contained within the first region identified by both ALLMOTI5 and 107x178x4 motifs.

20       FIG. 42 depicts the search motif results conducted on a second Staphylococcus aureus toxin, enterotoxin A. Two regions were identified by the ALLMOTI5 motif, at amino acid residues 22-70 and amino acid residues 164-205. The 107x178x4 motif found two  
25       regions, the first at amino acid residues 26-69 and the second at amino acid residues 165-192. A P23LZIPC motif search revealed a region at amino acid residues 216-250. No coiled-coil regions were predicted by the Lupas program.

30       FIG. 43 shows the motif search results conducted on the E. coli heat labile enterotoxin A protein, demonstrating that identification of DP178/DP107 analogs corresponding to peptides located within this protein. Two regions were identified by the ALLMOTI5  
35       motif, with the first residing at amino acid residues

55-115, and the second residing at amino acid residues 216-254. The 107x178x4 motif identified a single region at amino acid residues 78-105. No coiled-coil regions were predicted by the Lupas program.

5 25. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS WITHIN VARIOUS  
HUMAN PROTEINS

10 The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to peptide sequences present within several different human proteins.

15 FIG. 44 illustrates the search motif results conducted on the human c-fos oncoprotein. The ALLMOTI5 motif identified a single region at amino acid residues 155-193. The 107x178x4 motif identified one region at amino acid residues 162-193. The Lupas program predicted a region at amino acid residues 148-201 to have coiled-coil structure.

20 FIG. 45 illustrates the search motif results conducted on the human lupus KU autoantigen protein P70. The ALLMOTI5 motif identified a single region at amino acid residues 229-280. The 107x178x4 motif identified one region at amino acid residues 235-292. The Lupas program predicted a region at amino acid residues 232-267 to have coiled-coil structure.

25 FIG. 46 illustrates the search motif results conducted on the human zinc finger protein 10. The ALLMOTI5 motif identified a single region at amino acid residues 29-81. The 107x178x4 motif identified one region at amino acid residues 29-56. A P23LZIPC motif search found a single region at amino acid residues 420-457. The Lupas program predicted no coiled-coil regions.

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26. EXAMPLE: POTENTIAL MEASLES VIRUS DP178/DP107  
ANALOGS: CD AND ANTIVIRAL  
CHARACTERIZATION

In the Example presented herein, measles (MeV) virus DP178-like peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 21, above, are tested for anti-MeV activity. Additionally, circular dichroism (CD) structural analyses are conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that none of the these peptides exhibit a substantial helical character.

26.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were determined from  $A_{280}$  using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-MeV antiviral activity syncytial reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of Vero cells acutely infected with MeV (*i.e.*, cells which are infected with a multiplicity of infection of 2-3) to fuse and cause syncytial formation on a monolayer of an uninfected line of Vero cells. The more potent the peptide, the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of Vero cells were grown in microtiter wells in 10% FBS EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum

[FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 10%, antibiotics/antimycotics (Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

5 To prepare acutely infected Vero cells for addition to the uninfected cells, cultures of acutely infected Vero cells were washed twice with HBSS (Bio Whittaker Cat. No. 10-543F) and cell monolayers were removed with trypsin (Bio Whittaker Cat. No. 17-161E).  
10 Once cells detached, media was added, any remaining clumps of cells were dispersed, and hemacytometer cell counts were performed.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the  
15 dilutions described below) in 10% FBS EMEM, and 50-100 acutely MeV-infected Vero cells per well. Wells were then incubated at 37°C for a maximum of 18 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the  
20 wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were  
25 then counted, using a dissecting microscope.

Anti-MeV antiviral activity plaque reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of MeV to infect permissive, uninfected Vero cells, leading to  
30 the infected cells' fusing with uninfected cells to produce syncytia. The lower the observed level of syncytial formation, the greater the antiviral activity of the peptide.

35 Monolayers of uninfected Vero cells are grown as described above.



The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the dilutions described below) in 10% FBS EMEM, and MeV stock virus at a final concentration of 30 plaque forming units (PFU) per well. Wells were then incubated at 37°C for a minimum of 36 hours and a maximum of 48 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Peptides: The peptides characterized in the study presented herein were peptides T-252A0 to T-256A0, T-257B1/C1, and T-258B1 to T-265B0, and T-266A0 to T-268A0, as shown in FIG. 47. These peptides represent a walk through the DP178-like region of the MeV fusion protein.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

## 26.2 RESULTS

The data summarized in FIG. 47 represents antiviral and structural information obtained via "peptide walks" through the DP178-like region of the MeV fusion protein.

As shown in FIG. 47, the MeV DP178-like peptides exhibited a range of antiviral activity as crude peptides. Several of these peptides were chosen for purification and further antiviral characterization.

The IC<sub>50</sub> values for such peptides were determined, as shown in FIG. 47, and ranged from 1.35µg/ml (T-257B1/C1) to 0.072µg/ml (T-265B1). None of the DP178-like peptides showed, by CD analysis, a detectable level of helicity.

5        Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-MeV antiviral compounds.

10        27. EXAMPLE:     POTENTIAL SIV DP178/DP107 ANALOGS:  
                              ANTIVIRAL CHARACTERIZATION

              In the Example presented herein, simian immunodeficiency virus (SIV) DP178-like peptides  
15        identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9, 12 and 19, above, were tested for anti-SIV activity. It is demonstrated that several of the identified peptides exhibit potent antiviral  
20        capability.

27.1 MATERIALS AND METHODS

Anti-SIV antiviral assays: The assay utilized herein were as reported in Langolis et al. (Langolis,  
25        A.J. et al., 1991, AIDS Research and Human Retroviruses 7:713-720).

Peptides: The peptides characterized in the study presented herein were peptides T-391 to T-400, as shown in FIG. 48. These peptides represent a walk  
30        through the DP178-like region of the SIV TM protein.

              Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

## 27.2 RESULTS

The data summarized in FIG. 48 represents antiviral information obtained via "peptide walks" through the DP178-like region of the SIV TM protein.

5 As shown in FIG. 48, peptides T-391 to T-400 were tested and exhibited a potent antiviral activity as crude peptides.

10 Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-SIV antiviral compounds.

### 28. EXAMPLE: ANTI-VIRAL ACTIVITY OF DP107 AND DP-178 PEPTIDE TRUNCATIONS AND MUTATIONS

15 The Example presented in this Section represents a study of the antiviral activity of DP107 and DP178 truncations and mutations. It is demonstrated that several of these DP107 and DP178 modified peptides exhibit substantial antiviral activity.

20

#### 28.1 MATERIALS AND METHODS

Anti-HIV assays: The antiviral assays performed were as those described, above, in Section 6.1. Assays utilized HIV-1/IIIB and/or HIV-2 NIH2 isolates.  
25 Purified peptides were used, unless otherwise noted in FIGS. 49A-C.

Peptides: The peptides characterized in the study presented herein were:

- 30 1) FIGS. 49A-C present peptides derived from the region around and containing the DP178 region of the HIV-1 BRU isolate. Specifically, this region spanned from gp41 amino acid residue 615 to amino acid residue 717. The peptides listed contain  
35 truncations of this region and/or mutations

which vary from the DP178 sequence amino acid sequence. Further, certain of the peptides have had amino- and/or carboxy-terminal groups either added or removed, as indicated in the figures; and

- 5           2) FIG. 50. presents peptides which represent truncations of DP107 and/or the gp41 region surrounding the DP107 amino acid sequence of HIV-1 BRU isolate. Certain of the peptides are unblocked or biotinylated, as indicated  
10           in the figure.

Blocked peptides contained an acyl N-terminus and an amido C-terminus.

## 28.2 RESULTS

15           Anti-HIV antiviral data was obtained with the group 1 DP178-derived peptides listed in FIG. 49A-C. The full-length, non-mutant DP178 peptide (referred to in FIG. 49A-C as T20) results shown are for 4ng/ml.

20           In FIG. 49A, a number of the DP178 truncations exhibited a high level of antiviral activity, as evidenced by their low  $IC_{50}$  values. These include, for example, test peptides T-50, T-624, T-636 to T-641, T-645 to T-650, T-652 to T-654 and T-656. T-50  
25           represents a test peptide which contains a point mutation, as indicated by the residue's shaded background. The HIV-1-derived test peptides exhibited a distinct strain-specific antiviral activity, in that none of the peptides tested on the HIV-2 NIHZ isolate demonstrated appreciable anti-HIV-2 antiviral  
30           activity.

          Among the peptides listed in FIG. 49B, are test peptides representing the amino (T-4) and carboxy (T-3) terminal halves of DP178 were tested. The amino terminal peptide was not active ( $IC_{50} > 400 \mu g/ml$ ) whereas  
35           the carboxy terminal peptide showed potent antiviral

activity ( $IC_{50} = 3\mu g/ml$ ). A number of additional test peptides also exhibited a high level of antiviral activity. These included, for example, T-61/T-102, T-217 to T-221, T-235, T-381, T-677, T-377, T-590, T-378, T-591, T-271 to T-272, T-611, T-222 to T-223 and  
5 T-60/T-224. Certain of the antiviral peptides contain point mutations and/or amino acid residue additions which vary from the DP178 amino acid sequence.

In FIG. 49C, point mutations and/or amino and/or carboxy-terminal modifications are introduced into the  
10 DP178 amino acid sequence itself. As shown in the figure, the majority of the test peptides listed exhibit potent antiviral activity.

Truncations of the DP107 peptide (referred to in IG. 50 as T21) were also produced and tested, as shown  
15 in FIG. 50. FIG. 50 also presents data concerning blocked and unblocked peptides which contain additional amino acid residues from the gp41 region in which the DP107 sequence resides. Most of these peptides showed antiviral activity, as evidenced by  
20 their low  $IC_{50}$  values.

Thus, the results presented in this Section demonstrate that not only do the full length DP107 and DP178 peptides exhibit potent antiviral activity, but  
25 truncations and/or mutant versions of these peptides can also possess substantial antiviral character.

29: EXAMPLE: POTENTIAL EPSTEIN-BARR DP178/DP107  
ANALOGS: ANTIVIRAL CHARACTERIZATION

In the Example presented herein, peptides derived  
30 from the Epstein-Barr (EBV) DP-178/DP107 analog region of the Zebra protein identified, above, in the Example presented in Section 20 are described and tested for anti-EBV activity. It is demonstrated that among these peptides are ones which exhibit potential anti-  
35 viral activity.

## 29.1 MATERIALS AND METHODS

### Electrophoretic Mobility Shift Assays (EMSA):

Briefly, an EBV Zebra protein was synthesized utilizing SP6 RNA polymerase in vitro transcription and wheat germ in vitro translation systems (Promega Corporation recommendations; Butler, E.T. and Chamberlain, M.J., 1984, J. Biol. Chem. 257:5772; Pelham, H.R.B. and Jackson, R.J., 1976, Eur. J. Biochem. 67:247). The in vitro translated Zebra protein was then preincubated with increasing amounts of peptide up to 250 ng/ml prior to the addition of 10,000 to 20,000 c.p.m. of a <sup>32</sup>P-labeled Zebra response element DNA fragment. After a 20 minute incubation in the presence of the response element, the reaction was analyzed on a 4% non-denaturing polyacrylamide gel, followed by autoradiography, utilizing standard gel-shift procedures. The ability of a test peptide to prevent Zebra homodimer DNA binding was assayed by the peptide's ability to abolish the response element gel migration retardation characteristic of a protein-bound nucleic acid molecule.

Peptides: The peptides characterized in this study represent peptide walks through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. Specifically, the peptide walks covered the region from amino acid residue 173 to amino acid residue 246 of the EBV Zebra protein.

Each of the tested peptides were analyzed at a range of concentrations, with 150ng/ml being the lowest concentration at which any of the peptides exerted an inhibitory effect.

## 29.2 RESULTS

The EBV Zebra protein transcription factor contains a DP178/DP107 analog region, as demonstrated in the Example presented, above, in Section 20. This protein appears to be the primary factor responsible for the reactivation capability of the virus. A method by which the DNA-binding function of the Zebra virus may be abolished may, therefore, represent an effective antiviral technique. In order to identify potential anti-EBV DP178/DP107 peptides, therefore, peptides derived from the region identified in Section 20, above, were tested for their ability to inhibit Zebra protein DNA binding.

The test peptides' ability to inhibit Zebra protein DNA binding was assayed via the EMSA assays described, above, in Section 28.1. The data summarized in FIG. 51A-B presents the results of EMSA assays of the listed EBV test peptides. These peptides represent one amino acid "walks" through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. As shown in FIG. 51A-B, the region from which these peptides are derived lies from EBV Zebra protein amino acid residue 173 to 246. A number of the test peptides which were assayed exhibited an ability to inhibit Zebra protein homodimer DNA binding, including 439, 441, 444 and 445.

Those peptides which exhibit an ability to inhibit Zebra protein DNA binding represent potential anti-EBV antiviral compounds whose ability to inhibit EBV infection can be further characterized.

The present invention is not to be limited in scope by the specific embodiments described which are intended as single illustrations of individual aspects

of the invention, and functionally equivalent methods  
and components are within the scope of the invention.  
Indeed, various modifications of the invention, in  
addition to those shown and described herein will  
become apparent to those skilled in the art from the  
5 foregoing description and accompanying drawings. Such  
modifications are intended to fall within the scope of  
the appended claims.

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